COMBINING ABILITY AND HETEROTIC GROUPING OF ELITE MAIZE (*Zea mays* L.) INBRED LINES

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COMBINING ABILITY AND HETEROTIC GROUPING OF ELITE MAIZE (*Zea mays* L.) INBRED LINES

A Thesis Submitted to the School of Graduate Studies
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In Partial Fulfillment of the Requirements for the Degree of
MASTER OF SCIENCE IN AGRICULTURE (PLANT BREEDING)

By

NIGUS BELAY

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Jimma University

APPROVAL SHEET
JIMMA UNIVERSITY
SCHOOL OF GRADUATE STUDIES

As Thesis Research advisors, we here by certify that we have read and evaluated this thesis prepared, under our guidance, by **Nigus Belay**, entitled "**Combining Ability and Heterotic Grouping of Elite Maize (*Zea mays* L.) Inbred Lines**" we recommend that it can be submitted as fulfilling the thesis requirement.

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As member of the Board of Examiners of the M.Sc Thesis Open Defense Examination, We certify that we have read and evaluated the thesis prepared by Nigus Belay, and examined the candidate. We recommended that the thesis be accepted as fulfilling the thesis requirement for the Degree of Master of Science in Agriculture (Plant breeding).

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DEDICATION

I dedicated this thesis to my mother, Amelework Negash

STATEMENT OF THE AUTHOR

First, I declare that this thesis is my own work and that all sources of material used for this thesis have been duly acknowledged. This thesis has been submitted in partial fulfillment of the requirements of M.Sc. degree at Jimma University, College of Agriculture and Veterinary Medicine and is deposited at the University Library to be made available to users under rules of the Library. I seriously declare that this thesis is not submitted to any other institution anywhere for the award of any academic degree, diploma, or certificate.

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BIOGRAPHICAL SKETCH

The author was born on June 08, 1983 in Arsi Zone in the town of Assela. He attended his elementary school at Assela Saint Gabriel Elementary School and his junior secondary school at Assela Junior Secondary School. He completed his high school study at Assela Comprehensive Secondary School. Passing the Ethiopian School Leaving Certificate Examination (ESLCE), he joined the then Alemaya University, now Haramaya University in 2001 and graduated with B. Sc. Degree in Plant Sciences in July 2004.

Right after his graduation, the author was recruited as a junior instructor by Ministry of Agriculture and assigned at Shire Endeselassie Agricultural Technical and Vocational Training College from January 2005 to May 2006. Then, he joined The Ethiopian Institute of Agricultural Research (EIAR) and he was assigned as researcher in Crop Research Department at Pawe Agricultural Research Center (PARC). He was working there till he joined the School of Graduate Studies at Jimma University in October 2010 for M.Sc. degree in plant breeding.

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ACRONYMS AND ABBREVIATIONS

ANOVA	Analysis of variance
CIMMYT	International Center for Maize and Wheat Improvement
CSA	Central Statistics Authority
CML	CIMMYT maize line
CV	Coefficient of variation
cm	Centimeter
^{0}C	Degree Celsius
DAP	Diamonium phosphate
Df	Degrees of freedom
F1	First filial generation
F2	Second filial generation
FAO	Food and Agriculture Organization of the United Nation
GCA	General combining ability
gm	Gram
M.a.s.l	Meter above sea level
QPM	Quality protein maize
SAS	Statistical Analysis Software
SCA	Specific combining ability
t/ha	Ton per hectare

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COMBINING ABILITIY AND HETEROTIC GROUPING OF ELITE MAIZE (*Zea mays* L.) INBRED LINES

ABSTRACT

The national average maize yield in Ethiopia is low and thus, choice of promising germplasm, knowledge of combining ability and heterotic grouping are a prerequisites to develop high yielding maize varieties. A line x tester analysis involving 86 test-crosses generated by crossing 43 elite maize inbred lines with two testers and two standard checks were studied for different yield and agronomic traits during 2010 cropping season at Melkasa, Ziway, Dhera, Mieso and Pawe Research Sites. The objectives of the present study were to identify promising test cross hybrid combinations, estimate combining ability of elite maize inbred lines for grain yield and related agronomic traits and classify the inbred lines into different heterotic groups. The genotypes were evaluated in alpha lattice design replicated twice in all the locations. Analyses of variances showed significant mean squares due to genotypes and crosses for most traits in each and across locations. Among the crosses, L23 x T2, L24 x T2, L41 x T1, L23 x T1, L13 x T1 and L17 x T1 showed high grain yield, which could be utilized for future evaluation for possible release or used in maize breeding activities.General combining ability (GCA) mean squares due to lines were highly significant for most studied traits while specific combining ability (SCA) mean squares were significant only for few traits at all locations. The relative importance of GCA and SCA variances observed in the current study for most studied traits revealed the predominance of additive genetic variance in controlling these traits. This suggests that selection would be effective for the improvement of traits of interest. Inbred lines L23, L24 and L41 were the best general combiners for grain yield, and hence were promising parents for hybrids as well as for inclusion in breeding program. Inbred lines L2, L3, L5, L7, L8 and L11 had negative and significant GCA effects for days to anthesis and silking, indicating that the lines had gene combinations that can enhance early maturity. L1, L5, L7, L8 and L37 showed negative and significant GCA effects for plant height in most cases, indicating that these lines had a tendency to decrease plant stature. Crosses L4 x T1, L14 x T1, L22 x T2, L23 x T2, L24 x T2 and L33 x T2 exhibited good specific combining ability effects for grain yield, indicating that the crosses had desirable gene combinations for increased grain yield. Inbred lines L23, L24, L25, L32, L33, and L36 were grouped in to heterotic group A. while inbred lines L7,L13, L14, L17, L25, L27, L29, L30, L34 L41 and L42 were grouped in to heterotic group B. Further studies should explore the possibility of separating the other inbred lines used in this study into distinct heterotic groups using other more divergent testers. In general, the information from this study could be useful for researchers who need to develop high yielding varieties of maize mainly adapted to the rift valley areas of Ethiopia.

1. INTRODUCTION

Maize (*Zea mays* L.), together with wheat and rice, is one of the three cereals that feed the world, with a total production of 689 million tons (FAO, 2007). Maize grains have long been used for feed, food consumption and raw material industrial products. Nowadays there is also strong demand of maize grains for bio-fuel production especially in the two main maize producing countries, United State and China (FAO, 2007). The global maize production is predicted to grow continuously as demand and price in the world market increase.

Maize is believed to be originated in Mexico and was introduced to West Africa in the early 1500s by Portuguese traders and then to Ethiopia during the 1600s and 1700s (Dowswell *et al*., 1996). Today, maize is one of the most important food crops throughout the country. In terms of area, it is the second most important commodity next to tef (*Eragrostis tef*) (CSA, 2011). In Ethiopia, maize is one of the top priority food crops selected to achieve food security. It is the staple food and one of the main sources of calorie, particularly in the major maize producing regions. Overall, the area allocated and the productivity level of maize has been increasing since 1994. The area allocated in 1994 was about one million ha, which has increased to about 1.96 million ha of land in 2010/11 production season. Similarly, the average national productivity of maize has increased from about 1.5 t/ha in 1994 to about 2.54 t/ha in 2010/11 mainly due to the strong public push of improved seed and fertilizer (CSA, 1994-2011).

Maize grows in different agro-ecological zones of Ethiopia ranging from sea level up to 2800 m a.s.l (IAR/CIMMYT, 1993). It is grown in areas with light to heavy soils, wide ranges of temperatures and rainfall, indicating that maize has good adaptability to different arrays of environmental variables. However, in spite of its wide adaptation and efforts made to develop improved maize technologies for different maize agro-ecological zones still many biotic and abiotic constraints limit maize production and productivity in different maize producing agro-ecological zones. In mid-altitude and lowland sub-humid areas the major maize production constraints include: grey leaf spot (GLS), turcicum leaf blight (TLB), common leaf rust (CLR), phaesphorea leaf spot (PLS), maize streak virus (MSV), stalk borer, termite, storage pests, low soil fertility and weeds (parasitic and non-parasitic). In low moisture stress areas drought, low soil fertility, weeds (parasitic and non-parasitic), CLR, TLB, stalk borers and storage pests are the major constraints to maize production while in the highland sub-humid areas frost, water logging, low soil fertility, weeds, TLB, CLR, PLS and stalk borer are the major problems in maize production (EARO/CIMMYT, 2002).

Although the average yield of maize in developed world is high (7.2 t ha^{-1}), the national average yield in Ethiopia is still as low as 2.54 t ha^{-1} (CSA, 2011) and thus, increasing maize productivity is a high national priority. To increase maize yield on the farmers' field, maize research in Ethiopia has been on-going since 1952. Over the years several improved varieties have been released or recommended for commercial production in the country (IAR/CIMMYT, 1993; EARO/CIMMYT, 2002). With the dissemination and utilization of improved maize technologies by the farmers, the national average yield has been increasing starting in late 1990s. This level of productivity is still very low as compared to the average maize yield of 5 t ha^{-1} attained on-farmers' field under national extension intervention program in potential areas (EARO/ CIMMYT, 2002). In drought stressed areas, however, the average yield is lower than 1.5 t ha^{-1} in most of the years. This indicates the need to develop high yielding maize varieties that perform well under both stress and non-stress conditions. In order to achieve this, potentially suitable parents and superior combinations must be identified.

Development of improved maize germplasm that perform better under biotic and abiotic maize production constraints should be a continues process. In maize breeding program, analysis of general combining ability (GCA), specific combining ability (SCA) and heterosis would help to identify best inbred lines for hybrid development and hybrid combinations for better specific combining ability. Combining ability is an effective tool which gives useful genetic information for the choice of parents in terms of their performance in series of crosses (Sprague and Tatum, 1942). Simmonds (1979) emphasized the need of screening parents and crosses before their use in breeding programme and suggested that combining ability analysis based on progeny test data is a useful method for evaluating parents and crosses for a wide range of quantitative characters. The development of populations with high combining abilities has a fundamental role in the efficient use of heterosis (Vasal *et al.*, 1992a). Determination of combining abilities also provides information on the nature of gene action involved in the expression of quantitative traits (Falconer, 1989). Therefore germplasm evaluation is a decisive aspect in maize breeding programs.

Heterosis can be maximized by crossing genetically diverse inbred lines. The higher the genetic diversity between the inbred lines the higher the heterosis expressed by the hybrid variety (Mungoma and Pollak, 1988). In maize, therefore, genetic diversity and heterosis can be maximized by crossing inbred lines belonging to different heterotic groups. Heterotic group A and B designate broad classes in maize with diverse genetic base that are complimentary and result in expression of heterosis after crossing. Therefore, knowledge on the heterotic groups of inbred lines is paramount important before they can be deployed in variety development.

Line x tester (Kempthorne, 1957) is useful in deciding the relative ability of female and male lines to produce desirable hybrid combinations. It also provides information on genetic components and enables the breeder to choose appropriate breeding methods for hybrid variety or cultivar development programmes. Information on combining ability effects helps the breeder in choosing the parents with high general combining ability and hybrids with high specific combining. In the current study, a Line x Tester mating scheme study involving 43 elite maize inbred lines introduced from CIMMYT-Zimbabwe and two testers was conducted with the objectives to:

1. Estimate combining abilities for grain yield and other agronomic traits in elite maize inbred lines using Line x Tester mating design.
2. Classify the elite inbred lines into different heterotic groups for future use in the breeding program.
3. Identify better performing test-cross hybrid combination for possible release for commercial production

2. LITERATURE REVIEW

2.1. Taxonomy and Reproductive Biology of maize

Maize (*Zea mays* L.) is a diploid (2*n* = 20) and a monocot of the family Poaceae (Gramineae), or grass family. The genus has four species: *Z. mays* (cultivated corn and teosinte), *Z. diploperennis* Iltis et al. (diploperennial teosinte), *Z. luxurians*, and *Z. perennis* (perennial teosinte) (Doeblay, 1994).

Maize is a monoecious annual and one of the largest of the cereals, capable of reaching 4.5 m in height. The male flowers (staminate) occur in the terminal panicle or tassel at the top of the stalk, while the female inflorescence (pistillate) is borne in the axils of leaves as clusters, called a cob, at a joint of the stalk. Long silks (long styles) hang from the husk of each cob. These pollen tubes are the longest known in the plant kingdom. As pollen receptors, each silk must be individually pollinated in order to produce a fruit or kernel. A fertilized cob (also called an ear) may contain eight or more rows of kernels. Furthermore, a stalk may bear 1–3 cobs (Khehra, 1997).

Corn has a variety of morphological features. Some early maturing types maturing in 50 days may attain a height of 0.6 m and produce 8–9 leaves, while tall late maturing types (330 days) may attain a culm or stalk height of 6 m and bear 42–44 leaves (Acquaah, 2007)

Corn pollen is primarily dispersed by wind. Consequently, corn is about 95% cross-pollinated, most of the effective pollination of an ear originating from sources in the immediate vicinity of the ear. Pollen dispersal is favored by warm temperature and low humidity. Being predominantly open-pollinated, natural populations of corn are highly heterozygous and genetically variable. In theory, each kernel on the ear could be produced from the fertilization of an ovule by a different pollen parent (Acquaah, 2007).

2.2. Development of Parental Inbreds

Maize is a cross-pollinated species that shows high heterosis (i.e., superior performance of crosses relative to their parents) for various traits that include grain yield. This high expression of heterosis is exploited in maize hybrids and constitutes the foundation of the maize seed industry. Maize hybrids were first developed in the United States in the mid-1930s and by the early 1960s practically all the maize area in the US was planted to hybrids (Duvick & Cassman, 1999). Improved productivity and selection gain with the use of hybrids has stimulated increased investment in hybrid development, resulting in impressive genetic progress. 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 (Acquaah, 2007). Selected inbreds are then evaluated in hybrid combinations across locations to select superior hybrids and to estimate their combining abilities.

An inbred is a nearly homozygous line obtained through continuous inbreeding of cross pollinated species with selection accompanying inbreeding (Singh, 2005). Different type of segregating populations can be used as the source in line development: open-pollinated cultivars (OPC), synthetic cultivars, single crosses, backcrosses, double crosses, and exotic germplasm (Acquaah, 2007). Overall, major emphasis goes to the use of breeding populations created by hybridization of complementary inbreds and the selection of progenies possessing the desirable traits from both parents (Hallauer, 1990). Selection within F_2 and backcross populations using pedigree breeding is the most important breeding method to develop maize inbreds (Hallauer et al., 2010). Breeding programs that emphasize pedigree selection within populations developed from elite inbred lines are therefore cyclical creating second-, third-, fourth-, etc. generation recycled improved inbreds (Hallauer, 1990). The incorporation and introgression of exotic germplasm brings new desirable alleles and genetic diversity to this recycling of elite lines (Goodman *et al.*, 2000). A backcross or multiple backcross to the best parental inbred is used commonly to increase the probability of maintaining favorable combinations of alleles (Troyer, 2001). Maize breeders use multiple traits, multistage, and multiple environment selection methods (Betrán *et al.*, 2003). Multiple environment and multiyear inbred general combining ability values with validated performance in hybrids are considered carefully for choosing parents to start breeding populations.

Hybrid development requires the development of parental inbred lines. The inbred parents used to produce the hybrids are developed through a process of inbreeding and selection. The consequence of inbreeding is the increase in homozygosity that leads to homogeneous expression of traits and to inbreeding depression (i.e., loss of vigor and productivity). Self-pollination is the most common and fastest system of inbreeding (Acquaah, 2007). As inbreeding reduces the genetic variation within families and increases the genetic variation among families, the efficiency of selection among lines increases while it decreases within lines. The level of inbreeding depression depends on the trait. Traits that show high inbreeding depression also show high heterosis (e.g., grain yield). Vigor, plant size, grain yield components, and grain yield are reduced while time to flowering and incidence of barrenness increase with inbreeding (Hallauer and Miranda, 1988). Development of inbred parents can follow different breeding methods such as pedigree breeding, backcrossing, bulking, single seed descent, double haploids, etc (Hallauer, 1990; Singh, 2005).

Pedigree breeding is the most widely used breeding system to develop maize inbreds. Typically, specific crosses are made between inbred lines, and then self-pollination is applied to the F_1 and subsequent generations to develop inbred lines that are superior to either parent (transgressive segregants) through genetic segregation and recombination (Singh, 2005). Selection is applied among progeny rows and among plants within S_1 families and it is common to have replicated nurseries for the S_1 families exposed to different disease, insect, or abiotic stresses. (Hallauer *et al*., 2010). This process of selfing and selection is repeated in successive generations (S_2, S_3, S_4, S_5, . . .S_n) 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, etc (Acquaah, 2007).

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 advent of genetically modified organisms, major emphasis is devoted to accelerate backcrosses to transfer the transgenes to elite inbreds (Hallauer *et al*., 2010; Acquaah, 2007). The use of DNA molecular markers has facilitated both the speed and accurate recovery of the recurrent parent, and the reduction of linkage drag (Acquaah, 2007).

The bulk method, where the seeds 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, are also used in inbred line development because of their simplicity and low space requirements (Acquaah, 2007; Hallauer *et al.*, 2010).

2.3. Testers and Test Crossing

In the use of testcross, selection of tester is the most important step that provides the best discrimination among genotypes according to the purposes of selection (Hallauer and Miranda, 1988). According to Hallauer and Miranda (1988), the use of a common tester to evaluate lines for general combining ability was introduced by Davis in 1927 and Jenkins and Brunson in 1932. Following the introduction of the top cross procedure by Davis in 1927, Johnson and Hayes, in 1936, also reported that inbred lines giving high yields in top crosses were more likely to produce better single crosses (Hallauer and Miranda, 1988).

Artificial crossing or mating is a common activity in plant breeding programs for generating various levels of relatedness among the progenies that are produced. A mating may be as simple as a cross between two parents, to the more complex diallel mating. Diallel mating is a commonly used experimental design for crossing inbred lines in which each line is crossed with every other line (Falconer, 1989). When a large number of maize inbred lines are available from a breeding program, breeders cannot evaluate the combining ability of the lines in diallel crosses because the number is prohibitive. When a large number of inbred lines generated, line x tester mating design proved to be efficient in testing of inbred lines for combining ability because with its use it was possible to identify more promising inbred lines by making fewer numbers of crosses than are required for making all possible crosses. The line x tester basically an extension of top crosses analysis in the sense that instead of one tester as used in top crossing; more than one tester are employed under line x tester design (Kempthorne, 1957).

The use of testers in maize breeding has one of the following objectives: (1) evaluation of combining ability of inbred lines in a hybrid breeding programme, or (2) evaluation of breeding values of genotypes for population improvement (Hallauer and Miranda, 1988). In each instance, the choice is essentially to find a tester that provides the best discrimination among genotypes according to the purpose for selection. Matzinger (1953) defined a desirable tester as one that combines the greatest simplicity in use with maximum information on performance to be expected from tested lines when used in other combinations or grown in other environments. Rawlings and Thompson (1962) defined a good tester as one that classifies correctly relative performance of lines and discriminates efficiently among lines under test. For improvement of breeding populations, Allison and Curnow (1966) defined the best tester as one that maximizes the expected mean yield of the population produced from random mating of selected genotypes. Hallauer (1975) pointed out that in general a suitable tester should include simplicity in use, provide information that correctly classifies the relative merit of lines and maximize genetic gain.

Every hybrid breeding program has to invest considerable effort in choosing an appropriate tester for assessing the combining ability of segregating lines. A tester may be an inbred line, an OPV, or a single-cross hybrid (Vivek *et al.*, 2008). A desirable tester must facilitate discrimination among genotypes for combining ability and desirable traits, simultaneously identify useful hybrid products for direct use, and are compatible with a practical maize breeding program (Vasal *et al.*, 1997). The choice of testers involves a mix of theoretical and practical considerations (Bänziger *et al.*, 2000).

2.4. Hybrid Development and Performance Evaluation

The only reason maize breeders isolate inbred lines is to develop parental inbred lines for the production of hybrids. Hybrid varieties are the first filial generations (F_1) from crosses between two or more pure lines, inbreds, open-pollinated varieties, clones or other populations that are genetically dissimilar (Singh, 2005). Maize hybrid development began in the early 1900s (Hallauer *et al.*, 1988). 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 F_1'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 to identify appropriate heterotic combinations to maximize the vigour of the hybrid (Kim and Ajala, 1996). The general process to develop maize hybrids starts with the creation of a source segregating breeding population that is used to develop inbred lines through inbreeding and selection

(Betran *et al*., 2004). Selected inbred lines are then evaluated in hybrid combinations across locations to select superior hybrids and to estimate their combining ability.

The commercial applications of hybrid breeding started with a cross of two inbred lines (a single cross: A × B) and later shifted to the more economic double cross [(A × B) × (C × D)] and then back to a single cross (Acquaah, 2007). Other parent combinations in hybrid development have been proposed, including the three way cross [(A × B) × C] and modified versions of the single cross, in which closely related crosses showed that the single cross was superior in performance to the other two in terms of average yield (Acquaah, 2007). Today, commercial hybrids are predominantly single crosses. Breeders continue to develop superior inbred lines. The key to using these materials in hybrid breeding is identifying pairs of inbreds with outstanding combining ability. Shull (1908) gave the original concept for production and growing of single cross hybrids, but the cost of seed production has limited its utility. Jones (1918) suggested that double cross hybrids can be produced from two single cross hybrids to reduce the cost of seed production subsequently with the improvement in vigour and yield potential of inbred lines and development of better cultural practices, single crosses were adapted for commercial cultivation in the advanced countries. The recent trends even in the developing and under developed countries single cross hybrids are more popular due to their higher yield levels under favorable environment and uniformity in expression (Hallauer et.al, 2010). Hence, there is a greater scope for the exploitation of heterosis through single cross hybrids, than double cross hybrids.

Much research in maize has assessed the efficiency of per se versus test cross evaluation of new genetic material for use in hybrid production. Predicting the grain yield of single crosses in maize based on the *per se* performance of their parental inbred lines has not been effective due to masking non-additive effects (Smith, 1986; Hallauer, 1990). Further, genotype-environment interactions also lower this correlation (Bernardo, 1991).

The number of potential single crosses to evaluate increases substantially with the number of parental inbreds. The possibility of using inbred line information, as indicative of hybrid performance, is desirable to reduce the number of hybrid evaluations. The correlation between parental inbreds and hybrids depends on the trait. In general, the correlation is relatively high for some additively inherited traits (e.g., plant morphology, ear traits, maturity, and quality characters) but is relatively low for grain yield (Acquaah, 2007). The correlation for grain yield has been consistently positive and significant but not high enough to predict hybrid performance. The correlations between parental genetic diversity estimated with molecular markers, pedigree, or phenotypic traits and hybrid performance also have been too low to have predictive value (Melchinger, 1999). Although these recent approaches facilitate hybrid selection, hybrid testing is required ultimately to identify the inbreds with the best breeding values. Combining ability of inbred lines is the ultimate factor determining future usefulness and commercial potential of the lines for hybrids (Hallauer *et al*., 1988).

Efforts are allocated in preliminary tests to evaluate as many hybrids as possible in a few locations with intensive selection, leaving relatively few hybrids to proceed to the more advance stages. As the numbers of lines to be tested at various stages of inbreeding increase over time, their evaluation in all possible hybrid combinations is not feasible. Therefore, testcrossing with appropriate testers has been adopted extensively to evaluate the relative combining ability of experimental inbred lines. Usually combining ability is first tested at the S1 (F_3) or S_2 (F_4) stage (Vivek *et al.*, 2008). Breeding programs may have hundreds of early generation lines being test-crossed and evaluated across locations. The best 5-20% of the lines are selected and advanced. By the time combining ability is tested for the second time (usually at the S_3 [F_5] or S_4 [F_6] stage), the chosen inbred lines are fairly fixed and may be test-crossed to more testers in order to identify final products (Vivek *et al*., 2008).

2.5. Combining Ability and Gene Action

Combining ability has been defined as the performance of a line in hybrid combinations (Kambal and Webster, 1965). Since the final evaluation of inbred lines can be best determined by hybrid performance, it plays an important role in selecting superior parents for hybrid combinations and in studying the nature of genetic variation (Hallauer and Miranda, 1988). Sprague and Tatum (1942) introduced the concepts of general combining ability (GCA) and specific combining ability (SCA). The authors defined GCA as the average performance of a line in hybrid combinations, while SCA as those instances in which certain hybrid combinations are either better or poorer than would be expected of the average performance of the parent inbred lines included. For random individuals, GCA is associated with additive effects of the genes, while SCA is related to dominance and epistatic effects (non-additive effects) of the genes. However, Rojas and Sprague (1952) verified that the variance of SCA also contains deviations due to the interaction between genotypes and environments, in addition to those that come from dominance and epistasis. GCA and SCA is an indication of genes having largely additive and non-additive (dominance and epistatic) effects, respectively. Sprague and Tatum (1942) found that GCA was relatively more important than SCA for unselected inbred lines, whereas SCA was more important than GCA for previously selected lines for influencing yield and stalk lodging. However, studies have indicated that inbred yields predicted GCA more accurately than SCA (Duvick, 1999). GCA effects quantitatively measure the comparative performance of parents and cross combinations in relation to one another.

The term additive gene action denotes those gene effects in heterozygote where every dominant gene or allele contributes a unit increment without affecting the other dominant allele at another locus and the heterozygote, accordingly perform exactly intermediate between the two homozygotes with respect to a particular character. Dominance indicates a type of gene action where the heterozygote genotype gives the same response as the homozygous dominants, while epitasis refers to a condition where two or more gene loci (non-allelic gene) interact to determine the performance of a genotype (Acquaah, 2007).

Combining ability studies enable classification of selected parental materials with respect to breeding behavior in addition to provision of information on the nature of gene action. The choice of the method to be used for the purpose of genetic improvement of crop plants is dependent on the type of gene action each gene that controls quantitative characters, since quantitative inheritance involves large number of genes (Falconer, 1996). Knowledge of these variances is important to the breeder since it indicates the possibility and extent to which improvement is possible through selection (Allard, 1960; Singh, 1993).

In Ethiopia and other countries, combining ability studies have been made by many workers to estimate the combining ability effects for yield and other traits of maize. A chain of combining ability studies have been also made by many workers from the International Maize and Wheat Improvement Center (CIMMYT) to establish heterotic patterns among several maize populations and gene pools and to maximize their yield for hybrid development (Beck et al., 1990).

Pswarayi and Vivek (2008) studied the combining ability amongst CIMMYT's early maturing germplasm using diallel design and found significant GCA mean squares for grain yield, plant height, days to anthesis, grain texture, husk cover, ear position and anthesis-silking interval. Similary, they reported significant SCA mean squares for plant height, ear position, days to anthesis and husk cover. The authors reported significant GCA x location interaction effects for all studied traits while SCA x location interaction was significant for grain yield, anthesis-silking interval, root lodging and number of ears per plant. Pswarayi and Vivek (2008) reported GCA sums of squares were larger than SCA sums of squares for grain yield (87%), days to anthesis (84%), grain texture (72%) and plant height (65%), while SCA sums of squares were larger for anthesis-silking interval (52%) and ears per plant (55%).

Kim and Ajala (1996) studied combining ability among tropical and temperate maize inbred lines and reported that a major proportion of crosses sum of squares for grain yield was explained by GCA. San Vincente *et al.* (1998) reported greater relative importance of non-additive than additive genetic effects for grain yield in diallel crosses among improved tropical white endosperm populations. In crosses among subtropical and temperate CIMMYT germplasm, Beck *et al.* (1991) observed highly significant GCA effects for grain yield, time to silk and plant height. In a diallel cross among Mexican races of maize, Crossa *et al.* (1990) reported highly significant GCA and SCA mean squares for grain yield, days to anthesis and ears per plant. They further reported that GCA effect was the most important component of variation among the entries for grain yield. In population diallel crosses, Glover *et al.* (2005) observed significant GCA and SCA mean squares for grain yield, stalk lodging, ear height and days to silking.

Makumbi *et al.* (2004) estimated GCA and SCA effects of 15 tropical maize inbred lines for anthesis date, silking date, plant height, anthesis-silking interval, ears per plant and grain yield under stressed and optimal conditions. The authors reported that both GCA and SCA effects across locations were significant for all traits and GCA x location and SCA x location interaction effects were significant for grain yield and ears per plant. They further stated that additive genetic effects were more important for grain yield under drought and well-watered conditions and non-additive genetic effects were found to be more important under low N stress conditions for ears per plant in the set of studied inbred lines.

Cordova *et al.* (2003) reported the importance of GCA effects for grain yield in a factorial crosses between QPM inbred lines from two heterotic groups. Fan *et al.* (2004) analyzed the combining ability of 10 yellow QPM indreds from CIMMYT and China, and reported significant GCA and SCA effects for grain yield. Bhatnagar *et al.* (2004) studied combining ability of white and yellow QPM inbreds for grain yield, days to silk, plant and ear heights, lodging and grain moisture and reported presence of significant GCA effects for all traits except for grain yield in both diallel sets across locations. Xingming *et al.* (2004) evaluated combining ability and heterotic groups of yellow QPM inbreds and observed significant differences among the crosses and GCA of lines for grain yield, plant height, rows per ear, kernels per row and thousand seed weight and non-significant difference in SCA mean squares for all traits.

Vasal *et al.* (1992a) evaluated seven tropical white maize populations crossed in a diallel mating design for grain yield, plant height, and days to silking at seven locations. They reported GCA to account for 67%, 85%, and 78% of the sums of squares among crosses for grain yield, days to silk, and plant height, respectively. Vasal *et al.* (1992a) reported that GCA x location interaction for grain yield was not significant while that for days to silk and plant height were significant. Positive and significant GCA effects for grain yield for three of the populations and negative significant GCA effects for two populations were reported but no significant SCA effects were found for grain yield.

Vasal *et al.* (1993a) observed highly significant GCA for grain yield, ear height, time to silk and endosperm hardness and non-significant SCA effects for all the traits they studied in three locations in the study of heterosis and combining ability in CIMMYT's subtropical QPM germplasm. In another set of experiment, Vasal *et al.* (1992b) conducted on combining ability of CIMMYT tropical and subtropical maize materials, significant GCA effects were observed for grain yield in both tropical and sub-tropical locations but significant SCA effect was observed for grain yield only in sub tropical location. Vasal *et al.* (1993b) reported that GCA effects were highly significant for all traits he studied and non-significant SCA effects indicating minor importance of non-additive gene action. Singh and Asnani (1979) found significant mean squares for GCA and SCA for yield and 100- grain weight, number of kernel rows per ear, number of kernels per row, ear length and ear diameter in a 8 x 8 diallel cross of maize inbred lines. These authors concluded that both GCA (additive) and SCA (non-additive) effects play an important role in the inheritance of yield and its components.

For a 7 x 7 diallel cross among maize lines in Ethiopia, Shewangizaw *et al.* (1985) reported significant GCA and SCA for most traits, but predominance of non-additive genetic variance in the case of yield. On the other hand, Younnes and Andrew (1978) reported more importance of additive gene action than non-additive components in previously unselected materials. Similarly, Shewangizaw (1983) reported GCA to be more important than SCA for days to 50% tasseling, silking, maturity, kernel rows per ear and 1000-kernel weight. However, his results indicate SCA to be more important than GCA for grain yield and ear height where as Yoseph (1998) reported highly significant GCA and SCA for days to tasseling, and silking, plant and ear height, number of kernel rows per ear, 1000 seed weight and grain yield.

Leta *et al.* (1999), observed highly significant mean square due to GCA effects for grain yield, ear height, plant height, and time to silking using diallel crosses among seven maize populations. They reported high GCA effects than SCA effects and reached at the conclusion that additive gene action was important in controlling all traits.

Significant mean square due to GCA effects for days to tasseling, days to silking, days to maturity, plant height, ear height, ear length and ear diameter, kernel rows per ear, kernel per row, thousand kernel weight, and grain yield at Bako, Hwassa, and Areka as well as from combined data over three locations was reported by Jemal (1999). He reported significant mean squares due to SCA effects only for some traits at all locations and across locations. Shewangizaw (1983), Kebede (1989), Yoseph (1998), and Mandefro (1999) reported the importance of both additive and non-additive types of gene actions in the inheritance of number of days- to-tasseling-and -silking.

Teshale (2001) evaluated 27 crosses of tropical highland maize genotypes for eleven agronomic characters with objective of generating information on combining ability and heterotic pattern between inbreed lines and testers, and found significant GCA mean squares due to lines for all the traits except for number of kernel rows per ear but significant GCA due to testers only for grain yield, ear length and 100 seed weight. He also found significant line x tester interaction for all traits considered indicating the presence of differences among the F_1 progenies. His results revealed significant GCA x location both for lines and testers for days to maturity, 100 seed weight and yield; and significant SCA x location interaction for most characters except number of kernel rows per ear, ear length and ear diameter. He also reported as additive genetic variance is more important in controlling most of the studied traits.

Dagne *et al*. (2007) reported the importance of both additive and non-additive gene effects in controlling days to tasseling, days to silking, days to maturity, plant height and ear height, number of ears per plant, ear length, ear diameter, number of kernel rows per ear, number of kernels per row, 1000 kernel weight and grain yield. He also found the dominant role of additive gene effects in an expression of all characters studied except for grain yield. Dagne *et al*. (2010) evaluated crosses between CIMMYT and Ethiopia lines resulted from North Carolina Design II and found significant GCA and SCA effects for most traits.

Hadji (2004) found highly significant differences among entries, parents, crosses, and parents versus crosses for most traits in a diallel study 10 QPM inbred lines. He reported significant differences for GCA and SCA effects for all traits evaluated except endosperm hardness. The author further reported the dominance of additive gene effects in the expression of all traits studied, except for ear length, number of kernels per row and grain yield.

Gudeta (2007) evaluated eighty crosses, 24 parents (20 female parents and four testers) at four high land locations (Ambo, Holeta, Kulumsa and Haramaya) found highly significant mean squares due to female GCA across location for ear rot, number of kernel rows per ear and ear diameter. He also found highly significant mean squares due to SCA for grain yield, ear rot, number of kernel rows per ear and ear diameter. Gudeta (2007) also reported highly significant mean squares due to SCA and male GCA for grain yield at the four locations including across locations while mean squares due to female GCA were highly significant at Holeta and Kulumsa. Genotype x location and SCA x location were significant for grain yield. He also found significant SCA effects for 11 of the crosses.

Legesse et al. (2009) studied GCA and SCA of highland transition maize inbred lines using line x tester analysis. They reported GCA mean squares due to lines and testers were highly significant for all the traits. Similarly SCA mean squares for most traits except for days to physiological maturity and for northern leaf blight (NLB, caused by *Exserohilum turcicum*) were found highly significant. Legesse *et al*. (2009) reported estimates of GCA effects and they indicated that three inbred lines showed good combiners for grain yield and for days to silking. They also indicated significantly different SCA effects were revealed for crosses involving most traits.

A number of combining ability studies have been conducted on maize for grain yield where the magnitude of GCA was reported to be greater than that of SCA (Rameeh *et al*., 2000; Pal and Prodhan, 1994). In contrary, some researchers reported that dominance deviation is more important in controlling grain yield (Kumar *et al*., 1999; Kalla *et al*., 2001; Kara, 2001). Other scientists, on the other hand, concluded that grain yield in maize is controlled by both additive and non-additve type of gene action (Dubey *et al*., 2001; Sujiprihati *et al*., 2001).

Flowering in maize is controlled by additive type of gene action and is more important than dominant gene action (Konak *et al*., 1999). Additive gene action was also observed to be more important than dominant gene action for days to silking (Satyanarayana *et al*., 1994). Similarly, in the evaluation of maize inbred lines derived from seven late white CIMMYT populations using line x tester design, additive gene effects were found more important for days to silking (Lemos *et al*., 1999). Nirala and Jha (2001) in a study on combining ability in maize using seventy crosses reported that the magnitude of GCA were more pronounced than SCA for days to anthesis and silking. In contrary to these findings, other investigators reported the importance of dominant gene effects for days to anthesis and silking (Reddy and Agarwal, 1992; Santyanara, 1995; Singh and Singh, 1998).

Reddy and Agarwal (1992), reported the importance of additive genetic variances in maize for plant and ear height while Kumar and Gangashetti (1998) and Paul and Debanth (1999) have reported that both additive and dominant gene actions to be involved in the inheritance of plant height. The results from line x tester analysis on maize showed that plant height is controlled by additive type of gene action and ear height by dominant gene action (Konak et *al*., 1999; Lemos *et al*., 1999). In combining ability study in maize it was reported that plant height is controlled by additive gene action (Revilla *et al*., 1999; Konak *et al*. 2001). Desai and Singh (2001), Kalla *et al*. (2001) and Vicente *et al*. (2001) in separate studies reported that plant and ear height controlled by additive type of gene action. Using line x tester mating design, Dodiya and Joshi (2002) reported the importance of non-additive gene effects in controlling plant height in maize. In some other studies in maize, combining ability results showed the importance of non-additive gene effects for plant and ear height (Vacro *et al*., 2002; Venugopal *et al*., 2002).

Singh and Singh (1998) through line x tester analysis reported that ear length is mainly attributed to line GCA. While Konak *et al*. (1999), Kalla *et al*. (2001) and Venugopal *et al*. (2002) have reported that non-additive gene action was predominant for ear length. Singh and Singh (1998) and Venugopal *et al*. (2002) have reported that ear diameter in maize is under the control of non-additive gene action. Rosa *et al*. (2000) in their study on maize have reported that ear diameter is controlled by additive gene action.

Number of kernel rows per ear is controlled by non-additive gene action (Kumar *et al*., 1999; Rameeh *et al*., 2000). Kalla *et al*. (2001) in a combining ability study conducted on maize inferred that both additive and non-additive gene actions were involved in the control of number of kernel rows per ear.Vankatesh *et al*. (2001) carried out line x tester analysis and reported that non-additive gene action involved in the control of number of kernel rows per ear. Similarly Venugopal *et al*. (2002) carried out diallel analysis for number of kernels rows per ear and reported non-additve gene action was involved for the character. Pal and Prodhan (1994) reported estimates of SCA were higher than those of GCA for number of kernels per row. Rameeh *et al*.(2000), Vankatesh et al. (2001) and Venugopal *et al*. (2002) in combining ability studies in maize have reported that both additive and non-additive gene in controlling the number of kernels per row.

The study conducted by Rameeh *et al*. (2001) revealed that there was preponderance of additive gene action for 100-grain weight. Whereas in a study conducted by Dudey *et al*. (2001) on 45 hybrids derived from, 15 maize lines crossed with 3 testers, they reported that both GCA and SCA are important for 100-grain weight. In another study conducted on maize inbred lines, Kalla *et al*. (2001) and Kara (2001) observed that both additive and non additive gene actions were involved in the inheritance of 100-grain weight.

2.6. Heterotic Pattern

Appropriate knowledge about the performance of maize genotypes in crosses is required to organize germplasm in applied breeding programs. In species that exhibit heterosis, information about combining ability with genetically divergent testers is useful when classifying the germplasm into heterotic groups.

The recognition of heterotic groups simplified decisions relative to choices of testers and crosses to test between newer inbred lines. The concept of heterotic groups is different from the one for heterotic patterns. A heterotic group may be defined as a group of related or unrelated genotypes from the same or different populations, which display a similar combining ability when crossed with genotypes from other germplasm groups (Acquaah, 2007). Heterotic pattern refers to a specific pair of two heterotic groups, which express high heterosis and high performance in hybrid combination and it is collection of germplasm, which when crossed to a germplasm external to its group tend to exhibit more heterosis (on average) than when crossed to a member of its own group (Allard, 1960). Knowledge of the heterotic groups and patterns is helpful in plant breeding. It helps breeders to utilize their germplasm in a more efficient and consistent manner through exploitation of complementary lines for maximizing the outcomes of a hybrid breeding program (Hallauer, 1990). To increase efficiency and to facilitate hybrid development, it is imperative that source populations should be heterotic to each other exhibiting high level of cross performance.

Heterotic group classification methods used by researchers have great influence on how a maize line is assigned to a maize heterotic group. Two major heterotic group-classification methods are currently used widely across the world. The traditional method uses SCA with some line-pedigree information and/or field hybrid-yield information (SCA_PY) to assign a maize line to a heterotic group (Wu *et al.*, 2007). Another method employs various molecular markers to compute genetic similarity (GS) or genetic distance (GD) to assign maize lines to different heterotic groups (Menkir *et al.*, 2004).

Heterotic groups in maize are more clearly determined in temperate germplasm (European flint × US dent lines used in Europe and Reid Yellow Dent × Lancaster used in the US) than in tropical germplasm. General information about the heterotic patterns being used in the tropics indicates that crosses of ETO or Suwan I with Tuxpeño are most common (Hallauer et al., 1988). The extensive use and investigations of a well-established heterotic pattern, Reid × Lancaster, have been made and has culminated in the development and use of many good maize hybrids in China (Fan *et al.*, 2002; Yuan *et al.*, 2002; Wu *et al.*, 2007) and many parts of the world (Vasal *et al*., 1992a, 1992b; Menkir *et al*., 2004; Barata and Carena, 2006). Heterotic patterns are very critical for maximizing the expression of hetorosis in hybrids. However, they have not been well established and improved in a systematic manner by the majority of maize improvement programmes in the tropics (Paliwal, 2000).

In studies to determine the combining ability and heterotic patterns of tropical maize (*Zea mays* L.) developed at CIMMYT, using four line testers Vasal *et al*. (1992a) identified and formed two divergent tropical heterotic groups (THGA and THGB). Lines showing negative SCA with Tester 1 “Pop 21” (Tuxpeno-1) and positive SCA with Tester 3 “Pop 25” (Blanco Cristalino) were classified under Tropical Heterotic Group “A”. Those showing positive SCA with Tester 1 and negative with Tester 3 were classified under Tropical Heterotic Group “B”.

In a similar study in the same year using subtropical CIMMYT maize lines, Vasal *et al*. (1992b), identified and formed two divergent subtropical heterotic groups (STHGA and STHGB). Lines that had negative SCA with Tester 2 (Pop 44) and positive SCA with Tester 4 (Pop 34) were classified under Subtropical Heterotic Group “A” and those showing positive SCA with Tester 2 and negative with Tester 4 were classified under Subtropical Heterotic Group “B”. The hypothesis was that positive SCA effects between inbred lines generally indicate that lines are in opposite heterotic groups and lines in the same heterotic group tended to exhibit negative SCA effects when crossed.

Fan *et al*. (2001) used a diallel design to study combining abilities among 10 maize lines (five lines from the International Maize and Wheat Improvement Center [CIMMYT] and five major commercial lines from China). According to SCA_PY method, they classified CML171, CML161, CML166 into one heterotic group; Chang 631/o2, Zhongxi 096/o2 into another heterotic group; and Qi 205 into a third heterotic group. Xingming *et al*. (2004) studied combining ability of 10 quality protein maize inbred lines and the 10 lines were divided into 4 groups: CML171, CML166, CML161 and CML164 were in group A; CML194 was in group B; Chang631/O2, CA339 and Zhongxi096/O2 were in group C; Xin9101/O2 and Qi205 were in group D. While Wu *et al*. (2007) used North Carolina design II (NC II design) to classify 27 maize inbred lines into four known maize heterotic groups widely accepted in China.

Menkir *et al*. (2004) used two testers representing the flint and dent heterotic patterns to test 38 tropical maize inbred lines. The two testers successfully classified 23 of the 38 tested inbred lines into two heterotic groups based on the SCA_PY method. Barata and Carena (2006) conducted a similar study as that of Menkir *et al*. (2004) to classify 13 elite North Dakota maize inbred lines into current U.S. Corn Belt heterotic groups. Menkir *et al*. (2003) evaluated 30 tropical lowland inbred lines at six environments and classified some of the inbred lines into two heterotic groups based on SCA effects and testcross mean grain yields.

CIMMYT-Zimbabwe works with two major heterotic groups A (N3, Tuxpeno, Kitali and Reid) type and B (SC, ETO Blanco, Ecuador and Lancaster) type (Mickelson *et al.*, 2001). Based on results from CIMMYT-Zimbabwe's regional trials conducted over several years, single cross testers CML312/CML442 (group A) and CML395/CML444 (group B) have proved useful in hybrid formation for subtropical and mid altitude environments and are currently in wide use. These single crosses are intermediate and late maturing respectively (Pswarayi and Vivek, 2008). Mawere (2007) studied combining ability of maize inbred lines and assigned them into groups using yield SCA averages across sites with CML312/CML442 (Group A) and CML395/CML444) (Group B). Five lines were assigned into heterotic group A, five lines were assigned into group B and three lines were classified as AB.

Among well-known heterotic groups in the world, Kitale Syn.II and Ecuador 573 are widely used in Eastern Africa including Ethiopia (Darrah, 1986). Legesse *et al*. (2009) examined combining ability of 26 highland transition maize inbred lines for grain yield and other desirable traits with two testers Pool9A-MHM and 142-1-e for assigning the inbred lines in to heterotic groups, each group involving 13 and 10 inbred lines, respectively.

3. MATERIALS AND METHODS

3.1. Experimental Locations

The field experiments were conducted at five maize testing locations in Ethiopia; namely, Melkasa, Mieso, Ziway, Dhera and Pawe. Melkasa, Ziway, Dhera and Mieso are located Oromia National Regional State while Pawe is located in Benishangul Gumuz National Regional State, in the north western part of Ethiopia. Description of the locations is given in Table 1.

Table 1. Description of the testing locations

Location	Annual rainfall (mm)	Altitude (m.a.s.l)	Latitude	Longitude	Soil type
Melkasa	710	1550	$8^0$24’ N	$39^0$21’ E	sandy-clay-loam
Ziway	640	1637	$7^0$56’ N	$38^0$35’ E	silt
Dhera	520	1680	$8^0$20’ N	$39^0$23’ E	sandy-clay
Mieso	560	1470	$9^0$12’ N	$40^0$52’ E	clay-loam
Pawe	1579	1120	$11^0$09’ N	$36^0$03’ E	clay

Source: Seboksa *et al.* (2001)

3.2. Experimental Materials

The experiment comprised 88 maize genotypes (including 86 test crosses formed by crossing 43 elite inbred lines to two testers in line x tester mating design) and two standard checks (BH-543 and Melkasa-2). The inbred lines were introduced from CIMMYT-Zimbabwe and were bred for resistance to various biotic and abiotic stresses of Africa. The most important stresses against which the inbred lines were selected include diseases (maize streak virus, grey leaf spot, leaf rust and turcicum leaf blight), low nitrogen, high density and drought. The two testers used are single crosses of commercial CIMMYT inbred lines of known heterotic groups; viz. CML312/CML442 (tester A) and CML202/CML395 (tester B), which are commonly used by CIMMYT and many other national maize research programs in Africa. The lines x tester crosses were made at Melkassa Agricultural Research Center during the main season of 2009. From the checks, BH543 is a three way-cross commercial hybrid released by Bako National Maize Research Project in 2005. It is a medium maturing hybrid that matures in about 145 days at Bako and similar environments. The hybrid is a high yielding, tolerant/resistance to major maize diseases known in the country and well adapted to mid-altitude to transitional highland environments (1000-2000 m.a.s.l) receiving high rainfall. Melkasa-2 is relatively early maturing and drought tolerant variety released by Melkasa Agricultural Research Center in 2004 for drought stressed areas of the rift valley.

3.3. Experimental Design and Field Management

The experiment was conducted in 2010 at all the locations. The experimental design for the field evaluation of the materials was 8 x 11 alpha-lattice design (Patterson and Williams, 1976) with eight plots per an incomplete block and 11 incomplete blocks in each replication. The experiment was planted in two replications. Design and randomization of the trials were generated using CIMMYT's computer software known as Fieldbook (Banziger and Vivek, 2007). Each plot consisted of one row of 5 m length with 75 cm and 25 cm spacings between rows and plants, respectively. Two seeds were planted per hill to ensure uniform and sufficient plant stand and then thinned to one plant per hill. As recommended by MARC, 100 kg/ha DAP was applied at planting and 50 kg/ha urea was side dressed at 35 days after planting for the experiments conducted at Melkasa, Dhera, Meiso and Ziway. At Pawe 100 kg/ha DAP and 50 kg/ha urea was applied at planting while 50 kg/ha urea was side dressed at knee height following the research recommendation given for the area. Urea and diamonium phosphate (DAP) were used as sources of N and P_2O_5, respectively. Other crop management practices such as land preparation, weeding, disease and insect control were applied following research recommendations for each locality.

Table 2. Code and pedigree of inbred lines, testers and checks used in the study

Line code	Pedigree
1	[[Ent320:92SEW2-77/[DMRESR-W]EarlySel-#I-2-4-B/CML386]-B-11-3-B-2-#-B*4]
2	[INTA-F2-192-2-1-1-1-B*7-6-B]
3	[ZEWBc1F2-216-2-2-B-1-B]
4	[[SC/CML204//FR812]-X-30-2-3-2-1-BBB]
5	[ZEWAc1F2-219-4-3-B-1-B*5]
6	[[CML141/[CML141/CML395]F2-1sx]-4-2-1-B*6]
7	[[[Ent52:92SEW1-2/[DMRESR-W]EarlySel-#L-2-1-B/CML386]-B-22-1-B-4-#/[TIWD-EarlySelSynS1#-2-XX-2-B/[SW1SR/COMPE1-W]-126-2-1-B]-B-11-4-B-2-#]-B-2-B-1-B*5]
8	[Syn01E2-64-2-B-2-B]
9	[[INTA-2-1-3/INTA-60-1-2]-X-11-6-3-BBB]
10	[[[P501c2/[EV7992#/EV8449-SR]C1F2-334-1(OSU8i)-1-1-X-X-BB]-4-1-1-4-2-1-B/[[[K64R/G16SR]-39-1/[K64R/G16SR]-20-2]-5-1-2-B*4/CML390]-B-38-1-B-3-#]-B-7-B-1-B*6]
11	[PL15QPMc7-SR(BC0FS#)-balbreedbulk-31-1-4-4-2-B-3-B]
12	[DTPWC9-F104-5-6-1-1-B*4]
13	[(CLQRCWQ50/CLQRCWQ26)-B-47-BB]
14	[[NC348-BB/[Ent67:92SEW1-17/[DMRESR-W]EarlySel-#I-3-3-B/CML391]-B-31-B-3-#-2-B//[[NAW5867/P30-SR//NAW5867]-84-1/[NAW/P30//NAW]-3-1]-6-2-2-1-3-B-3-B]-2-1-1-BBB]
15	[[INBRED-A/INBRED-B]-BBB-1-BBB]
16	[[(CML395/CML444)-B-4-1-3-1-B/CML444//[[TUXPSEQ]C1F2/P49-SR]F2-45-7-1-2-BBB]-2-1-2-2-B*5]
17	[[CML198/90323(B)-1-X-5-SN]-B-31-2-1-B*6]
18	[[CML199/[EV7992#/EV8449-SR]C1F2-334-1(OSU8i)-6-3-Sn]-B-23-2-2-B*8]
19	[[CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-B*4]-1-5-1-1-1-B*7]
20	[[CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-B*4]-1-5-1-1-2-B*6]
21	[[CML312/CML445//[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BBB]-1-2-1-1-2-B*5]
22	[[CML312/CML445//[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BBB]-1-2-1-1-3-B*5]
23	[[CML442/CML197//[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-1-1-B*4]
24	[[CML442/CML197//[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-2-1-B*4]
25	[[CML442/CML197//[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-2-3-B*5]
26	[[CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-1-B*4]
27	[[CML444/CML395//SC/ZM605#b-19-2-X]-1-2-X-1-1-B*6]-2-2-2-1-B*5]
28	[[LZ955355/LZ956441]-B-2-3-3-B-3-B*7]

Table 2 (Continued)

29	[[SYN-USAB2/SYN-ELIB2]-12-1-1-1-B*4]
30	[[SYN-USB2/SYN-ELIB2]-81-1-1-1-B*6]
31	[[TS6C1F238-1-3-3-1-2-#-BB/[EV7992#/EV8449-SR]C1F2-334-1(OSU8i)-10-7(I)-X-X-X-2-BB-1]-1-1-2-1-1-B*6]
32	[CML312-B]
33	[CML442-B]
34	[CML443-B]
35	[CML489-B]
36	[MAS[206/312]-23-2-1-1-B*5]
37	[MAS[MSR/312]-117-2-2-1-B*4]
38	[P501SRc0-F2-4-2-1-1-BBB]
39	[P501SRc0-F2-47-3-1-1-BBB]
40	[Z97SYNGLS(B)-F2-188-2-1-2-B*6]
41	[ZM523A-16-2-1-1-B*4]
42	[ZM523B-29-2-1-1-B*4]
43	[ZM621A-10-1-1-1-2-B*6]
Testers	
1	CML 312 / CML 442 (tester A)
2	CML 202 / CML 395 (tester B)
Standard checks	
1	BH- 543
2	Melkasa-2

3.4. Data Collected

1. **Anthesis date (AD):** Measured as number of days after planting to when 50% of the plants shed pollen..

2. **Silking date (SD):** It is the number of days from planting to when 50% of the plants in the plot showed up silks of 2-3 cm length.

3. **Plant height (PH):** Measured as the height from the soil surface to the base of tassel branching; the record was taken two weeks after pollen shed has ceased.

4. **Ear height (EH):** Measured as height from the soil surface to the node bearing the upper most ear of the same plant used to measure plant height two weeks after pollen shed has ceased..

5. **Stand count at harvest (SCH)**: The total number of plants per plot at harvest was recorded.

6. **Number of ears harvested:** The total number of ears harvested per plot at harvest was recorded.

7. **Ears per plant (EPP):** The number of harvested ears in each plot was divided by the stand count at harvest.

8. **Grain moisture (MOI):** Percent water content of grain was measured at harvest.

9. **Thousand kernel weight (TKWT)**: The weight in grams of 1000 random kernels were weighed from each plot using sensitive balance and was adjusted to 12.5 % moisture level.

10. **Number of rows per ear (RPE):** The total number of kernel rows of the ear were counted from five randomly taken ears and the average value were used as number of rows per ear.

11. **Number of kernels per row (KPR):** Number of kernels per row was recorded by counting kernels in each row from five randomly taken ears and the average value was recorded.

12. **Ear length (EL):** The lengths of five random taken ears were measured from the base to the tip in cm and the average value was used.

13. **Ear diameter (ED):** The diameters of 5 random taken ears were measured at mid-length in cm and the average value was used. The same ears used for measuring ear length were used to measure ear diameter.

14. **Grain yield (GY):** The total grain yield from all the ears of each experimental unit were used to estimate grain yield (in ton per hectare) after moisture level was adjusted to 12.5%.

3.5. Statistical Analysis

3.5.1. Analysis of variance

Analyses of variances (ANOVA) were conducted for grain yield and other agronomic traits for each location. Genotypes were considered fixed effects while replications and incomplete blocks within replications were regarded as random effects. Prior to combined data analysis across locations, Bartlett's test for grain yield and related traits were conducted to test homogeneity of error variances (Gomez and Gomez, 1984). Means adjusted for incomplete block effects were used to conduct combined analysis of variance using PROC GLM in SAS (SAS, 2003). The pooled error mean squares were obtained by dividing the sum of the error sums of square from all location ANOVA with the corresponding sum of the error degrees of freedom. In the combined analysis, environments and replications within environments were considered random and genotypes as fixed effects.

Genotypic component of variation was partitioned into variation due to hybrids, checks and checks versus hybrids whereas the hybrid component of variation was partitioned into variation due to line (female), tester (male) and line (female) x tester (male) interaction.

3.5.2. Combining ability analysis

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

The F-test of mean square due to lines and crosses were computed against mean square due to error for individual location analysis (Singh and chaudary, 1999). For across locations ANOVA, the F-test for the main effects such as crosses, lines and lines x testers interaction mean square was tested against their respective interaction with the locations. The mean squares attributable to all the interactions with the locations were tested against pooled error mean square. Significances of GCA and SCA effects of the lines and hybrids were determined by t-test using standard errors of GCA and SCA effects. The main effects due to females and males were considered as GCA effects while, male x female interaction effects were represented as the SCA. Skeletons of ANOVA for individual and across locations are indicated in Tables 3 and 4, respectively.

Table 3. Skeleton of ANOVA for combining ability for individual location

	Mean squares	
Source of variation	Df	Ms
Block/Rep	Rep(Bloc-1)	
Genotype(G)	G-1	MSg
Cross(Cr)	Cr-1	MScr
Line(L)	L-1	MSl
Tester(T)	T-1	MSt
Line x Tester (L x T)	(L-1)(T-1)	MS(lxt)
Cheks (Ck)	Ck-1	MSck
Ck vs Cr	1	MS ck vs cr
Error	(R-1) (G-1)	MS error

The mathematical model used for the combining ability analysis for one location is given as:

$\mathbf{Y_{ijk} = \mu + l_i + t_j + (l \times t)_{ij} + e_{ijk}}$;

Where, Y_{ijk} is the k^{th} observation on i x j^{th} progeny,

µ is the general mean,

l_i is the effects of the i^{th} line,

$(l \times t)_{ij}$ is the interaction effect of the cross between the i^{th} line and j^{th} tester and

e_{ijk} is the error term associated with each observation.

Table 4. Skeleton of ANOVA for combining ability combined over locations

	Mean squares	
Source of variation	df	Ms
Location (Loc)	Loc-1	
Rep/loc	Loc(r-1)	
Genotype(G)	G-1	MSG
Crosses(Cr)	Cr-1	MSCr
Line(L)	L-1	MSL
Tester(T)	T-1	MST
Line x Tester (L x T)	(L-1)(T-1)	MS(LxT)
Cheks (Ck)	Ck-1	MSCk
Ck vs Cr	1	MS Ck vs Cr
Loc*G	(G-1)(Loc-1)	MS(LocxG)
Cr*Loc	(Cr-1)(Loc-1)	MS(LocxCr)
L*Loc	(L-1)(Loc-1)	MS(LocxL)
T*Loc	(T-1)(Loc-1)	MS(LocxT)
L x T(Loc)	(L-1)(T-1)(Loc-1)	MS(LxT) x Loc
Ck*Loc	(Ck-1)(Loc-1)	MS(CkxT)
Cr vs Ck (Loc)	Loc-1	MS(Ck vs Cr x Loc)
pooled error	Loc (G-r(block-1))	MS pooled error

Ck= checks, Cr = crosses, G= genotypes, L= lines or females, Loc = location, MScr = mean sum of squares due to crosses, MSG = mean sum of squares due to genotypes , MSck = mean sum of squares due to checks, MSl =mean sum of squares due to females (lines), MS l x t = mean sum of squares due to females x male, MScross x Loc= mean sum of squares due to cross x loc, MS lxloc = mean sum of squares due to l x loc, MStxloc = mean sum of squares due to t x loc, MS (lxt)xloc = mean sum of squares due to (t x l) x loc, MS pooled error= mean sum of squares due to pooled error, r = replication, T = testers or males

The mathematical model used for the combining ability analysis for across location is given as: $\mathbf{Y_{ijkl} = \mu + a_l + v_{ij} + (av)_{ijl} + e_{ijkl}}$

Where Y_{ijkl} = observed value from each experimental unit,

μ = the general mean,

a_l = location effect,

v_{ij} = F_1 hybrid

$(av)_{ijl}$ = interaction effect between i^{th} F_1 hybrid and l^{th} location,

e_{ijkl} = residual effect.

3.5.2.1. General and specific combining ability effects

The GCA effects due to lines and testers were calculated as a deviation of line or tester mean from the overall hybrid mean, as follows:

Lines: $g_i = \frac{X_i..}{tr} - \frac{X...}{ltr}$

Where, g_i = GCA effect for i^{th} line; g_j = GCA effect for j_{th} tester; $X_{.j.}$ = sum of the j^{th} tester; $X_{i..}$ = Sum of the ith line; X… = grand sum; l = number of lines; t = number of testers and r = number of replications.

The specific combining ability effects of LxT cross combinations were calculated as:

$$S_{ij} = \frac{X_{ij}.}{r} - \frac{X_i..}{tr} - \frac{X._j.}{lr} + \frac{X...}{ltr}$$

Where, S_{ij} = SCA effect of the ij^{th} cross; X_{ij}**.** = i x j cross sum; X_i**..** = ith line sum; $X_{.j.}$= j^{th} tester sum; l = number of lines, t = number of testers and r = number of replications.

For GCA and SCA effects of lines and tester, and cross combinations, the restriction $\sum g_i = \sum g_j = 0$ and $\sum S_{ij} = 0$ was imposed.

3.5.2.2. Standard errors for combining ability effects

Standard errors for the combining ability effects were calculated to test the significance of GCA and SCA effects or that of the difference between any two GCA and SCA effects; that is SE and SED were calculated as follows:

1. Standard error (SE) for general combining ability effects (GCA)
   a) Line: SE (GCA for line) = (Mse/rt) $^{1/2}$
   b) Tester: SE (GCA of tester) = (Mse/rl) $^{1/2}$
2. Standard error (SE) for specific combining ability effects
   SE (SCA effects) = (Mse/r) $^{1/2}$
3**.** Standard error of the differences (SED) between general combining ability effects

$SE (g_i-g_j)$ line = $(2Mse/rt)^{1/2}$

$SE (g_i-g_j)$ tester = $(2Mse/rl)^{1/2}$

4. Standard error of the differences (SED) between specific combining ability effects

$SE (S_{ji}-S_{kl}) = (2Mse/r)^{½}$

3.5.3. Classification of the inbred lines into heterotic groups

Grain yield SCA estimates were used to determine the heterotic grouping of the lines used for the current study. Lines that showed positive and significant grain yield SCA effects with CML312/CML442 (heterotic group A), and negative and significant SCA effect with CML202/CML395 (heterotic group B) were classified as heterotic group B, and vice versa. In addition, inbred lines with positive and significant GCA effects were classified into heterotic groups based on positive or negative SCA effects they exhibited when crossed with the two testers. Inbred lines that showed low GCA effects and non-significant SCA effects when crossed with the testers were not classified into heterotic groups.

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance

Analyses of variances were conducted for grain yield (GY), anthesis date (AD), silking date (SD), plant height (PH), ear height (EH), number of ears per plant (EPP), 1000-kernel weight (TKWT), number of rows per ear (RPE), number of kernels per row (KPR), ear length (EL) and ear diameter (ED) for five locations; namely, Melkasa, Ziway, Dhera, Mieso and Pawe (Appendices 1-5). Combined analyses were performed for the traits that showed significant genotypic mean squares for individual location analysis and homogenous error variance analyzed using Barttlet's test (Gomez and Gomez, 1984). Accordingly, the combined analyses of variances were performed for EPP, ED and RPE across all locations, for GY and EL across four locations (excluding Dhera), for PH and EH across four locations (excluding Melkasa) for TKWT across four locations (excluding Ziway), for KPR across four locations (excluding Pawe) and for AD and SD across three locations (Melkasa, Ziway and Pawe) (Tables 5)**.**

Highly significant differences (P<0.01) were observed among the genotypes for AD and SD at all locations. The mean squares due to genotypes were significant at all locations for GY, RPE, EL, ED, KPR and PH. Genotypic effects were significant for EPP for all locations except for Dhera and Pawe. Mean square due to genotypes for TKWT was significant at most locations except at Ziway and mean square for genotype was significant for EH at most locations except at Melkasa (Appendices 1-5). On the other hand, mean squares due to checks and checks versus crosses were not significant for most of the traits at all locations.

Across locations analysis of variance showed highly significant (p<0.01) differences among environments for all studied traits. Mean squares due to entries were significant for all traits except for EPP and TKWT. Mean squares due to checks and checks versus crosses were not significant for most of the traits. Entry (genotype) by environment interactions were highly significant (p<0.01) for all traits except EPP (Table 5).

The combined analyses of variances revealed highly significant (P<0.01) differences among the 88 genotypes for most of the traits studied, indicating the presence of inherent variation among the materials, which makes selection possible. Desirable genes from this germplasm can effectively be utilized to develop high performing hybrids. Similarly, several previous studies reported significant differences among genotypes for GY and GY related traits in different sets of maize genotypes (Dagne *et al*., 2007; Teshale, 2001; Jemal, 1999; Amiruzzaman *et al*., 2010; Hadji, 2004; Gudeta, 2007).

The interaction between genotypes and locations (G x loc) were highly significant for most of the traits, indicating that genotypes performed differently across locations, that is, the relative performances of the genotypes were influenced by the varying environmental conditions. In consistent with the present findings, Jumbo and Carena (2008) reported significant G x loc interaction for GY, AD, SD, EH, EL and ED. Similarly, Pswarayi and Vivex (2008) reported significant G x loc interaction for GY, AD, SD, PH and EH and Gudeta (2007) reported significant G x loc interaction for GY, RPE and ED whereas he reported non-significant G x loc interaction for EPP.

Table 5. Combined analysis of variance for GY, PH, EH, EL, KPR and TKWT (across four locations), AD and SD (across three locations) and EPP, RPE and ED (across five locations) of line by tester crosses involving 43 lines and two testers.

Source	DF	GY t/ha	PH cm	EH cm	EL cm	KPR #	TKWT gm	DF	AD days	SDdays	DF	EPP #	RPE #	ED cm
Location(Loc)	3	420.10*	112963.0**	15834.0*	367.60*	909.9**	521867.60*	2	2386.6**	2004.1*	4	0.97**	5.79**	9.80**
Entry(E)	87	2.15**	256.08**	235.43*	3.66**	16.74**	2139.70	87	12.55**	12.62**	87	0.02	1.66**	0.12**
Cross(Cr)	85	2.08**	254.84**	238.49**	3.53**	16.93**	2158.59	85	12.31**	12.41**	85	0.02	1.67**	0.13**
GCA line(L)	42	2.51**	396.17**	379.30**	5.10**	19.05**	3212.06	42	21.60**	21.16**	42	0.03*	2.82**	0.19**
GCAtester(T)	1	1.57	14.61	325.85	3.94	22.41	22.16	1	18.99*	23.95*	1	0.001	0.19	0.42
SCA(L x T)	42	1.67**	119.23	95.59*	1.96**	14.68*	1155.98	42	2.86**	3.39**	42	0.01	0.56**	0.06**
Check(Ck)	1	5.28	76.26	208.08	13.01	12.01	397.62	1	44.83	42.67	1	0.02	0.58*	0.001
Ck vs Cr	1	5.15**	18.95	3.02	4.84	5.22	2276.56	1	0.38	0.45	1	0.01	1.43**	0.05
Loc*E	261	0.92**	96.38**	69.38	1.26**	6.64*	2172.40**	174	1.49**	1.51**	348	0.02**	0.31	0.04**
Cr*Loc	255	0.92**	94.92**	68.12	1.22**	6.65*	2176.74**	170	1.45**	1.49**	340	0.02**	0.31	0.04**
L*Loc	126	1.22**	95.72**	74.31	1.33**	6.88*	2404.72**	84	1.45**	1.73**	168	0.02**	0.32	0.04**
T*Loc	3	0.91	351.40**	45.41	1.40	4.17	4425.90*	2	0.91	0.08	4	0.03**	0.41	0.06*
L x T x Loc	126	0.61*	88.02*	62.48	1.10	6.47	1895.20**	84	1.47**	1.27**	168	0.02**	0.31	0.03**
Ck*Loc	3	1.30	279.28**	465.73	5.12	7.31	2196.97	2	1.02	2.22	4	0.01	0.03	0.09*
Cr vs Ck(Loc)	4	0.53	40.57	90.90*	1.36	4.99	1182.39	3	2.64	1.48	5	0.02	0.01	0.14**
Pooled Error	268	0.45	63.08	62.47	0.90	5.30	1151.41	201	0.59	0.70	335	0.01	0.28	0.02
% contr. GCA		60	77	80	83	57	76		89	86		78	83	77
% contr. SCA		40	23	20	27	43	24		11	14		22	17	23

4.2. Mean Performance of Genotypes

The results observed in individual locations suggested that, higher mean GY were obtained from Pawe (7.26 t/ha) and Melkasa (8.18 t/ha) while lower mean GY were obtained from Dhera (2.6 t/ha), Mieso (3.68 t/ha) and Ziway (4.3 t/ha) (Appendices 6-10). The low yield could be attributed to moisture stress in these areas. Even though Melkasa is a low moisture stress area, the genotypes had high grain yield as compared to the other locations, which could be attributed to the favorable rainfall amount and distribution received in the evaluation year. In line with the current finding, Zerihun (2011) reported high grain yield performances of maize varieties evaluated at Pawe and Melkasa at during the same season.

On average, the genotypes evaluated were late in anthesis and silking at Dhera, Melkasa and Ziway as compared to Pawe and Mieso. This is because these locations have relatively, lower temperature as the locations are situated at higher altitudes as compared to Pawe and Miesso (Appendices 6-10). Similar to the present results, Zerihun (2011) reported later anthesis and silking of maize varieties at Ziway and Melkasa, as compared to Pawe. Most of the crosses produced higher GY across locations also had taller PH and EH relative to the mean value of checks. These results agree with the findings of Zerihun (2011), who reported higher grain yields in late maturing and taller varieties.

In combined analysis across locations, mean GY of the genotypes were 4.85 t/ha ranging from 7.5 t/ha to 4.02 t/ha. Cross L23 x T2 (7.5 t/ha) followed by the crosses L24 x T2 (7.38 t/ha) and L41 x T2 (7.27 t/ha) had higher GY while crosses L14 x T2 (4.02 t/ha) and Melkasa-2 (4.25 t/ha) showed lower GY. AD ranged from 74.83 (L23 x T1) to 66 (L5 x T1) with overall mean of 71.18. Mean SD was 72.94 with a range of 76.8 (L14 x T2) to 67.3 (L5 x T1). PH ranged from 201.18 cm (L23 x T1) to165.1 cm (L5 x T1) with a mean of 187.18 cm while EH ranged from 117.45 cm (L30 x T2) to 74.7 cm (L9 x T2) with a mean of 96.72 cm (Table 13). Mean EPP of genotypes were 1.1 ranged from 0.8 (L32 x T1) to 1.4 (L15 x T2). TKWT ranged from 230.2 (L15 x T1) to 335.6 (L14 x T2) gm with overall mean of 283.47 gm. Mean RPE was 13.80 ranged from 12.5 (L5 x T1) to 15.5 (L3 x T2). Mean KPR was 33.8 with the lowest 28.63 (L21 x T2) and the highest 39.08 (L34 x T1) (Table 6).

A number of crosses showed better performances for more than one trait as compared to the best hybrid check used in the study. Therefore, crosses that had high grain yield could be used in the breeding program to improve the grain yield and other traits of interest. Similarly, hybrids that were 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. In agreement with the present results, a several investigators in their studies identified experimental varieties performing better than the best check for most yield and related traits (Dagne *et al*., 2010; Gudeta, 2007; Zerihun, 2011).

Table 6. Across location estimates of mean values for grain yield and related trait

Crosses	GY (t/ha)	AD(days)	SD(days)	PH (cm)	EH (cm)	EL (cm)	KPR (#)	EPP (#)	RPE (#)	ED (cm)	TKWT(gm)
L1 x T2	5.36	69.40	70.60	170.93	85.18	14.33	34.90	1.00	14.72	4.52	250.1
L2 x T2	5.84	67.53	69.43	190.80	88.45	15.10	35.45	1.18	13.96	4.52	296.4
L3 x T2	5.00	68.07	69.20	186.10	96.40	14.63	32.93	1.02	15.48	4.40	231.9
L4 x T2	5.31	71.67	73.97	195.63	99.05	15.43	34.98	0.96	13.80	4.44	278.1
L5 x T2	4.58	67.77	69.53	173.60	88.80	13.53	33.18	1.06	13.04	4.18	263.5
L6 x T2	5.21	72.90	74.63	196.03	103.53	15.43	35.30	1.00	13.52	4.36	261.5
L7 x T2	5.37	69.37	71.40	192.08	89.03	16.30	34.48	0.90	14.10	4.52	319.3
L8 x T2	5.70	68.83	70.87	179.53	83.70	15.15	31.98	1.04	13.40	4.18	295.2
L9 x T2	4.99	69.53	71.90	184.83	92.03	14.78	32.85	1.02	13.40	4.36	296.2
L10 x T2	5.99	72.60	74.43	184.8	99.25	15.75	34.40	1.08	14.28	4.34	247.1
L11 x T2	6.26	68.80	70.93	185.18	103.55	15.55	32.58	1.06	14.48	4.42	295.2
L12 x T2	5.41	71.77	73.47	181.15	90.98	13.75	33.53	1.26	13.14	4.16	251.1
L13 x T2	6.25	71.13	72.87	195.83	99.83	15.43	33.45	1.12	14.44	4.48	268.2
L14 x T2	4.02	74.63	76.80	181.60	103.08	15.13	32.63	0.94	13.44	4.42	335.6
L15 x T2	5.51	72.13	73.80	187.25	105.33	14.60	35.93	1.14	13.20	4.20	250.6
L16 x T2	5.54	71.63	73.43	184.75	95.20	14.85	31.68	1.10	14.34	4.40	293.6
L17 x T2	4.88	73.67	74.90	183.10	103.75	14.20	33.40	1.04	13.50	4.74	322.7
L18 x T2	4.87	70.87	73.27	181.13	92.90	15.05	34.55	1.06	13.64	4.32	278.1
L19 x T2	6.21	70.13	71.40	197.65	107.38	14.85	32.75	1.14	13.28	4.50	312.4
L20 x T2	5.52	70.50	73.27	193.93	101.63	14.73	31.40	0.98	14.24	4.64	294.5

Table 6 (Continued)

L21 x T2	6.33	69.83	72.40	191.28	105.30	13.20	28.63	1.06	13.90	4.62	294.0
L22 x T2	6.40	68.23	69.53	181.83	99.23	14.85	33.65	1.08	13.88	4.64	300.4
L23 x T2	7.50	73.37	74.90	187.20	100.48	15.85	36.28	1.16	13.28	4.56	289.6
L24 x T2	7.38	74.43	75.73	195.98	98.03	15.55	34.23	1.14	13.38	4.40	269.2
L25 x T2	6.90	73.07	74.40	191.53	98.48	15.48	36.80	1.18	13.04	4.44	245.9
L26 x T2	5.67	72.03	73.93	178.05	93.58	14.98	32.40	1.02	14.64	4.58	256.9
L27 x T2	6.38	71.93	74.13	198.55	96.08	15.30	35.35	1.00	13.08	4.50	286.8
L28 x T2	6.14	70.60	72.37	193.53	98.10	15.05	31.70	1.12	13.52	4.42	305.0
L29 x T2	6.25	72.60	74.03	193.05	105.33	16.08	34.10	1.20	14.04	4.36	276.6
L30 x T2	6.49	74.07	76.20	192.95	117.45	16.18	35.50	1.02	13.32	4.44	268.5
L31 x T2	5.84	70.83	72.73	186.68	94.45	15.53	35.23	1.00	13.76	4.38	289.1
L32 x T2	6.12	70.43	72.30	191.00	97.65	16.13	34.03	1.04	14.40	4.56	269.2
L33 x T2	6.78	71.40	73.47	190.08	98.10	17.83	37.40	1.02	13.80	4.48	273.2
L34 x T2	4.82	74.23	76.37	176.38	93.18	16.78	33.63	1.02	12.96	3.94	273.8
L35 x T2	4.78	74.27	76.23	182.23	94.43	17.50	35.95	1.00	13.40	4.06	305.3
L36 x T2	6.48	72.33	74.40	194.83	96.38	17.18	35.35	1.02	15.08	4.74	269.9
L37 x T2	6.29	70.30	71.77	175.03	92.55	16.50	37.25	1.06	13.80	4.38	309.6
L38 x T2	5.36	73.63	75.30	183.60	97.55	14.43	30.43	1.08	14.12	4.26	292.4
L39 x T2	5.89	73.27	75.07	185.20	97.03	17.00	34.9	1.08	13.86	4.32	301.7
L40 x T2	5.28	73.07	74.83	184.45	108.05	16.03	35.15	1.00	14.08	4.38	275.8
L41 x T2	6.49	73.00	73.93	188.38	88.98	16.78	35.73	1.04	12.98	4.48	327.1

Table 6 (Continued)

L42 x T2	6.00	72.53	73.70	186.83	103.08	15.95	35.83	1.04	13.84	4.20	278.7
L43 x T2	6.44	70.43	71.90	187.15	97.68	15.50	35.05	1.04	13.72	4.48	262.4
L1 x T1	5.91	68.13	69.70	175.45	93.73	13.83	31.85	1.18	14.34	4.48	253.2
L2 x T1	6.21	67.23	69.17	191.05	85.18	14.95	32.55	1.06	14.28	4.58	302.7
L3 x T1	5.70	68.43	70.20	178.53	96.23	15.75	35.88	1.00	15.12	4.4	258.1
L4 x T1	6.25	69.43	71.50	194.00	90.18	15.78	35.35	0.94	13.18	4.42	290.2
L5 x T1	5.42	66.00	67.30	165.10	79.25	14.20	32.98	1.02	12.48	4.32	282.8
L6 x T1	5.59	73.27	74.80	196.85	107.95	14.88	33.30	1.02	14.84	4.52	248.1
L7 x T1	6.75	67.10	69.37	177.78	88.03	16.48	36.93	0.94	13.60	4.58	322.7
L8 x T1	5.19	67.30	68.60	165.43	74.70	15.73	33.55	1.04	13.36	4.18	272.9
L9 x T1	5.48	70.00	73.13	186.15	98.03	14.58	32.10	1.04	13.80	4.46	269.0
L10 x T1	6.20	72.13	74.13	192.88	105.83	15.00	35.03	1.06	14.38	4.46	256.7
L11 x T1	5.78	68.07	69.57	190.40	101.05	15.70	34.65	1.10	14.04	4.34	300.6
L12 x T1	5.19	73.43	74.77	183.00	90.15	13.38	30.90	1.18	13.40	4.28	281.2
L13 x T1	7.02	69.97	72.03	200.83	97.73	15.98	35.08	1.12	15.24	4.64	267.6
L14 x T1	5.88	72.80	73.77	195.18	99.33	15.10	31.00	0.96	14.14	4.64	280.2
L15 x T1	5.52	70.43	72.83	184.83	99.00	15.25	37.20	1.16	13.32	4.36	230.2
L16 x T1	4.81	70.77	72.97	190.30	95.78	14.83	34.30	1.04	14.28	4.54	268.5
L17 x T1	6.75	71.73	73.23	194.08	102.90	14.80	33.68	1.06	13.62	4.76	301.1
L18 x T1	5.96	69.50	71.40	177.28	84.40	14.85	35.75	1.04	13.76	4.54	295.1
L19 x T1	5.24	71.30	72.70	194.40	95.60	14.03	28.85	1.06	13.36	4.56	276.4

Table 6 (Continued)

L20 x T1	5.46	71.67	73.27	186.68	96.70	14.08	29.30	1.02	13.92	4.46	284.7
L21 x T1	6.73	70.27	71.80	191.13	104.95	14.73	32.25	1.06	13.80	4.72	322.3
L22 x T1	5.36	69.30	70.80	186.23	105.83	15.43	31.10	1.08	13.68	4.52	276.8
L23 x T1	7.04	74.83	76.30	201.18	102.88	15.68	34.20	1.10	13.52	4.56	291.0
L24 x T1	6.46	72.97	74.33	199.33	96.33	15.60	34.60	1.14	13.22	4.52	315.7
L25 x T1	6.32	74.30	76.10	199.65	108.03	14.85	32.43	1.12	12.82	4.26	274.0
L26 x T1	6.44	70.67	72.30	182.53	92.38	15.30	35.55	1.00	14.32	4.80	312.1
L27 x T1	6.67	71.70	73.70	189.70	95.63	16.08	35.95	1.04	13.24	4.62	277.1
L28 x T1	6.00	69.87	71.60	187.13	98.98	15.33	33.75	1.04	13.64	4.48	291.7
L29 x T1	6.48	72.47	74.23	200.00	108.65	15.63	34.30	1.10	15.04	4.64	272.0
L30 x T1	7.11	72.77	74.47	194.93	106.15	16.30	34.88	1.04	13.60	4.56	293.5
L31 x T1	6.10	69.43	71.07	182.00	84.48	15.25	34.43	1.02	13.76	4.48	291.7
L32 x T1	4.38	73.43	75.17	178.50	85.75	14.10	29.20	0.96	14.28	4.30	242.8
L33 x T1	4.42	73.27	75.67	183.35	82.63	14.18	31.18	1.02	13.88	4.24	243.2
L34 x T1	6.28	70.97	72.40	189.85	95.45	17.15	39.08	1.16	13.86	4.34	288.5
L35 x T1	5.44	72.40	74.43	184.90	93.53	16.35	36.03	1.10	14.20	4.28	267.0
L36 x T1	5.04	71.83	73.90	183.20	90.88	14.63	32.00	1.04	14.24	4.46	256.3
L37 x T1	5.81	69.60	71.57	167.85	80.13	15.83	32.85	1.06	13.70	4.34	292.2
L38 x T1	5.84	72.60	73.67	190.30	101.70	15.53	34.13	1.04	14.16	4.56	307.5
L39 x T1	5.54	72.70	74.47	193.13	111.93	17.15	34.83	1.12	13.32	4.34	314.2
L40 x T1	6.03	72.10	73.20	192.20	100.90	14.35	32.68	1.02	14.16	4.60	288.2

Table 6 (Continued)

L41 x T1	7.27	71.17	73.17	197.28	99.40	15.48	32.00	1.14	13.6	4.52	326.8
L42 x T1	6.88	70.13	71.33	177.70	96.53	16.53	36.50	1.04	13.46	4.32	298.8
L43 x T1	5.65	72.03	73.43	187.13	91.65	14.40	30.80	1.06	13.12	4.44	298.8
BH-543	5.88	73.67	75.33	188.75	102.43	17.40	35.90	0.98	14.44	4.36	293.1
Melkasa-	4.25	68.20	70.00	182.58	92.23	14.85	33.45	1.06	13.96	4.38	307.2
Cr mean	5.88	71.19	72.94	187.22	96.70	15.34	33.85	1.10	13.80	4.40	283.08
Ck mean	5.07	70.93	72.67	185.66	97.32	16.12	34.67	1.00	14.2	4.40	300.2
Mean	4.85	71.18	72.94	187.18	96.72	15.36	33.88	1.10	13.8	4.40	283.5
LSD (5%	1.87	2.14	2.33	22.11	22.00	2.64	6.41	0.30	1.50	0.40	89.3
CV	19.6	1.50	1.60	6.00	11.50	8.70	9.60	12.90	5.40	4.50	16.9
Min	4.25	66.00	67.30	165.10	54.70	13.20	28.63	0.90	12.50	3.90	227.2
Max	7.50	74.83	76.80	201.18	117.45	17.83	39.08	1.30	15.50	4.80	323.1

AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, RPE = Number of rows per ear, SD = number of days to silking, TKWT = thousand kernels weight

4.3. Combining Ability Analysis

Significant differences were observed among test crosses for grain yield at all individual locations and combined across four locations. The partitioning of significant crosses mean squares into general combining ability (GCA) and specific combining ability (SCA) showed that SCA mean squares to be significantly different for grain yield at most individual locations except at Mieso (Appendices 6-10). In combined analysis, significant GCA and SCA mean squares were observed for grain yield (Table 5). Line GCA means squares were significantly different for grain yield at Melkasa, Dhera, Mieso and Pawe (Appendices 1-5) and combined across locations (Table 5) while tester GCA mean squares were significant only at Dhera and Pawe. Significant GCA and SCA mean squares implied the importance of both additive and non-additive gene actions in governing grain yield. In agreement with 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. Mandefro (1999), Mandefero and Habtamu (2001), Dagne *et al*. (2007, 2010) and Demissew *et al*. (2011) have also reported the importance of both additive and non-additive gene actions in governing grain yield in maize. On the other hand, Bayisa (2004) found non-significant GCA effects for grain yield in line x tester study of transition highland inbred lines at Kulumsa. Gudeta (2007) carried out line x tester analysis of QPM versions of early generation highland maize inbred lines and reported significant GCA mean squares due to lines at Holeta and Kulumsa but non-significant at Ambo and Haramaya. He also found highly significant GCA mean squares for grain yield due to testers and line x tester interactions at all locations. Similarly Legesse *et al*. (2009) reported significant GCA mean squares due to lines and testers and significant SCA mean squares for grain yield. Pswarayi and Vivek (2008) carried out diallel analysis among CIMMYT’s early maturing maize grmplsam and reported significant GCA mean squares and non-significant SCA mean squares for grain yield indicating that the importance of both additive and non-additive gene action for this trait.

GCA sums of squares were larger than SCA sums of squares for GY at Melkasa (55%), Dhera (57%), Mieso (59%) and Pawe (77%) and when combined across the four locations (60 %) while SCA sums of squares were larger for GY (52%) at Ziway (Tables 5-10). The predominance of GCA sums of squares to SCA sums of squares for GY at most locations indicated the relative importance of additive gene action to non-additive gene action for this trait (Beck *et al*. 1990). In line with this study Pswarayi and Vivek (2008), and Legesse et al.

(2009) reported the preponderance of additive gene action in the inheritance of grain yield while in contrast to these findings, Bhatnagr *et al.* (2003) and Dagne *et al.* (2007) previously reported dominant role of SCA gene action in the grain yield of maize.

Mean squares due to crosses for anthesis and silking date were highly significant ($P < 0.001$). Line GCA and SCA mean squares were significant for anthesis and silking date at all locations and across three locations (Tables 5-10). Results of this study are in accordance with the findings of Ahmad and Saleem (2003) who reported significant mean squares due to GCA and SCA for days to anthesis and silking. Tester GCA mean squares were significant at Melkasa, Ziway, Pawe and across three locations while it was not significant at Dhera and Mieso (Tables 5-10). In line with this study Gudeta (2007) reported significant GCA effects due to testers at Ambo and Holeta but non-significant GCA effect due to tester at Kulumsa and Haramaya.

GCA sums of squares were larger than SCA sums of squares for anthesis and silking dates at all locations (Appendices 1-5) and across three locations (Table 5). The predominance of GCA sums of squares to SCA sums of squares for these traits indicate the relative importance of additive gene action to non-additive gene action for the inheritance of these traits. In line with this study Ahmad and Saleem (2003) reported the preponderance of additive gene action in the inheritance of days to anthesis and days to silking. Legesse *et al.* (2009) reported the predominance of additive gene action in inheritance of days to silking.

Mean squares due to crosses were significant for ear and plant heights across four locations and at all individual locations (Appendices 1-5) except for ear height, which showed non-significant mean square at Melkasa. Combining ability analysis revealed highly significant GCA effects of lines for plant and ear height except at Mieso for plant height. On the other hand, tester GCA and SCA mean squares were significant at all locations except at Melkasa, Ziway (Appendices 1-5) and in combined analysis across four locations (Tables 5). Tester GCA and SCA mean squares were significant for ear height at Dhera (Appendix 3) and Pawe (Appendix 5) and also in combined analysis across four locations (Table 5). In line with these findings, Gudeta (2007) reported significant GCA and non-significant SCA mean squares for plant height. However, Hadji (2004), Dagne *et al.* (2010) and Demissew *et al.* (2011) found significant GCA and SCA mean squares for plant and ear height.

GCA sums of squares were larger than SCA sums of squares for plant height and ear height across four locations (Table 5) and at all locations except for ear height at Mieso (Appendices 1-5). Similar to the present findings Glover *et al*. (2005)and Dagne *et al*. (2007) reported the preponderance of additive gene action in the inheritance of plant height.

Mean squares due to crosses for number of ears per plant were significant only at Melkasa (Appendix 1) and Ziway (Appendix 2) while mean square due to SCA for the same trait was non-significant in all locatons (Appendices 1-5). Similar to the finding of the current study, Mandefro (1999), and Pswarayi and Vivek (2008) reported that non-additive gene action is not important in controlling number of ears per plant. Mean squares due to line GCA and tester GCA for number of ears per plant were significant only at Melkasa (Appendix 1). Similar to the current findings, Gudeta (2007) reported significant and non-significant mean squares due to tester GCA.

GCA sums of squares were larger than SCA sums of squares for number of ears per plant at all locations except Pawe (Appendices 1-5). In contrast to present findings Pswarayi and Vivex (2008) reported the preponderance of non additive gene action in the inheritance of number of ears per plant.

Significant differences were observed among crosses for thousand-kernel weight at all locations except at Ziway (Appendices 1-5) and across the five test locations (Table 5). Tester GCA and SCA mean squares were significant for thousand-kernel weight at Dhera and Mieso while line GCA mean squares were significant at Melkasa, Dhera, Mieso, Pawe (Appendices 1-5) and combined across the five locations (Table 5). In agreement with the present results, Amiruzzaman *et al*. (2010), and Malik *et al*. (2004) and Dagne *et al*. (2007) reported significant mean squares due to GCA and SCA for thousand-kernel weight while Gudeta (2007) reported non-significant SCA mean squares.

Mean squares due to crosses for number of kernels per row were significant at all locations (Appendices 1-5) and across four locations (Table 5). For number of kernels per row, mean squares due to line GCA were non-significant at Mieso but significant at the remaining four locations and across four locations while the mean square due to tester GCA was highly significant at Ziway but non-significant at the remaining four locations and across four locations where as mean squares due to SCA were significant at Melkasa and Mieso

(Appendices 1-5) and across four locations (Table 5) implying different genetic expressions at different locations. The current result is similar to the works of Dagne *et al*. (2007) and Hadji (2004) who reported the importance of both GCA and SCA at some locations**.** Even though, mean squares due to line GCA, tester GCA and SCA were variable at different locations both additive and non-additive gene actions would have involved in the inheritance of kernel rows per ear, which is in agreement with the work of Yoseph (1998). Based on across site result, both mean squares due to line GCA and SCA were highly significant for number of kernels per row (Table 10) and hence both additive and non-additive gene actions might have involved in the inheritance of this trait.

Analysis of variance further indicated that mean squares due to crosses and line GCA were significant for ear length at all locations (Appendices 1-5) and combined across four locations (Table 5). This result is in line with the findings of Dagne *et al*. (2007), who reported significant mean squares due to GCA for ear length. Mean square due to tester GCA was highly significant at Ziway but not at other locations and also non-significant across locations where as mean squares due to SCA were significant at Mieso and across locations but not at the other locations (Appendices 1-5). Similar results were previously reported by Gudeta (2007), who reported significant tester GCA mean squares at one location among the four test locations but non-significant tester mean squares at the other three locations. On the other hand, Mandefro (1999) reported that non-additive gene action is not important for ear length. On the other hand, Dagne *et al*. (2007) confirmed the importance of additive gene action in controlling ear length.

For number of rows per ear, mean squares due to line GCA was highly significant at all locations and across locations but tester GCA was not significant at all locations and across locations except at Mieso. Mean square due to SCA for the same trait was significant at Dhera, Pawe and across locations but not at Melkasa, Ziway and Mieso (Table 5) and (Appendices 1-5), which confirm the findings of Khotyleva and Tarutina (1973) who concluded that expression of genetic variances depends on the location in which the material has been evaluated. In the current study, even though inconsistencies of mean squares were observed at different locations, the importance of both additive and non-additive genetic components was clearly observed. The present results are in line with the findings of Kalla *et al*. (2001) and Gudeta (2007), who found additive and non-additive gene actions in the inheritance of number of rows per ear.

For ear diameter, mean square due to line GCA was highly significant at Melkasa, Ziway, Dhera and Pawe and across locations (Table 5) and (Appendices 1-5). Mean square due to tester GCA was significant at Pawe, Melkasa and across locations but not significant at Ziway and Dhera (Table 5) and (Appendices 1-5). Mean square due to SCA was significant at Melkasa, Dhera, Pawe and across locations but not at Ziway (Tables 5) and (Appendices 1-5). In line with the current findings, Khotyleva and Tarutina (1973) reported that variability of genetic variances in different locations. Even though inconsistence of mean squares were observed at different locations in current study, the importance of both additive and non-additive genetic components were observed to responsible for ear diameter. The present result is in line with the findings of Jemal (1999), Hadji (2004), Dagne *et al*. (2007) and Gudeta (2007).

Knowledge of the genetic control of characters is essential to the breeder when deciding on the selection method and breeding procedure to follow (Acquaah, 2007). In the present study, significance of mean squares due to GCAs of lines and testers, and SCA of crosses for the traits, indicate the role of additive and non-additive gene action in the inheritance of these characters. This has breeding implications, since hybridization methods such as multiple crossing and/or reciprocal recurrent selection, which utilizes both additive and non-additive gene effects simultaneously, could be useful in genetic improvement of the characters under consideration. However, GCA sum of squares components were greater than SCA sum of squares for most of the studied traits, suggesting that variations among crosses were mainly attributed to additive rather than non-additive gene effects. Several studies involving the inheritance of various quantitative traits in maize have revealed the importance of additive gene action (Vacaro *et al.*, 2002; Vasal *et al.*, 1992a; Betran *et al.*, 2003; Shewangizaw, 1985). Hence these parents can be crossed to develop high-yielding composites and synthetics that can be used directly or for further breeding work.

Combined analysis of variance and combining ability effects across locations further indicated that entry and cross by environment interactions were highly significant ($P < 0.01$) for all traits except for number of rows per ear and ear height (Table 5). Partitioning of the cross by environment interactions (Cr x Loc) sum of squares into GCA by environment (GCA x loc) and SCA by environment (SCA x loc) showed that line GCA x loc effects were significant for all traits except for number of kernels row per ear and ear height, tester GCA x loc were non-significant for grain yield, ear length, number of kernels per row, days to anthesis and silking and SCA x loc were significant for grain yield, plant height, number of ears per plant, ear diameter, thousand kernel weight, days to anthesis and silking (Table 10). Significant line GCA x loc interactions indicates the variation of inbred line for their GCA effects under different environments and the need for selecting different parental inbred lines for specific location, whereas non-significant tester GCA x loc interactions for five traits above is an indication of similarity in general combining ability of testers under different environments. Significant SCA x loc interactions for the above seven traits suggesting that different hybrids are required for different locations. In line with the current study, Pixley and Bjarnason (1993) observed significant interaction of GCA and SCA with environments in diallel study of QPM inbred lines. Teshale (2001) reported significant mean squares due to female GCA x location for grain yield, thousand kernel weight and plant height and significant mean squares due to tester GCA x location for grain yield, ear diameter, thousand kernel weight, and plant height. He also found significant SCA x location mean squares for grain yield and some yield related traits. Similarly, Jemal (1999) reported significant mean squares due to interaction of GCA x location and SCA x location for grain yield and most of yield related quantitative traits. Similarly Dagne *et al.* 2010 found significant mean squares due to GCA x location for grain yield, days to anthesis and silking and plant height but found non-significant mean squared due to SCA x location for all traits. In line with the present results, Pswayari and Vivek (2008) reported significant GCA x location and SCA x location for grain yield, plant height, days to anthesis and number of ears per plant. In contrary to present findings, Bayisa (2004) reported non-significant mean squares due to both interaction of female GCA x location and male GCA x location for grain yield, ear height and ear length. In the present study, significant interaction of genotype and cross with the location suggests that the crosses (genotypes) reacted differently to different environments.

4.3.1. General combining ability estimates

General combining ability effects of grain yield and related agronomic traits are presented for individual locations (Appendices 11-15) and combined across locations (Table 7).

Grain yield

At Melkasa, line GCA effects for grain yield ranged between -1.65 t/ ha (L14) to 1.96 t/ ha (L23) (Appendix 11). Even though a total of 18 lines showed positive GCA effects for grain yield, only five inbred lines (L21, L23, L24, L37 and L41) were found to be the best general combiners for grain yield as these lines had positive and significant GCA effects. These inbred lines are desirable parents for hybrid development as well as for inclusion in the breeding program, as the lines may contribute favorable alleles in the synthesis of new varieties. Inbred lines with negative and significant GCA effects were L6, L9, L14 and L16, indicating that these lines were poor general combiners for grain yield (Appendix 11).

Inbred parents L2 and L37 had higher GCA effects for grain yield (1.22 and 0.92 t/ha, respectively) at Dhera (Appendix 13). Although, 22 inbred lines showed positive GCA effects while only two inbred lines had significant GCA effects, indicating that these lines were good general combiners for high grain yield at this specific location. Four inbred lines such as L32 (-1.18), L33 (-0.63), L38 (-0.73) and L42 (-0.68) exhibited significant and negative GCA values suggesting that the lines were poor general combiners for grain yield.

At Mieso, L13 and L41 had higher GCA effects for grain yield (1.63 and 1.53 t/ha, respectively) and L38 and L11 had lower GCA effects for the same trait (-0.81 and -0.78 t/ha, respectively) (Appendix 14). Even though, 17 inbred lines had positive GCA effects for grain yield, only four, L2 (0.80 t/ha), L13 (1.63 t/ha), L21 (0.80 t/ha) and L41 (1.53 t/ha), showed significant GCA effects.

At Pawe, L30 (3.41 t/ha) and L23 (2.85 t/ha) had higher GCA effects whereas L12 (-2.69 t/ha) and L33 (-1.72 t/ha) had lower GCA effects for grain yield. A total of 17 lines expressed positive GCA estimates among which 10 lines (L13, L23, L24, L25, L27, L28, L30, L31, L38 and L42) showed significant GCA effects. On the other hand nine inbred lines (L39, L35, L32, L18, L12, L8, L5, L2 and L33) exhibited significantly-negative GCA effects for grain yield (Appendix 15).

In combined analysis across four locations, 18 inbred lines showed positive GCA effects for grain yield. Ten inbred lines (L13, L23, L24, L25, L27, L29, L30, L41 and L42) showed positive and significant GCA effects indicating the potential advantage of the inbred lines for the development of high-yielding hybrids. L23 (1.4 t/ha) followed by L24 (1.04) had higher GCA effects. Ten inbred lines (L3, L5, L6, L9, L12, L14, L16, L18, L32 and L35) were poor general combiners for grain yield as they showed negative and significant GCA effects for grain yield (Table 7). Results of the current study are in accordance with the findings of Amiruzzaman *et al*. (2010), Legesse *et al*. (2009), Gudeta (2007), Hadji (2004) and Dagne *et al*. (2007) who reported significant positive and negative GCA effects for grain yield in maize germplasm. Lines with positive GCA effects for grain yield can be extensively used in hybridization program as they contribute favorable alleles in the development of high yielding varieties.

Days to anthesis and Silking

At Melkasa, line GCA effects for days to anthesis ranged between -4.63 days (L2) to 2.37 days (L14, L35). Among 17 inbred lines with negative GCA effects, twelve inbred lines had significant GCA effects (Appendix 11), indicating that the inbred lines had gene combinations that enhance early maturity. Fifteen inbred lines exhibited positive and significant GCA effects for days to anthesis, indicating that the inbed lines had the tendency to increase late maturity.). L14 had higher GCA effect for number of days to silking (3.39 days) and L2 had lower GCA effect (-4.81 days) for the same trait. A toal of 27 inbred lines showed positive GCA effects, among which 13 inbred lines had significant GCA effects for days to silking and 11 inbred lines exhibited significant and negative GCA effects for the same trait; hence, the inbred lines had the tendency to increase early maturity. Inbred lines L1, L2, L3, L5, L7, L8, L11 and L22 were the best general combiner for early maturity as they showed the tendency to increase early flowering and silking.

At Ziway, line GCA effects for days to anthesis ranged between -4.18 days (L7) to 4.12 days (L23). Among 23 inbred lines which showed negative GCA effects, 12 inbred lines had significantly negative GCA effects for days to anthesis, indicating that the lines were good general combiners for early maturity. Sixteen inbred lines exhibited significantly positive GCA effects for days to anthesis. L25 had higher GCA effect (3.61 days) and L5 had lower GCA effect (-4.24 days) for days to silking. Twenty-two inbred lines showed positive GCA effects among which 11 inbred lines had significant GCA effects for days to silking. Eight inbred lines exhibited significant and negative GCA values for days to silking. L1, L2, L3, L5, L7, L8, L11 and L22 were the best general combiners for early maturity (Appendix 12).

At Dhera, line GCA effects for days to anthesis ranged between -5.99 days (L8) to 3.51 days (L14). A total of 18 inbred lines showed negative GCA effects among which nine inbred lines (L1, L2, L3, L5, L7, L8, L9, L11 and L22) had significant GCA effects for days to anthesis. Ten inbred lines exhibited significantly positive GCA effects for the same trait (Table 16). L25 and L23 had higher GCA effects (3.61 and 3.01 days), respectively and L2 had lower GCA effect for days to silking (-5.29 days). Among 25 inbred lines that showed positive GCA effects, nine inbred lines had significant GCA effects. Eight inbred lines (L1, L2, L3, L5, L7, L8, L11 and L9) exhibited significantly negative GCA effects for days to silking (Appendix 13).

At Mieso, L20 had higher positive GCA effects (3.82 days) and L2 had higher negative GCA effects (-4.98 days) for days to anthesis. Even though 23 inbred lines showed negative GCA effects for days to anthesis, only six inbred lines (L1, L2, L3, L5, L13 and L22) had significant GCA effects. On other hand, only seven inbred lines (L20, L24, L25, L34, L35, L38 and L39) exhibited significantly positive GCA effects for days to anthesis (Table 17). L34 had higher GCA effect for number of days to silking (5.62 days) whereas L2 had lower GCA effect (-5.63 days). Among 19 inbred lines showed positive GCA effects for days to silking among which 10 inbred lines (L34, L35, L20, L38, L32, L39, L25, L33, L24 and L30) had significant GCA effects. Six inbred lines such as L1, L2, L3, L5, L13 and L21 exhibited significantly negative GCA values for days to silking (Appendix 14).

At Pawe, L24 and L23 had higher positive GCA effects (3.39 and 2.89 days, respectively) and L5 and L2 had lower GCA effects for days to anthesis (-5.06 and -3.36 days, respectively). Twenty inbred lines showed negative GCA effects among which 15 inbred lines had significant and negative GCA effects whereas 16 inbred lines exhibited significantly positive GCA effects for days to anthesis. Inbred lines, L24 and L23 had higher GCA effects of 3.07 and 2.92 days, respectively while L5, L3,L9 and L11 had lower GCA effects for days to silking (-4.88, -3.18 and -3.13 days, respectively). Among 22 inbred lines which showed positive GCA effects, 21 inbred lines had significant GCA effects while 17 inbred lines exhibited significantly negative GCA effects for days to silking.

Line GCA effects for days to anthesis ranged between -4.31 days (L5) to 2.91 days (L23) in combined analysis across three locations. Eighteen inbred lines showed negative GCA effects among which 16 inbred lines had significant GCA effects for days to anthesis, indicating that these lines were good general combiners for early maturity while 20 inbred lines exhibited significant and positive GCA effects for days to anthesis, indicating that these lines were undesirable as they show the tendency to increase late maturity. In combined analysis across three locations, L23 had higher GCA effect for days to silking (2.66 days) whereas L5 had lower GCA effect (-4.53 days). Among 25 inbred lines which showed positive GCA effects, 19 inbred lines had significant GCA effects for days to silking while 13 inbred lines exhibited significant and negative GCA effects for days to silking. L1, L2, L3, L5, L7, L8, L11, L22, L28, L31 and L37 were the best general combiners for early maturity (Table 7).

These results are in agreement with Gudeta (2007) and demissew *et al*. (2011) who reported significant positive and negative line and tester GCA effects for days to anthesis and silking. Similar findings were also reported by Dagne *et al*. (2010) and Teshale (2001).

Plant and ear height

At Melkasa, line GCA effects of plant height ranged between -29.05 (L1) to 20.1 (L23). Even though a total of 25 inbred lines showed positive GCA effects, only five inbred lines (L4, L19, L23, L27, and L30) showed significant GCA effects while six inbred lines (L1, L3, L5, L7, L12 and L16) showed significant and negative GCA effects for plant height, indicating the inbred lines were good general combiners for shorter plant stature (Appendix 11).

At Ziway, line GCA effects for plant height ranged between -29.64 cm (L5) to 16.36 cm (L19). Even though a total of 25 inbred lines showed positive GCA effects, only two inbred lines (L19, L13) showed significant GCA effects for tallness while four inbred lines (L1, L5, L8, and L37) showed significant GCA effects for shortness of plant height (Table 15). Line GCA effects for ear height ranged between -22.41 cm (L8) to 16.24 cm (L17). Among a total of 22 inbred lines that showed positive GCA effects for ear height, only five inbred lines (L6, L17, L19, L22 and L39) showed significant GCA effects. On other hand, only four inbred lines (L2, L5, L8, and L31) showed significantly negative GCA effects for ear height (Appendix 12) hence desirable GCA effects for ear height as short plants are less prone to lodging.

At Dhera, line GCA effects for plant height ranged between -20.94 cm (L37) to 13.46 cm (L20). A total of 22 inbred lines showed positive GCA effects but only three inbred lines (L6, L20, and L39) showed significant GCA effects for tallness. Four inbred lines (L5, L8, L36, and L37) showed significant and negative GCA effects for shortness of plant height. Line GCA effects for ear height ranged between -20.98 cm (L8) to 17.47 cm (L30). Among 22 inbred lines which showed positive GCA effects for ear height, only four inbred lines (L3, L10, L20, and L30) showed significant GCA effects for ear height (least desirable). On other hand, only five inbred lines (L4, L8, L26, L33 and L36) showed significantly negative GCA effects for ear height (Appendix 13).

At Mieso, line GCA effects for ear height ranged between -14.45 cm (L12) to 12.75 cm (L30). Even though 21 inbred lines expressed positive GCA effects for ear height, only four inbred lines (L14, L21, L23, and L30) showed significant GCA effects. On other hand, four inbred lines (L1, L7, L12, and L37) showed significantly negative GCA effects for ear height.

At Pawe, line GCA effects for plant height ranged between -25.32 cm (L1) and 18.73 cm (L24). A total of 23 inbred lines showed positive GCA effects among which 16 inbred lines showed significant GCA effects for plant height, indicating that these lines had a tendency to increase tallness. On other hand, 16 inbred lines showed significant and negative GCA effects for plant height, indicating a tendency to increase shortness in plant height. Line GCA effects for ear height ranged between -17.93 cm (L8) to 18.77 cm (L30). Among the 21 inbred lines that showed positive GCA effects, 12 inbred lines had significant GCA effects for ear height (least desirable). On other hand, 17 inbred lines showed significant and negative GCA effects for ear height (Appendix 15).

Even though 20 inbred lines showed negative GCA effects for plant height in combined analysis across locations (Table 19), only six inbred lines (L1, L5, L8, L18, L26 and L37) showed significant GCA effects, implying the tendency of these lines to reduce plant height. Among all, 11 inbred lines (L4, L6, L13, L30, L19, L23, L24, L25, L27, L29 and L41) were the poor general combiners for plant height as they showed positive and significant GCA effects. For ear height, 22 inbred lines showed negative GCA effects among which nine inbred lines (L1, L2, L5, L7, L8, L18, L31, L33 and L37) showed significant GCA effects for ear height (Table 7) suggesting that these inbred lines were good general combiners for shorter plant stature.

In line with the present study Dagne *et.al* (2010), Demissew *et al.* (2011) and Hajji (2004) found significant positive and negative GCA effects for plant and ear height.

Number of ears per plant

For this trait, 16 inbred lines showed positive GCA effects among which seven inbred lines (L12, L21, L23, L24, L25, L29 and L34) had significant GCA effects. L12 had higher positive and significant GCA effect for number of ears per plant (0.39) hence it was the best general combiner for prolificacy. On the other hand, five inbred lines (L3, L5, L7, L9, L14 and L16) showed significantly negative GCA effects for the same trait. L7 had the smallest GCA effect of -0.21 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.

Number of rows per ear

At Melkasa, line GCA effects for number of rows per ear ranged between -0.92 (L19, L41) and 1.98 (L3). Even though a total of 18 inbred lines showed positive GCA effects, only four inbred lines (L1, L3, L29 and L36) had significant GCA effects hence they were good general combiners for high number of rows per year. Three inbred lines (L12, L19 and L41) exhibited significant and negative GCA effects for number of rows per ear (Appendix 11).

At Ziway, L3 had higher GCA effect for number of rows per year (2.03). L4 had lower GCA effect for number of rows per year (-1.77). Even though a total of 20 inbred lines showed positive GCA effects, only five inbred lines (L3, L10, L13, L26 and L32) had significant GCA effects for number of rows per year. Two inbred lines (L4 and L5) exhibited significantly negative GCA effects for number of rows per year (Appendix 12).

At Dhera, L3 and L29 showed higher GCA effects for number of rows per ear (1.49). L5 had lower GCA effect for the same trait (-1.81). Among 17 inbred lines that showed positive GCA effects, eight inbred lines (L1, L3, L6, L13, L29, L32, L36 and L38) had significant GCA effects. Five inbred lines (L5, L8, L22, L25, and L42) showed negative and significant GCA effects for number of rows per ear (Appendix 12).

At Mieso, L13 had higher GCA effects for number of rows per ear (1.15). L25 had lower GCA effects for the same trait (-1.4). Even though a total of 23 inbred lines showed positive GCA effects, only one inbred line (L13) had significant GCA effect. Three inbred lines (L23, L18 and L25) exhibited significantly negative GCA effects for number of rows per ear.

At Pawe, L3 had higher GCA effects for number of rows per ear (1.25). L27 had lower GCA effect for the same trait (-1.65). A total of 24 inbred lines expressed positive GCA effects among which nine inbred lines (L3, L10, L11, L13, L16, L26, L29, L36 and L40) had significant GCA effects. Six inbred lines (L5, L17, L19, L24 L27 and L34) exhibited significantly negative GCA values for number of rows per ear.

In combined analysis across locations, 18 inbred lines showed positive GCA effects among which 11 inbred lines had significant GCA effects. Inbred lines, L1, L3, L10, L13, L16, L26, L29, L32 and L36 were the best general combiners for number of rows per ear as they showed significant and positive GCA effects (Table 19) (Table 7). These results were in agreement with the investigations of Dagne *et al.* (2007), Hadji (2004) and Mandefro (1999).

Number of kernels per row

At Melkasa, line GCA effects for number of kernels per row ranged between -4.68 (L20) to 5.02 (L4). Even though a total of 23 inbred lines showed positive GCA effects for number of kernels per row, only four inbred lines (L4, L25, L27 and L42) had significant GCA effects. Four inbred lines (L14, L19, L20 and 41) exhibited significantly negative GCA effects for number of kernels per row.

At Ziway, line GCA effects for number of kernels per row ranged between -3.02 (L16, L22) and 3.93 (L34). Even though 22 inbred lines showed positive GCA effects for number of kernels per row, only one inbred line (L34) had significant GCA effect. None of the inbred lines exhibited significant and negative GCA effects for number of kernels per row.

At Dhera, line GCA effects for number of kernels per row ranged between -6.16 (L21) to 5.44 (L15). Even though 24 inbred lines showed positive GCA effects for number of kernels per row, only two inbred lines (L15 and L41) had significant GCA effects. Four inbred lines (L14, L21, L22 and L32) exhibited significantly negative GCA effects for number of kernels per row.

At Pawe, line GCA effects for number of kernels per row ranged between -4.33 (L2) to 6.17 (L4). Among 22 inbred lines with positive GCA effects, only eight (L4, L15, L16, L24, L25, L27, L28 and L30) showed significant GCA effects. Nine inbred lines (L1, L2 L7, L8, L14, L15, L19, L20 and L21) exhibited significantly negative GCA effects for number of kernels per row.

In combined analysis across locations, GCA effects for number of kernels per row ranged between -3.51 (L20) and 2.49 (L34). Six inbred lines (L7, L15, L27, L34, L35 and L42) showed positive and significant GCA effects for number of kernels per row suggesting that these lines were good combiner for increasing number of kernels per row. Six inbred lines (L12, L14, L19, L20, L21 and L32) showed positive and significant GCA effects for number of kernels per row (Table 7).

These results were in agreement with the findings of Amiruzzaman *et al*. (2010), Dagne *et al*. (2007) and Gudeta (2007) who reported significant and positive GCA effects for some lines, and significant and positive GCA effects for others in number of kernels per ear.

Ear length

At Melkasa, 17 inbred lines recorded showed significant GCA effects among which eight inbred lines (L4, L7, L30, L33, L34, L35, L39 and L42) showed significant GCA effects. L7 and L34 had higher positive and significant GCA effects for ear length (2.1 cm) hence they were the best general combiners for longer ears. On the other hand, three inbred lines (L3, L12 and L19) had negative and significant GCA effects. L12 had the smallest GCA effect (-1.6 cm), implying the tendency of these line to reduce ear length.

At Ziway, even though 21 inbred lines showed positive GCA effects for ear length, only four inbred lines (L7, L34, L35 and L39) showed significant GCA effects. L34 had positive and significant GCA effects for ear length (2.52 cm) whereas three inbred lines (L1, L12 and L17) had negative and significant GCA effects. L1 had small (-2.03 cm) while T2 showed large but non-significant GCA effects for ear length.

At Dhera, even though a total of 21 inbred lines showed positive GCA effects for ear length, only two inbred lines (L41 and L34) showed significant GCA effects. L41 had higher positive and significant GCA effect for ear length (2.63 cm) whereas only four inbred lines (L5, L21, L22 and L26) had negative and significant GCA effects. L21 had negative and significant GCA effect (-2.72 cm).

At Mieso, even though a total of 23 inbred lines showed positive GCA effects, only two inbred lines (L35 and L39) had significant GCA effects. L35 had positive and significant GCA effect for ear length (1.82 cm) while inbred lines (L4 and L21) had negative and significant negative GCA effects. L4 had negative and significant GCA effects for ear length (-2.18 cm).

At Pawe, 21 inbred lines showed positive GCA effects for ear length among which nine inbred lines (L4, L23, L27, L28, L30, L34, L35, L39 and L41) showed significant GCA effects. Inbred lines L39 and L30 had positive and significant GCA effects for ear length

(2.05 and 1.95 cm, respectively). On the other hand, eight inbred lines (L1, L2, L5, L8, L12, L18, L20 and L22) had negative and significant GCA effects. L5 showed the smallest GCA effect (-2.18 cm) for the trait.

Across locations, GCA effects for ear length ranged from -1.78 cm (L12) to 1.74 cm (L39) and nine inbred lines (L7, L30, L33, L34, L35, L37, L39, L41 and L42) showed positive and significant GCA effects for ear length, suggesting that these inbred lines had a tendency to increase ear length. On the other hand, eight inbred lines (L1, L5, L9, L12, L17, L19, L20, and L21) found to be poor general combiners for ear length as they showed negative and significant GCA effects (Table 7).

Similar to the present findings, Amiruzzaman *et al*. (2010), Jumbo and Carena (2008) and Dagne *et al*. (2007) reported significant positive and negative GCA effects for this trait. Positive GCA effects for ear length are desirable as it indicates the tendency to increase ear length which directly contributes to increased grain yield in maize.

Ear diameter

At Melkasa, 17 inbred lines showed positive GCA effects among which seven inbred lines (L7, L17, L20, L21, L22, L27 and L40) showed significant GCA effects. L21 had the highest positive and significant GCA effect of 0.39 cm for ear diameter, indicating that the line has the tendency to increase ear diameter. In contrary, nine inbred lines (L10, L12, L24, L25, L34, L35, L39 and L42) showed negative and significant GCA effects for the trait. L12 had the lowest GCA effect of -0.41.

At Ziway, line GCA effects for ear diameter ranged between -0.3 cm (L12) to 0.5 cm (L26). Even though a total of 19 inbred lines showed positive GCA effects for ear diameter, only five inbred lines (L17, L20, L21, L22 and L26) had significantly positive GCA effects. Nine inbred lines (L4, L5, L8, L12, L15, L25, L34, L35 and L38) had negative and significant GCA effects for ear diameter.

At Dhera, line GCA effects for ear diameter ranged between -0.43 cm (L42) and 0.67 cm (L17). Even though a total of 22 inbred lines showed positive GCA effects for ear diameter, only three inbred lines (L2, L17 and L23) had significant and positive GCA effects. Four inbred lines (L25, L34, L35 and L42) had negative and significant GCA effects for ear diameter.

At Pawe, line GCA effects for ear diameter ranged between -0.43 cm (L12) to 0.37 cm (L21). Even though a total of 24 inbred lines showed positive GCA effects for ear diameter, only seven inbred lines (L13, L17, L20, L21, L22, L24 and L26) had significantly positive GCA effects. Five inbred lines (L5, L8, L12, L18 and L34) had negative and significant GCA effects for the trait.

In combined analysis across locations, 22 inbred lines showed positive GCA effects for ear diameter among which 12 inbred lines had significant GCA effects. L13, L17, L20, L21, L22, L23, L26 and L36 were the best general combiners for ear diameter as they had highly significant and positive GCA effect (Table 7). On the other hand, 11 inbred lines had significantly negative GCA effects. L34 was the worst general combiner for this trait (Table 19). The present study is in agreement with Amiruzzaman *et al*. (2010), Jumbo and Carena (2008), Dagne *et al*. (2007), and Gudeta (2007), who reported significant positive and negative GCA effects for ear diameter.

Thousand-kernel weight

At Melkasa, line GCA effects for thousand-kernel weight ranged from -104.62 (L6) to 134.34 gm (L37). Even though a total of 21 inbred lines showed positive GCA effects for thousand-kernel weight, only four inbred lines (L7, L19, L21 and L37) showed significant GCA effects in desired direction, indicating that the inbred lines were the best general combiners for thousand-kernel weight. These inbred lines might have favorable genes for larger kernels. On the other hand, L3, L6 and L25 showed negative and significant GCA effects, which are undesirable.

At Dhera, Line GCA effects for thousand-kernel weight ranged between -54.82 (L3) and 66.33 gm (L17). Even though a total of 21 inbred lines showed positive GCA effects for thousand-kernel weight, only two inbred lines (L3 and L15) showed significant GCA effects. On the other hand, L25, L3 and L6 showed negative and significant GCA effects for the same trait.

At Mieso, line GCA effects for thousand-kernel weight ranged from -70.41 (L4) to 73.19 gm (L14). Even though a total of 21 inbred lines showed positive GCA effects for thousand kernel weight, only three inbred lines (L2, L14 and L39) showed significant GCA effects in desired direction. On the other hand L4 and L15 showed negative and significant GCA effects in undesired direction.

At Pawe, three inbred lines (L24, L27 and L30) had positive GCA effects for thousand-kernel weight (75.55, 75.05 and 60.0 gm, respectively) and L36 and L12 had higher negative GCA effects (-59.80 and -57.45 gm, respectively). Even though a total of 22 inbred lines showed negative GCA effects for thousand-kernel weight, only four inbred lines (L36, L12, L15 and L37) had significant GCA effects.

The present results are in agreement with the findings of several researchers who reported significant positive and negative GCA effects for thousand-kernel weight (Demissew *et al.*, 2011; Amiruzzaman *et al.*, 2010; Dagne *et al.*, 2007; Teshale, 2001; Hadji, 2004).

Table 7. Across locations estimates of general combining ability effects (GCA) of 43 inbred lines and two testers for grain yield, 2010

Line	GY (t/ha)	AD (days)	SD(days)	PH(cm)	EH(cm)	EL (cm)	ED(cm)	KPR(#)	RPE(#)
L1	-0.24	-2.42**	-2.79**	-14.03**	-7.25**	-1.26**	0.06	-0.48	0.71**
L2	0.15	-3.81**	-3.64**	3.71	-9.89**	-0.31	0.11*	0.14	0.30
L3	-0.53*	-2.94**	-3.24**	-4.91	-0.39	-0.15	-0.04	0.54	1.48**
L4	-0.09	-0.64*	-0.21	7.59**	-2.09	0.26	-0.01	1.31	-0.33
L5	-0.87**	-4.31**	-4.53**	-17.87**	-12.68**	-1.48**	-0.19**	-0.78	-1.06**
L6	-0.48*	1.89**	1.77**	9.22**	9.03**	-0.19	0.00	0.44	0.36*
L7	0.19	-2.96**	-2.56**	-2.29	-8.18**	1.05**	0.11*	1.84*	0.03
L8	-0.43	-3.12**	-3.21**	-14.74**	-17.50**	0.1	-0.26**	-1.09	-0.44*
L9	-0.64*	-1.42**	-0.43	-1.73	-1.68	-0.66*	-0.03	-1.38	-0.22
L10	0.22	1.18**	1.34**	1.62	5.83*	0.04	-0.04	0.86	0.51**
L11	0.14	-2.76**	-2.69**	0.57	5.60*	0.29	-0.06	-0.24	0.44*
L12	-0.58*	1.41**	1.17**	-5.14	-6.14*	-1.78**	-0.22**	-1.64	-0.55**
L13	0.76**	-0.64*	-0.49	11.11**	2.07	0.36	0.12*	0.41	1.02**
L14	-0.92**	2.53**	2.34**	1.17	4.5	-0.23	0.09	-2.04*	-0.03
L15	-0.36	0.09	0.37	-1.18	5.46*	-0.41	-0.16**	2.71**	-0.56**
L16	-0.70**	0.01	0.26	0.31	-1.22	-0.5	0.03	-0.87	0.49**
L17	-0.06	1.51**	1.12**	1.37	6.62*	-0.84*	0.31**	-0.32	-0.26
L18	-0.46*	-1.01**	-0.61	-8.02**	-8.05**	-0.39	-0.01	1.29	-0.12
L19	-0.15	-0.47	-0.89*	8.81**	4.78	-0.90**	0.09	-3.06**	-0.50**
L20	-0.39	-0.11	0.32	3.08	2.46	-0.94**	0.11*	-3.51**	0.26

Table 7 (Continued)

L21	0.65**	-1.14**	-0.84*	3.98	8.42**	-1.38**	0.23**	-3.42**	0.03
L22	0	-2.42**	-2.78**	-3.19	5.82*	-0.2	0.14*	-1.48	-0.04
L23	1.40**	2.91**	2.66**	6.97*	4.97	0.42	0.12*	1.38	-0.42*
L24	1.04**	2.51**	2.09**	10.43**	0.47	0.24	0.02	0.56	-0.52**
L25	0.73**	2.49**	2.31**	8.37**	6.55	-0.18	-0.09	0.76	-0.89**
L26	0.18	0.16	0.17	-6.93*	-3.73	-0.2	0.25**	0.12	0.66**
L27	0.65**	0.63*	0.97**	6.91*	-0.85	0.35	0.12*	1.79*	-0.66**
L28	0.19	-0.96**	-0.96**	3.11	1.83	-0.15	0.01	-1.13	-0.24
L29	0.49*	1.34**	1.19**	9.31**	10.28**	0.51	0.06	0.34	0.72**
L30	0.93**	2.23**	2.39**	6.72*	15.10**	0.90**	0.06	1.33	-0.36*
L31	0.09	-1.06**	-1.04**	-2.88	-7.24**	0.05	-0.01	0.97	-0.06
L32	-0.63**	0.74**	0.79*	-2.47	-5.00	-0.23	-0.01	-2.24**	0.52**
L33	-0.28	1.14**	1.62**	-0.51	-6.34*	0.66*	-0.08	0.43	0.02
L34	-0.33	1.41**	1.44**	-4.11	-2.39	1.62**	-0.30**	2.49**	-0.41*
L35	-0.77**	2.14**	2.39**	-3.66	-2.73	1.59**	-0.27**	2.13**	-0.02
L36	-0.11	0.89**	1.21**	1.79	-3.08	0.56	0.16**	-0.18	0.84**
L37	0.17	-1.24**	-1.28**	-15.78**	-10.37**	0.82*	-0.08	1.19	-0.07
L38	-0.28	1.93**	1.54**	-0.27	2.92	-0.36	-0.03	-1.58*	0.32
L39	-0.16	1.79**	1.82**	1.94	7.77**	1.74**	-0.11*	1.01	-0.23
L40	-0.22	1.39**	1.07**	1.11	7.77**	-0.15	0.05	0.06	0.30
L41	1.00**	0.89**	0.61	5.61*	-2.52	0.79*	0.06	0.01	-0.53**
L42	0.56*	0.14	-0.43	-4.96	3.10	0.90**	-0.18**	2.31**	-0.17

Table 7 (Continued)

L43	0.17	0.04	-0.28	-0.08	-2.04	-0.39	0.02	-0.93	-0.40*
SE	0.24	0.32	0.34	2.81	2.73	0.33	0.06	0.81	0.18
SED	0.33	0.45	0.49	3.98	3.86	0.47	0.09	1.15	0.25

** = Significant at $P<0.01$ level of probability, * = Significant at $P<0.05$ Level of probability, AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, RPE = Number of rows per ear, SD = number of days to silking, SE= standard error, TKWT = thousand kernels weight

4.3.2. Specific combining ability estimates

The specific combining ability effects at individual and across locations were computed for traits that showed significant SCA mean squares in combining ability analysis. Specific combining ability effects for grain yield and related agronomic traits for each test locations (Appendices 16-20) and combined across locations were presented in Table 8.

Grain yield

At Melkasa, 50% of the crosses showed positive SCA effects for grain yield out of which three crosses, namely; L33 x T2 , L24 x T2 and L23 x T2 (Appendix 16) showed positive and significant SCA effects for grain yield with SCA values of 2.27, 1.97 and 1.32 t/ha, respectively, indicating that these crosses were good specific combinations for grain yield. Crosses with the higher value of SCA effect also showed higher values of mean grain yield performance, indicating good correspondence between SCA effects and mean grain yield. Hence such cross combinations could effectively be exploited in hybrid breeding program in maize research. On the other hand, three cross combinations L33 x T1, L24 x T1 and L23 x T1 expressed negative and significant SCA effects for grain yield which are undesirable as these crosses showed a tendency to reduce grain yield performance.

At Ziway, two crosses L4 x T1 (1.41 t/ha) and L33 x T2 (1.29 t/ha) (Appendix 17) showed significantly positive SCA effects, indicating that these crosses were good specific combiners for grain yield at this specific location. None of the crosses showed positive and significant SCA effects for grain yield at Dhera (Appendix 18). However, cross L34 x T1 had the highest positive SCA effect for grain yield, but yet not significant. At Pawe, three crosses namely L14 x T1 (2.30 t/ha), L22 x T2 (1.43) and L33 x T2 (1.36 t/ha) (Appendix 20) showed significant SCA effects for grain yield. In combined analysis across locations, seven crosses (L33 x T2, L32 x T2, L17 x T1, L14 x T1, L36 x T2, L34 x T1 and L7 x T1) showed positive and significant SCA effects. L33 x T2 (1.25 t/ha) was the best specific combiner for grain yield followed by L32 x T2 (0.94 t/ha) (Table 8). Thus, these crosses could be selected for their specific combining ability to improve grain yield. The finding of the current study are in agreement with that of Mandefro (1999) who reported significant positive and negative SCA effects for grain yield in 8 x 8 diallel study of drought tolerant maize populations at Melkasa.

Amiruzzaman *et al*. (2010), Dagne *et al*. (2007) and Bayisa (2004) also reported similar results for grain yield while Pswarayi and Vivek (2008) and Jumbo and Carena (2008) reported non-significant positive and negative SCA effects for grain yield.

Days to anthesis and Silking

At Melkasa, two crosses (L34 x T1 and L33 x T2) showed significantly negative SCA effects for days to anthesis and silking. L34 x T1 showed the highest negative SCA effect for days to anthesis (-1.63 days) and days to silking (-1.98 days) which were desirable for earliness (Appendix 16). Negative and significant SCA effects were found in crosses L4 x T1, L12 x T2, L19 x T2, L20 x T2, L23 x T2, L32 x T2 and L43 x T2 (Appendix 17) and the cross L12 x T2 showed the highest negative SCA effect (-3.12 days) for days to anthesis at Ziway. Only three crosses, L12 x T2 (-2.47 days), L23 x T2 (-2.47 days) and L43 x T2 (-2.42 days) showed negative and significant SCA effects for days to silking at Ziway (Appendix 17). Although 50% of the crosses showed negative SCA effects for number of days to anthesis and silking, only one cross combination had (L9 x T2) significant SCA effect at Dhera (Appendix 18), indicating that this cross was best specific combination for number of days to anthesis and silking. At Mieso, only four combinations (L21 x T1, L9 x T2, L17 x T1 and L12 x T1) (Table 23) had negative and significant SCA effects for days to anthesis and six crosses (L8 x T2, L9 x T2, L11 x T2, L12 x T1, L17 x T1 and L42 x T2) showed significantly negative SCA effects for days to silking. The cross combinations L17 x T1 and L9 x T2 (Appendix 19) had the highest SCA effects for days to anthesis and silking at Mieso. At Pawe four crosses (L9 x T2, L17 x T1, L32 x T2 and L34 x T1) showed significantly negative SCA effects for days to anthesis and five crosses (L8 x T1, L9 x T2, L17 x T1, L32 x T2 and L34 x T1) showed significantly negative SCA effects for days to silking. The cross combination L9 x T2 (Appendix 20) had the highest negative SCA effect for days to anthesis and silking at Pawe. In combined analysis across locations, 12 crosses showed negative and significant SCA effects and Cross L32 x T2 had the highest negative SCA effects for days to anthesis (-1.77 days) while 11 crosses showed negative and significant SCA effects for days to silking and Cross L32 x T2 had the highest negative SCA effect for days to silking (-1.74 days) (Table 8). Crosses with low estimate of SCA effects for days to anthesis and silking are desirable as they had earlier anthesis and silking than what have been expected based on GCA of their parents. These findings are in agreement with the findings of several researchers who reported significant positive-and-negative SCA effects for days to anthesis and silking (Dagne *et al*., 2010; Hadji, 2004; Gudeta, 2007)

Plant and ear height

For plant height, only two crosses (L37 x T1 and L32 x T1) at Dhera (Appendix 18) and two crosses (L7 x T2 and L28 x T2) at Pawe (Appendix 20) showed negative and significant SCA effects for the trait, indicating that these crosses had good specific combination for shorter plant stature. In line with the present results at these locations, Dagne *et al*. (2010), Legesse *et al*. (2009) and Mandefro (1999) reported significantly negative SCA effects for plant height. None of the crosses showed significantly negative and positive SCA effects for plant height at Mieso (Appendix 19) and for ear height at Pawe (Appendix 20) and across locations (Table 8). In contrary to these findings Demissew *et al*. (2011) and Gudeta (2007) found significantly positive and negative SCA effects for plant and ear height while Jumbo and Carena (2008) reported that estimated SCA effects for ear height were not significantly different from zero.

Ear length

For ear length, only one cross (L14 x T2) at Mieso (Appendix 19) and three crosses (L32 x T2, L33 x T2 and L36 x T2) across locations (Table 8) were good specific combination as they showed positive and significant SCA effect for this trait. Similarly, Bayisa (2004) and Dagne *et al*. (2007) reported positive and significant SCA effects for ear length.

Number of kernels per row

For number of kernels per row, two crosses (L3 x T1 and L16 x T1) at Melkasa (Appendix 16), one cross (L14 x T2) at Mieso (Appendix 19) and two crosses (L33 x T2 and L34 x T1) across locations (Table 8) showed significantly positive SCA effects for number of kernels per row, indicating that these crosses were good specific combinations for this trait. In line with the present findings, Gudeta (2007) and Dagne *et al*. (2007) reported positive and significant SCA effects for this trait.

Thousand-kernel weight

For thousand-kernel weight, only three crosses (L34 x T1, L41 x T2 and L39 x T2) at Dhera (Appendix 18), one cross (L14 x T2) at Mieso (Appendix 19) were the best combinations for thousand kernel weight as they showed positive and significant SCA effects for this trait. In line with the present findings, Amiruzzaman *et al.* (2010), Bayisa (2004) and Dagne *et al.* (2007) reported positive and significant SCA effects for this trait.

Ear diameter

For ear diameter, only two crosses (L34 x T1 and L23 x T2) at Melkasa (Appendix 16), two crosses (L29 x T1 and L34 x T1) at Dhera (Appendix 18), five crosses (L2 x T1, L9 x T1, L14 x T1, L33 x T2 and L36 x T2) at Pawe (Appendix 20) and seven crosses (L20 x T2, L25 x T2, L32 x T2, L33 x T2, L34 x L1, L36 x T2 and L38 x T1) across locations (Table 8) had significantly positive SCA effects for ear diameter, indicating that these crosses were good specific combinations for this trait. These findings are in agreement with several researchers who reported significantly positive SCA effects for ear diameter (Amiruzzaman *et al.*, 2010; Bayisa, 2004; Dagne *et al.*, 2007; Jemal, 1999; Gudeta, 2007).

Number of rows per ear

For number of rows per ear, only two crosses (L13 x T1 and L29 x T1) at Dhera (Appendix 18), two crosses (L34 x T1 and L2 x T1) at Pawe (Appendix 20) and two crosses (L6 x T1 and L29 x T1) across locations (Table 8) had significantly positive SCA effects for number of rows per ear, indicating that these crosses were good specific combinations for this trait. In line with the present findings, Amiruzzaman *et al.* (2010), Hadji (2004) and Gudeta (2007) reported positive and significant SCA effects for number of rows per ear.

Table 8. Estimates of specific combining ability effects (SCA) for line by tester crosses of maize inbred lines evaluated across locations, 2010

Crosses	GY(t/ha)	AD(days)	SD(days)	EH(cm)	EL(cm)	KPR(#)	KRE(#)	ED(cm)
L1 x T1	0.21	-0.36	-0.15	5.25	-0.14	-1.27	-0.21	-0.05
L1 x T2	-0.21	0.36	0.15	-5.25	0.14	1.27	0.21	0.05
L2 x T1	0.12	0.12	0.17	-0.66	0.03	-1.19	0.14	0.00
L2 x T2	-0.12	-0.12	-0.17	0.66	-0.03	1.19	-0.14	0.00
L3 x T1	0.29	0.45	0.80	0.89	0.67	1.73	-0.20	-0.03
L3 x T2	-0.29	-0.45	-0.80	-0.89	-0.67	-1.73	0.20	0.03
L4 x T1	0.40	-0.85*	-0.93*	-3.46	0.28	0.44	-0.33	-0.04
L4 x T2	-0.40	0.85*	0.93*	3.46	-0.28	-0.44	0.33	0.04
L5 x T1	0.35	-0.61	-0.81	-3.80	0.44	0.16	-0.30	0.04
L5 x T2	-0.35	0.61	0.81	3.80	-0.44	-0.16	0.30	-0.04
L6 x T1	0.12	0.45	0.39	3.19	-0.17	-0.74	0.64**	0.05
L6 x T2	-0.12	-0.45	-0.39	-3.19	0.17	0.74	-0.64**	-0.05
L7 x T1	0.62*	-0.86*	-0.71	0.47	0.19	1.48	-0.27	0.00
L7 x T2	-0.62*	0.86*	0.71	-0.47	-0.19	-1.48	0.27	0.00
L8 x T1	-0.32	-0.50	-0.83	-3.53	0.39	1.04	-0.04	-0.03
L8 x T2	0.32	0.50	0.83	3.53	-0.39	-1.04	0.04	0.03
L9 x T1	0.18	0.50	0.92*	3.97	0.01	-0.12	0.18	0.02
L9 x T2	-0.18	-0.50	-0.92*	-3.97	-0.01	0.12	-0.18	-0.02
L10 x T1	0.04	0.04	0.15	4.26	-0.27	0.57	0.03	0.03
L10 x T2	-0.04	-0.04	-0.15	-4.26	0.27	-0.57	-0.03	-0.03
L11 x T1	-0.31	-0.10	-0.38	-0.28	0.18	1.29	-0.24	-0.07
L11 x T2	0.31	0.10	0.38	0.28	-0.18	-1.29	0.24	0.07
L12 x T1	-0.17	1.10*	0.95*	0.56	-0.08	-1.06	0.11	0.03
L12 x T2	0.17	-1.10*	-0.95*	-0.56	0.08	1.06	-0.11	-0.03
L13 x T1	0.31	-0.31	-0.11	-0.08	0.38	1.07	0.38	0.05
L13 x T2	-0.31	0.31	0.11	0.08	-0.38	-1.07	-0.38	-0.05
L14 x T1	0.86**	-0.65	-1.21	-0.90	0.09	-0.56	0.33	0.08
L14 x T2	-0.86**	0.65	1.21	0.90	-0.09	0.56	-0.33	-0.08
L15 x T1	-0.06	-0.58	-0.18	-2.19	0.43	0.89	0.04	0.05
L15 x T2	0.06	0.58	0.18	2.19	-0.43	-0.89	-0.04	-0.05
L16 x T1	-0.43	-0.16	0.07	1.26	0.09	1.57	-0.05	0.04
L16 x T2	0.43	0.16	-0.07	-1.26	-0.09	-1.57	0.05	-0.04
L17 x T1	0.87**	-0.70	-0.53	0.55	0.41	0.39	0.04	-0.02

Table 8 (Continued)

L17 x T2	-0.87**	0.70	0.53	-0.55	-0.41	-0.39	-0.04	0.02
L18 x T1	0.48	-0.41	-0.63	-3.28	0.01	0.86	0.04	0.08
L18 x T2	-0.48	0.41	0.63	3.28	-0.01	-0.86	-0.04	-0.08
L19 x T1	-0.55	0.85*	0.95*	-4.91	-0.31	-1.69	0.02	0.00
L19 x T2	0.55	-0.85*	-0.95*	4.91	0.31	1.69	-0.02	0.00
L20 x T1	-0.10	0.85*	0.30	-1.49	-0.22	-0.79	-0.18	-0.12*
L20 x T2	0.10	-0.85*	-0.30	1.49	0.22	0.79	0.18	0.12*
L21 x T1	0.13	0.49	0.00	0.80	0.87	2.07	-0.07	0.02
L21 x T2	-0.13	-0.49	0.00	-0.80	-0.87	-2.07	0.07	-0.02
L22 x T1	-0.59	0.80	0.94*	4.27	0.39	-1.02	-0.12	-0.09
L22 x T2	0.59	-0.80	-0.94*	-4.27	-0.39	1.02	0.12	0.09
L23 x T1	-0.3	1.00*	1.00*	2.17	0.02	-0.78	0.10	-0.03
L23 x T2	0.3	-1.00*	-1.00*	-2.17	-0.02	0.78	-0.10	0.03
L24 x T1	-0.53	-0.46	-0.40	0.12	0.13	0.44	-0.10	0.03
L24 x T2	0.53	0.46	0.40	-0.12	-0.13	-0.44	0.10	-0.03
L25 x T1	-0.36	0.89*	1.15*	5.75	-0.21	-1.93	-0.13	-0.12*
L25 x T2	0.36	-0.89*	-1.15*	-5.75	0.21	1.93	0.13	0.12
L26 x T1	0.32	-0.41	-0.51	0.37	0.27	1.83	-0.18	0.08
L26 x T2	-0.32	0.41	0.51	-0.37	-0.27	-1.83	0.18	-0.08
L27 x T1	0.08	0.15	0.09	0.75	0.49	0.56	0.06	0.03
L27 x T2	-0.08	-0.15	-0.09	-0.75	-0.49	-0.56	-0.06	-0.03
L28 x T1	-0.14	-0.10	-0.08	1.41	0.24	1.28	0.04	0.00
L28 x T2	0.14	0.10	0.08	-1.41	-0.24	-1.28	-0.04	0.00
L29 x T1	0.05	0.20	0.40	2.64	-0.12	0.36	0.48*	0.11
L29 x T2	-0.05	-0.20	-0.40	-2.64	0.12	-0.36	-0.48*	-0.11
L30 x T1	0.24	-0.38	-0.56	-4.68	0.17	-0.06	0.12	0.03
L30 x T2	-0.24	0.38	0.56	4.68	-0.17	0.06	-0.12	-0.03
L31 x T1	0.07	-0.43	-0.53	-4.01	-0.03	-0.14	-0.02	0.02
L31 x T2	-0.07	0.43	0.53	4.01	0.03	0.14	0.02	-0.02
L32 x T1	-0.94**	1.77**	1.74**	-4.98	-0.91*	-2.16	-0.08	-0.16*
L32 x T2	0.94**	-1.77**	-1.74**	4.98	0.91*	2.16	0.08	0.16*
L33 x T1	-1.25**	1.20**	1.40**	-6.76	-1.72**	-2.86*	0.02	-0.15*
L33 x T2	1.25**	-1.20**	-1.40**	6.76	1.72**	2.86*	-0.02	0.15*
L34 x T1	0.66*	-1.36**	-1.68**	2.11	0.29	2.98*	0.43	0.17*
L34 x T2	-0.66*	1.36**	1.68**	-2.11	-0.29	-2.98*	-0.43	-0.17*

Table 8(Continued)

L35 x T1	0.27	-0.66	-0.60	0.52	-0.47	0.29	0.38	0.08
L35 x T2	-0.27	0.66	0.60	-0.52	0.47	-0.29	-0.38	-0.08
L36 x T1	-0.79*	0.02	0.05	-1.78	-1.17*	-1.42	-0.44	-0.17*
L36 x T2	0.79*	-0.02	-0.05	1.78	1.17*	1.42	0.44	0.17*
L37 x T1	-0.31	-0.08	0.20	-5.24	-0.23	-1.94	-0.07	-0.05
L37 x T2	0.31	0.08	-0.20	5.24	0.23	1.94	0.07	0.05
L38 x T1	0.18	-0.25	-0.51	3.05	0.66	2.11	0.00	0.12*
L38 x T2	-0.18	0.25	0.51	-3.05	-0.66	-2.11	0.00	-0.12*
L39 x T1	-0.24	-0.01	0.00	8.42*	0.18	0.22	-0.29	-0.02
L39 x T2	0.24	0.01	0.00	-8.42*	-0.18	-0.22	0.29	0.02
L40 x T1	0.31	-0.21	-0.51	-2.60	-0.73	-0.98	0.02	0.08
L40 x T2	-0.31	0.21	0.51	2.60	0.73	0.98	-0.02	-0.08
L41 x T1	0.32	-0.65	-0.08	6.19	-0.54	-1.61	0.29	-0.01
L41 x T2	-0.32	0.65	0.08	-6.19	0.54	1.61	-0.29	0.01
L42 x T1	0.37	-0.93*	-0.88	-2.30	0.39	0.59	-0.21	0.03
L42 x T2	-0.37	0.93*	0.88	2.30	-0.39	-0.59	0.21	-0.03
L43 x T1	-0.46	1.07*	1.07*	-2.04	-0.44	-1.87	-0.32	-0.05
L43 x T2	0.46	-1.07*	-1.07*	2.04	0.44	1.87	0.32	0.05
SE	0.33	0.45	0.49	3.86	0.47	1.15	0.25	0.08
SED	0.47	0.64	0.69	5.46	0.67	1.63	0.35	0.11

** = Significant at P<0.01 level of probability, * = Significant at P<0.05 Level of probability, AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, RPE = Number of rows per ear, SD=number of days to silking, SE=standard error, TKWT = thousand-kernels weight

4.4. Heterotic Grouping

On the basis of pooled ANOVA from four testing locations (Melkasa, Ziway, Mieso and Pawe), SCA effects for grain yield of the testcrosses were used to classify the inbred lines into heterotic groups as presented in Table 26. In addition, inbred lines with positive and significant GCA effects in combined analyses were classified into heterotic groups based on positive or negative SCA effects they exhibited when crossed with the two testers, as such line have good breeding value. Inbred lines that showed low GCA effects and non-significant SCA effects when crossed with the testers were not classified into heterotic groups as such lines do not have exploitable breeding value and appropriate power to be discriminated by the testers used. They rather belong to other heterotic groups not used in the study.

Table 26 shows heterotic grouping of the 43 inbred lines. Even though most inbred lines showed either positive or negative SCA and GCA effects when crossed with the testers, the SCA and GCA effects were not significant in most cases, indicating that the estimates did not have appropriate power to distinctively discriminate the inbred lines into different heterotic groups. However few inbred lines showed significant SCA effects when crossed with the testers. Such lines can confidently be assigned into heterotic groups and be instantly used in hybrid development program. These lines were L32, L33 and L36 (Heterotic group A) and L7, L14, L17 and L34 (heterotic group B). On the other hand, seven inbred lines (L13, L21, L27, L29, L30, L41 and L42) which showed positive and significant GCA effects and had negative SCA effects with tester B (CML202/CML395) were classified in to heterotic group B while three inbred lines (L23, L24 and L25) which showed positive and significant GCA effects and had negative SCA effects with tester A (CML312/CML442) were assigned to hetrotic group A. Most inbred lines evaluated in the current study neither revealed significant SCA in their cross combinations with the testers nor significantly higher GCA effects for grain yield, indicating that neither of the two testers used for the study are genetically divergent to provide the best discrimination among the inbred lines nor the inbred lines were good general combiners for grain yield. Similar to the present findings, Mosisa *et al.* (1996) found significant SCA effects only for few crosses combinations. Bayisa (2004) reported high and positive specific combining ability estimates for five transitional highland inbred lines and clearly grouped the inbred lines under Ecuador and Kitale heterotic groups. Similarly, in line by tester study of highland inbered lines, Gudeta (2007) classified six inbred lines under Kitale and seven inbred lines under Ecuador heterotic group.

Based on the SCA and GCA effects for grain yield, 17 elite maize inbred lines were classified into A and B heterotic groups. Inbred lines within the same group are genetically similar while those in different groups are dissimilar. Crossing two lines belonging to different heterotic groups will result to the development of high yielding hybrids.

In the future, maize breeding programs should exploit the groups identified in the current study in order to maximize genetic gain from heterotic effects. In hybrid variety development process using the inbred lines identified in this study, parents from heterotic group A should be crossed with those belonging to heterotic group B. In the case of the development of synthetic varieties, inbred lines belonging to the same heterotic group should be recombined. These should be the future research strategy to further exploit the genetic potential of the inbred lines.

Table 9. Combined mean grain yield, GCA, SCA effects and heterotic group of inbred lines

	GY (t/ha)		SCA		GCA	Heterotic group
	T1	T2	T1	T2		
L1	5.91	5.36	0.21	-0.21	-0.24	-
L2	6.21	5.84	0.12	-0.12	0.15	-
L3	5.70	5.00	0.29	-0.29	-0.53*	-
L4	6.25	5.31	0.4	-0.4	-0.09	-
L5	5.42	4.58	0.35	-0.35	-0.87**	-
L6	5.59	5.21	0.12	-0.12	-0.48*	-
L7	6.75	5.37	0.62*	-0.62*	0.19	B
L8	5.19	5.7	-0.32	0.32	-0.43	-
L9	5.48	4.99	0.18	-0.18	-0.64*	-
L10	6.2	5.99	0.04	-0.04	0.22	-
L11	5.78	6.26	-0.31	0.31	0.14	-
L12	5.19	5.41	-0.17	0.17	-0.58*	-
L13	7.02	6.25	0.31	-0.31	0.76**	B
L14	5.88	4.02	0.86*	-0.86*	-0.92**	B
L15	5.52	5.51	-0.06	0.06	-0.36	-

Table 9 (Continued)

L16	4.81	5.54	-0.43	0.43	-0.70**	-
L17	6.75	4.88	0.87*	-0.87*	-0.06	B
L18	5.96	4.87	0.48	-0.48	-0.46*	-
L19	5.24	6.21	-0.55	0.55	-0.15	-
L20	5.46	5.52	-0.1	0.10	-0.39	-
L21	6.73	6.33	0.13	-0.13	0.65**	B
L22	5.36	6.40	-0.59	0.59	0.00	-
L23	7.04	7.50	-0.3	0.30	1.40**	A
L24	6.46	7.38	-0.53	0.53	1.04**	A
L25	6.32	6.90	-0.36	0.36	0.73**	A
L26	6.44	5.67	0.32	-0.32	0.18	-
L27	6.67	6.38	0.08	-0.08	0.65**	B
L28	6.00	6.14	-0.14	0.14	0.19	-
L29	6.48	6.25	0.05	-0.05	0.49*	B
L30	7.11	6.49	0.24	-0.24	0.93**	B
L31	6.1	5.84	0.07	-0.07	0.09	-
L32	4.38	6.12	-0.94**	0.94**	-0.63**	A
L33	4.42	6.78	-1.25**	1.25**	-0.28	A
L34	6.28	4.82	0.66*	-0.66*	-0.33	B
L35	5.44	4.78	0.27	-0.27	-0.77**	-
L36	5.04	6.48	-0.79*	0.79*	-0.11	A
L37	5.81	6.29	-0.31	0.31	0.17	-
L38	5.84	5.36	0.18	-0.18	-0.28	-
L39	5.54	5.89	-0.24	0.24	-0.16	-
L40	6.03	5.28	0.31	-0.31	-0.22	-
L41	7.27	6.49	0.32	-0.32	1.00**	B
L42	6.88	6.00	0.37	-0.37	0.56*	B
L43	5.65	6.44	-0.46	0.46	0.17	-
SE			0.33	0.33	0.24	
SED			0.47	0.47	0.33	

5. SUMMARY AND CONCLUSIONS

This study was conducted at five locations (Melkasa, Ziway, Dhera, Mieso and Pawe) during The study was conducted with the objective of identifying better performing test-cross hybrid combination for possible release for commercial production, estimating combining abilities for grain yield and other agronomic traits in elite maize inbred lines and classifying the elite inbred lines into different heterotic groups for future use in the breeding program using Line x Tester mating design. A total of 88 maize genotypes including 86 test crosses developed by crossing 43 elite maize inbred lines with two testers and two standard checks were planted across five locations (Melkasa , Ziway, Dhera, Mieso and Pawe) during the 2010 cropping season in 8 x 11 alpha lattice design replicated twice. Data were recorded on for grain yield, anthesis date, silking date, plant height, ear height, number of ears per plant, 1000-kernel weight, number of rows per ear, number of kernels per row, ear length and ear diameter.

Analysis of variance indicated significant mean squares due to genotypes for grain yield, anthesis date, silking date, plant height, ear height, number of rows per ear, number of kernels per row, ear length and ear diameter at most locations and across locations. Furthermore, significant differences were not found among the checks and checks vs crosses for most traits.

Among the crosses, Crosses L24 x T2 (11.67 t/ha), L23 x T2 (11.42 t/ha) and L33 x T2 (11.19 t/ha) from Melkasa, L39 x T2 (6.4 t/ha), L42 x T1 (6.0 t/ha), L4 x T1 and L41 x T1 (5.9 t/ha) from Ziway L2 x T2 (4.0 t/ha), L37 x T2 (3.9 t/ha) and L17 x T1 (3.8 t/ha) from Dhera, L13 x T1 (5.64 t/ha), L41 x T1 (5.51 t/ha) and L17 x T1 (5.32 t/ha) from Mieso, L23 x T1 (10.9 t/ha), L30 x T2 (10.8 t/ha) and L30 x T1 (10.6 t/ha) from Pawe and L23 x T2 (7.5 t/ha), L24 x T2 (7.38 t/ha) and L41 x T1 (7.27 t/ha) from across locations showed higher grain yield. These hybrids could be included in further investigation for grain yield and related traits and could be possible candidates of future release. Higher 1000-kernel weight was recorded for L14 x T2. Cross combination L5 x T1 was the earliest cross for anthesis and silking date with corresponding values of 66 and 67.3 days, respectively. Shorter plant and ear heights were recorded for crosses L5 x T1, L8 x T1, and L37 x T1. Higher number of ears per plant, kernels per row and rows per ears were recorded for crosses L12 x T2, L34 x T1 and L3 x T2, respectively.

Results of L x T analysis showed that line GCA mean squares were significant for all studied traits at most of the study locations, except for number of ears per plant which showed significant line GCA only at Melkasa. Across locations, line GCA means squares were significant for all traits except for number of ears per plant and 1000-kernel weight. Testers GCA mean squares were significant for few traits at certain locations. Across locations, tester GCA mean squares were significant only for days to anthesis and silking.

SCA mean squares were significant mainly for grain yield, days to anthesis and silking, and plant height at most locations. In across location analysis, SCA means squares were significant for most traits except plant height, number of ears per plant and thousand kernel weight.

Significant GCA and SCA mean squares for most traits measured indicated that both additive and non-additive gene actions are important in determining the inheritance of these traits. In most cases, GCA sum of squares component was greater than SCA sum of squares for most of the studied traits, suggesting that variations among crosses were mainly due to additive rather than non-additive gene effects; and hence, selection would be effective in improving grain yield and other agronomic traits.

Based on individual and across locations combining ability analysis, L23, L24, and L41 at Melkasa, L2 and L23 at Dhera, L13 and L41 at Mieso, L25, L23 and L30 at Pawe, and L13, L21, L23, L25, L27, L30 and 41 in comined analysis across locations were found the best general combiners for grain yield. These inbred lines with a high GCA effects for grain yield were desirable parents for hybrids as well as for inclusion in the breeding program, since they may contribute favorable alleles in the synthesis of new varieties.

For days to anthesis and silking, L2, L3, L5, L8 and L11 were the best combiners at most locations and across locations, indicating that these lines had favorable alleles for early maturity.

Inbred lines L1, L5, L8 and L37 were good general combiners for shorter plant height, which are desirable for lodging resistance.

For grain yield, test crosses L4 x T1, L14 x T1, L22 x T2, L23 x T2, L24 x T2 and L33 x T2 has better specific combining ability for grain yield in different locations. These hybrids could be included for further studies for the improvement of grain yield or for direct release for commercial production.

Based on the SCA and GCA effects for grain yield, only 17 elite maize inbred lines were established into A and B heterotic groups. These heterotic groups could serve as sources for developing inbred line and hybrids. However, the testers used in the current study could not clearly discriminate most of the inbred lines into distinict heterotic groups. Therefore further studies should explore the possibility of separating these and other inbred lines into distinct heterotic groups using the currently used and other more divergent testers.

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

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7. APPENDIX

Appendix Table 1. Analysis of variance for grain yield and other agronomic traits of line by tester crosses involving 43 lines and two testers evaluated at Melkasa in 2010

		Mean squares										
Source	df	GY(t/ha)	AD(days)	SD(days)	EPP (#)	PH (cm)	EH (cm)	RPE (#)	KPR (#)	EL(cm)	ED (cm)	TKWT (gm)
Rep	1	22.01**	28.64**	31.11**	0.0005	829.11	1145.46*	0.36	13.09	6.88**	0.57**	47160.01**
Block(Rep)	20	2.10**	3.26**	2.88*	0.02	446.33**	225.10	0.28	6.25	1.73	0.06**	3966.80
Entry	87	1.34*	4.13**	4.54**	0.03*	228.65*	171.57	0.44*	7.34**	1.58**	0.05**	3397.06**
Crosses(Cr)	85	1.32*	3.95**	4.34**	0.03*	229.68*	174.24	0.45*	7.47**	1.59**	0.05**	3471.54**
GCA line	42	1.46**	6.99**	7.52**	0.04*	300.29**	216.27	0.69*	9.10**	2.17**	0.06**	4935.42**
GCA tester	1	0.47	2.41**	6.26**	0.05**	11.39	515.24	0.01	1.62	0.23	0.15**	0.01
SCA	42	1.19**	0.94**	1.12*	0.01	164.28	124.10	0.22	5.98*	1.03	0.03*	2091.05
Ck	1	0.50	22.45**	25.21	0.00	41.11	112.50	0.08	2.88	0.32	0.18	36.13
Ck vs Cr	1	4.31**	1.05	0.98	0.03	327.91	3.23	0.16	0.91	2.36	0.05**	396.43
Error	67	0.53	0.59	0.70	0.01	114.04	145.06	0.21	3.47	0.85	0.01	1943.19
% contribution.GCA		55	88	87	81	65	65	76	60	68	67	70
% contribution.SCA		45	12	13	19	35	35	24	40	32	33	30

** = Significant at P<0.01 level of probability, * = Significant at P<0.05 Level of probability, AD = number of days to anthesis, Df = degrees of freedom, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, Rep= replication, RPE = Number of rows per ear, SD = number of days to silking, TKWT = thousand kernels weight

Appendix Table 2. Analysis of variance for grain yield and other agronomic traits of line by tester crosses involving 43 lines and two testers evaluated at Ziway in 2010

		Mean squares										
Source	df	GY (t/ha)	AD(days)	SD(days)	EPP (#)	PH (cm)	EH (cm)	RPE (#)	KPR (#)	EL (cm)	ED (cm)	TKWT (gm)
Rep	1	41.74**	5.46*	0.69	0.05	0.28	164.20	0.27	248.43**	60.98**	2.12**	69713.68**
Block(rep)	20	2.20**	1.35	4.38*	0.03	244.56	165.76	0.80	11.66	2.40	0.08*	2535.64*
Entry	87	0.76*	5.98**	5.73**	0.02*	143.78*	129.71*	0.63*	7.62*	1.76**	0.04**	794.98
Crosses (Cr)	85	0.74*	5.97**	5.78**	0.02*	146.70*	132.41*	0.64*	7.52*	1.78**	0.04**	787.46
GCA line	42	0.64	9.03**	8.86**	0.02	205.98**	182.18**	0.97**	7.42*	2.06**	0.06**	1032.75
GCA tester	1	0.14	11.99**	8.54*	0.01	54.40	76.48	0.22	28.95*	6.04*	0.05	235.13
SCA	42	0.87*	2.77**	2.63**	0.02	89.62	83.96	0.33	7.12	1.41	0.03	555.33
Ck	1	0.98	7.61	4.50	0.01**	28.13	2.42	0.08**	23.12	1.28	0.02	2217.78
Ck vs Cr	1	1.68	4.82**	2.40	0.01**	11.14	27.32	0.37	0.34	0.36	0.12*	11.52
Error	67	0.47	0.57	1.26	0.01	88.45	77.32	0.41	4.91	0.90	0.02	583.75
% contribution.GCA		42	77	78	55	70	69	75	53	61	69	65
% contribution.SCA		58	23	22	45	30	31	25	47	39	31	35

** = Significant at P<0.01 level of probability, * = Significant at P<0.05 Level of probability, AD = number of days to anthesis, Df = degrees of freedom, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, Rep= replication, RPE = Number of rows per ear, SD = number of days to silking, TKWT = thousand kernels weight

Appendix Table 3. Analysis of variance for grain yield and other agronomic traits of line by tester crosses involving 43 lines and two testers evaluated at Dhera in 2010

		Mean squares										
Source	df	GY (t/ha)	AD (days)	SD(days)	EPP(#)	PH (cm)	EH (cm)	RPE (#)	KPR(#)	EL (cm)	ED (cm)	TKWT(gm)
Rep	1	10.59**	0.01	0.62	0.02	1250.82**	90.67	1.98**	38.18**	55.88**	1.12**	127.97
Block(rep)	20	0.47	9.77**	8.71	0.02	317.59**	291.97**	0.57*	12.26	2.23	0.11	2268.31
Entry	87	0.38**	6.79**	6.56**	0.01	122.27**	129.13*	0.74**	12.41*	2.24*	0.09**	1420.67**
Crosses(Cr)	85	0.37**	6.53**	6.37**	0.01	124.80**	130.14**	0.75**	12.58*	2.28*	0.09**	1453.54**
GCA line	42	0.41**	10.67**	9.93**	0.01	130.31**	162.15**	1.01**	14.65*	2.49*	0.11**	1437.76**
GCA tester	1	1.31*	0.49	3.24	0.0001	372.57*	298.79*	0.03	0.92	0.52	0.02	2800.98*
SCA	42	0.32*	2.54*	2.87*	0.01	113.39**	94.11	0.5*	10.78	2.12	0.08*	1437.24**
Ck	1	0.13	34.45	28.88	0.05	27.38	2.42	0.18	3.13	0.72	0.02	0.13
Ck vs Cr	1	0.91	0.56	0.94	0.02	1.79	170.02	0.30	7.38	0.28	0.11	47.48
Error	67	0.18	1.47	1.59	0.009	58.28	85.68	0.29	7.78	1.45	0.04	711.46
% contribution.GCA		58	81	78	60	55	64	67	58	54	56	51
% contribution.SCA		42	19	22	40	45	36	33	42	46	44	49

** = Significant at P<0.01 level of probability, * = Significant at P<0.05 Level of probability, AD = number of days to anthesis, Df = degrees of freedom, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, Rep= replication, RPE = Number of rows per ear, SD = number of days to silking, TKWT = thousand kernels weight

Appendix Table 4. Analysis of variance for grain yield and other agronomic traits of line by tester crosses involving 43 lines and two testers evaluated at Mieso in 2010

		Mean Squares										
Source	df	GY(t/ha)	AD (days)	SD (days)	EPP(#)	PH (cm)	EH (cm)	RPE (#)	KPR (#)	EL (cm)	ED(cm)	TKWT(gm)
Rep	1	39.69**	190.28**	166.14**	0.24**	136.51*	6.96	0.31	87.83**	25.54**	0.63**	15582.44*
Block(rep)	20	2.14**	11.95**	13.80**	0.02	184.75*	150.64**	0.41	18.22	6.41**	0.18**	4234.75*
Entry	87	0.52*	7.90**	9.66**	0.011*	104.76*	85.68*	0.48*	9.28*	2.18*	0.05*	2273.60**
Crosses(Cr)	85	0.53**	7.58**	9.31**	0.01	105.98*	87.48*	0.49*	9.30*	2.18*	0.04	2189.48**
GCA line	42	0.64**	10.73**	12.33**	0.01	81.28	119.91**	0.56*	8.53	2.10*	0.06	1873.20*
GCA tester	1	0.18	0.001	0.10	0.02	497.28**	0.62	1.16*	3.44	1.79	0.003	8249.64**
SCA	42	0.44	4.61**	6.50**	0.01	121.35*	57.11	0.41	10.22*	2.27*	0.03	2361.47**
Ck	1	0.02	2.88	1.81	0.00	1.62	10.13	0.02	4.81	0.13	0.05	5010.01
Ck vs Cr	1	0.004	40.09**	47.54**	0.00	104.83	8.62	0.25	11.55	4.23	0.31**	6687.34*
error	67	0.31	1.69	1.76	0.01	67.89	58.60	0.29	5.35	1.31	0.03	1071.04
% contribution.GCA		59	70	66	51	43	68	59	46	49	63	47
% contribution.SCA		41	30	34	49	57	32	41	54	51	37	53

** = Significant at P<0.01 level of probability, * = Significant at P<0.05 Level of probability, AD = number of days to anthesis, Df = degrees of freedom, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, rep = replication, RPE = Number of rows per ear, SD = number of days to silking, TKWT = thousand kernels weight

Appendix Table 5. Analysis of variance for grain yield and other agronomic traits of line by tester crosses involving 43 lines and two testers evaluated at Pawe in 2010

		Mean squares										
Source	df	GY (t/ha)	AD(days)	SD (days)	EPP(#)	PH (cm)	EH (cm)	RPE(#)	KPR(#)	EL (cm)	ED (cm)	TKWT (gm)
Rep	1	24.56**	5.46**	3.55	0.01	1452.45**	846.57**	1.58	15.66**	13.33**	0.38**	37115.53**
Block(rep)	20	2.57**	1.59	1.55	0.01	444.00**	311.20**	0.34	7.13**	2.89**	0.05**	2746.43**
Entry	87	2.29**	5.42**	5.38**	0.01	168.40**	99.07**	0.59**	6.54**	1.93**	0.05**	1565.47**
Crosses(Cr)	85	2.24**	5.29**	5.27**	0.01	162.14**	92.83**	0.59**	6.13**	1.63**	0.05**	1573.87**
GCA line	42	3.43**	8.47**	8.24**	0.01	265.77**	137.98**	0.86**	10.08**	2.76**	0.05**	2179.84**
GCA tester	1	3.49**	6.42**	9.31**	0.05	144.56*	86.20	0.39	0.003	0.09	0.45**	2249.12
SCA	42	1.01**	2.08**	2.19**	0.01	58.92*	47.84*	0.33*	2.33	0.55	0.03**	951.82
Ck	1	7.68	16.82	17.41**	0.02	856.98*	658.85*	0.32	27.38	26.64	0.08	1842.25
Ck vs Cr	1	1.39	5.06**	2.98*	0.01	12.48	369.76**	0.40	20.35**	1.98	0.03	574.87
error	67	0.49	0.55	0.64	0.01	36.45	29.68	0.21	2.10	0.60	0.01	817.78
% contribution.GCA		78	81	79	36	82	75	72	81	83	70	70
% contribution.SCA		22	19	21	64	18	25	28	19	17	30	30

** = Significant at P<0.01 level of probability, * = Significant at P<0.05 Level of probability, AD = number of days to anthesis, Df = degrees of freedom, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, Rep= replication, RPE = Number of rows per ear, SD = number of days to silking, TKWT = thousand kernels weight

Appendix Table 6. Estimates of mean values for grain yield and related traits at Melkasa

Genotypes	GY(t/ha)	AD(days)	SD(days)	EPP(#)	PH(cm)	EH(cm)	RPE(#)	KPR(#)	EL(cm)	ED(cm)	TKWT(gm)
L1 x T2	7.04	74.2	75.5	1.1	195.2	107.5	15.8	39	15.4	5	339.3
L2 x T2	8.57	70.9	72.1	1.2	226.6	107.5	14.6	39.2	15.8	4.7	337.7
L3 x T2	6.89	72.5	73.6	1.1	195.9	125	16.2	32.5	13.7	4.6	292.8
L4 x T2	7.72	75.7	77.5	1	239.8	125	13.6	42.9	17.8	4.9	407
L5 x T2	6.35	72.4	73.7	1	207.9	102.5	14	38.6	15.2	4.6	378.2
L6 x T2	6.64	76.7	77.8	1.1	229	132.5	13.6	40.2	16.3	4.7	287.4
L7 x T2	8.39	73.8	74.3	1	203.3	97.5	14.6	39.6	18.9	5	513.2
L8 x T2	7.87	73.1	74.2	1.1	223	105	13.6	35	16.9	4.6	409.5
L9 x T2	7.38	75.9	77.3	1	252.1	147.5	13.4	38.6	16	4.9	423.6
L10 x T2	8.13	76.9	78.1	1.2	230.5	122.5	14.2	39.3	17.5	4.6	282.4
L11 x T2	8.53	72.8	74	1.1	236.4	137.5	15	35	17.5	4.9	402.5
L12 x T2	8.2	76.8	77.8	1.5	201.6	110	13.8	36.4	14.8	4.3	367.9
L13 x T2	6.74	77.2	78.6	1.1	229.8	125	14.8	36.9	15.2	4.5	297.1
L14 x T2	5.53	78.8	81.3	1	218.6	125	14.4	34.4	15	4.7	430.8
L15 x T2	7.78	76	77.4	1.4	217.5	125	13.6	39.1	16.3	4.7	390.4
L16 x T2	7.37	76.7	78.1	1	191.9	115	14.4	34.7	14.8	4.5	334.1
L17 x T2	7.17	78	78.5	1.2	237.2	132.5	13.8	34.7	14.2	5	432.4
L18 x T2	6.62	74.6	76.9	1.1	220.9	117.5	14	38.4	15.1	4.5	402
L19 x T2	8.83	75.4	75.9	1.2	247.5	135	13.2	35	15	4.8	473.3
L20 x T2	7.97	74.5	77.1	1.1	213.6	112.5	14.2	35	16	5	413.9
L21 x T2	8.7	73.7	76.3	1.3	237.6	132.5	14.2	35.6	14.9	4.9	381.2
L22 x T2	8.46	72.8	73.7	1.2	217.4	115	14.4	39.4	15.7	4.9	368.5
L23 x T2	11.42	77.1	78.1	1.6	237.7	120	14	40.9	16	4.9	291.6
L24 x T2	11.67	77.8	78.5	1.6	240	120	13.8	37.2	16.4	4.7	309.1
L25 x T2	9.7	77.4	78.5	1.6	224.6	125	13	41.2	16.3	4.6	296.6
L26 x T2	7.61	76.2	77.9	1.1	206.7	125	14.8	38	15.6	4.7	301.9

Appendix Table 6 (Continued)

L27 x T2	8.09	76.6	78	1.1	236.5	137.5	13.8	41.5	17.1	5	327.5
L28 x T2	8.05	75	76.9	1.4	225.3	112.5	14	38.6	15.5	4.6	368.4
L29 x T2	8.98	75.3	77	1.2	230.5	142.5	15	40.2	17.3	4.9	410.8
L30 x T2	8.59	78.6	80.6	1	222.3	135	13.6	39	17.2	4.8	328.8
L31 x T2	8.56	74.5	76.6	1.1	227.9	135	13.6	37.6	16	4.5	361.8
L32 x T2	8.67	77.3	78.5	1.2	241.5	130	14.8	39.2	17.5	5	323.4
L33 x T2	11.19	75.2	76.7	1.2	212.1	130	13.8	42.5	20.4	4.8	353.9
L34 x T2	6.96	78.6	80	1.3	220	112.5	13.2	37.8	17.7	4.2	349.3
L35 x T2	6.54	79.3	80.8	1.2	206.8	107.5	13.2	38.8	18.1	4.4	477.4
L36 x T2	8.48	76.9	77.9	1.3	231	127.5	15.2	38.4	18.3	4.9	345.8
L37 x T2	9.9	73.5	74.6	1.1	222.3	135	14.2	37.1	17.6	4.9	480.2
L38 x T2	6.62	78	80	1.1	225.8	140	14.6	33.4	15.1	4.6	352.6
L39 x T2	7.94	77.3	78.4	1.2	218.8	135	14	37.3	16.9	4.4	398.1
L40 x T2	7.78	76.2	78.1	1.2	206	110	14.2	39.3	16.5	4.8	433.5
L41 x T2	9.44	77.5	78	1.2	235.5	127.5	13	31.8	16.3	4.6	365.8
L42 x T2	8.36	77.3	78.2	1.2	206.8	127.5	13.8	38.9	17.5	4.3	349.3
L43 x T2	8.6	76.6	77.8	1.1	231.9	127.5	14.4	38.1	15.8	4.8	352.4
L1 x T1	8.4	71.8	73	1.3	191.7	122.5	14	34	14.8	4.7	326.1
L2 x T1	9.16	71.2	72.2	1.1	222.4	105	14.8	32.9	15.6	4.8	381.3
L3 x T1	7.94	73.5	74.4	1	209.6	95	16	40.3	15.8	4.8	314.5
L4 x T1	8.81	75	76.9	1.2	236.2	140	14.2	42.5	17.8	4.7	381.9
L5 x T1	8.56	70.6	71.3	1.1	186.2	92.5	13.2	39.1	15.5	4.8	373.5
L6 x T1	7	77.6	78.6	1.2	243	137.5	14.6	36	15.8	4.9	244.9
L7 x T1	9.7	71.9	73.6	1	196.3	95	14	39	17.9	5	455.7
L8 x T1	7.04	72.8	73.8	1.1	192.5	97.5	14.4	38.7	18	4.8	354
L9 x T1	6.91	74.5	77.2	1.1	191.9	97.5	14.2	34.5	14.7	4.6	346.3

Appendix Table 6 (Continued)

L10 x T1	8.65	76	77.6	1.2	222.3	140	14.6	37.4	15.6	4.6	342.1
L11 x T1	9.86	72.1	73.6	1.4	214.5	120	14	37.9	17.3	4.7	382.9
L12 x T1	7.06	77	78	1.7	206	97.5	13	34.5	14.6	4.4	345
L13 x T1	8.23	76	77.6	1.2	220.6	100	14.6	36.8	15.6	4.8	348.2
L14 x T1	7.6	77.3	79.4	1.1	237.4	132.5	14.2	35.4	16.6	4.9	364
L15 x T1	7.75	76.2	77.6	1.2	242.4	140	13.6	38.8	16.1	4.7	287.3
L16 x T1	6.8	76.8	77.8	1.1	218.8	115	14.2	42.1	16.7	4.8	350.8
L17 x T1	9.53	75.4	76	1.2	230.8	120	14.4	35.9	16.2	5.2	412.4
L18 x T1	8.2	74.4	76	1.3	213.8	117.5	13.4	40.2	16.5	4.9	407.3
L19 x T1	7.56	74.2	75.7	1.3	229.4	110	13.2	31.1	14.6	4.7	423.9
L20 x T1	8.42	75.5	75.9	1.1	216.6	110	14.6	31	15.1	5	358.2
L21 x T1	10.61	74.8	75	1.4	231.9	142.5	13.8	37.9	16	5.4	488.5
L22 x T1	8.92	74.1	75	1.2	248.5	135	14.2	39.4	17	5.1	400.5
L23 x T1	8.92	77.7	79.2	1.5	247.5	135	14.2	35.5	15.3	4.5	368.7
L24 x T1	7.88	77.1	78.2	1.3	222.9	117.5	13.2	36.8	15.6	4.5	367.6
L25 x T1	8.5	77.9	78.8	1.5	235.9	130	13	39.6	15.7	4.6	314.3
L26 x T1	8.2	76	76.9	1.1	227.6	119.5	14	39.9	15.1	5	492.5
L27 x T1	9.11	76.2	77.6	1.1	243.4	127.5	13.8	40.5	16.3	5	288.5
L28 x T1	7.88	75.2	76.2	1.1	211.1	127.5	13.8	39.3	16.9	4.8	355.9
L29 x T1	9.04	78	78.8	1.5	221.4	115	15.4	38.8	16.4	4.7	392.9
L30 x T1	9.21	77.6	78.3	1.3	255	130	14	40	18.4	4.7	351.4
L31 x T1	7.18	74.4	74.8	1.1	219.4	120	14	39.1	16	4.9	373.9
L32 x T1	7.15	77.9	78.5	1.2	208.7	102.5	14.6	34.9	15.7	4.8	306.2
L33 x T1	6.79	78	80.1	1.3	230.3	115	14	36.2	15.5	4.6	266.7
L34 x T1	8.93	75	75.5	1.5	221.8	112.5	15.2	41.3	19.1	4.8	369.8
L35 x T1	8.32	76.8	77.8	1.4	221.2	127.5	14.2	39.1	17.5	4.5	318.3
L36 x T1	6.31	77.8	79.4	1.2	223.3	115	15.2	33.9	14.2	4.6	295.9
L37 x T1	9.08	74.7	75.9	1.1	215.8	105	14	37	16.9	4.9	530

Appendix Table 6 (Continued)

L38 x T1	8.51	76.9	77.7	1.3	225.8	140	14.6	37.7	15.2	5	372.5
L39 x T1	7.98	76.5	79.1	1.3	227.3	127.5	13	40.6	18.7	4.8	374.3
L40 x T1	8.37	76.1	76.5	1.1	215.5	120	14.4	38.5	16.1	5.1	405.3
L41 x T1	10.26	76.5	77.7	1.4	238.5	122.5	13.4	35.1	17.1	4.9	501.3
L42 x T1	7.93	74.7	75.7	1.1	216.5	120	13.6	42.7	18.1	4.6	448.8
L43 x T1	8.12	77.5	78.7	1.1	220.3	115	13.8	32.6	15.1	4.7	358.3
BH-543	7.23	78.3	79.8	1.1	230.9	115	14.6	38.2	17.8	4.3	350.2
Melkasa-2	6.23	71.6	72.7	1.1	240	130	14.2	35.8	17	4.9	366.7
Cr mean	8.21	75.7	77	1.2	222.5	121.2	14.1	37.7	16.3	4.8	370.8
Ck mean	6.73	75	76.3	1.1	235.5	122.5	14.4	37	17.4	4.6	358.5
Mean	8.18	75.7	76.9	1.2	222.8	121.2	14.1	37.7	16.3	4.8	370.5
LSD (5%)	2.04	2.2	2.4	0.3	30.1	34	1.3	5.3	2.6	0.3	124.4
CV	12.5	1.4	1.5	11.5	6.8	14	4.6	7	8	3.3	16.8
Min	5.53	70.6	71.3	1	186.2	92.5	13	31	13.7	4.2	244.9
Max	11.67	79.3	81.3	1.7	255	147.5	16.2	42.9	20.4	5.4	530

AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH=plant height, RPE= Number of rows per ear, SD= number of days to silking, TKWT= thousand kernels weight

Appendix Table 7. Estimates of mean values for grain yield and related traits at Ziway

Genotypes	GY(t/ha)	AD(days)	SD(days)	EPP(#)	PH(cm)	EH(cm)	RPE(#)	KPR(#)	EL(cm)	ED(cm)	TKWT(gm)
L1 x T2	4.5	70	70.2	0.8	190.5	95.6	15	36.6	12.5	4.5	276.6
L2 x T2	4.5	68.5	70.4	1.1	225	107	14.4	35.7	14.5	4.5	227
L3 x T2	4.5	69	69.4	1	210.8	110	16	37.7	15.2	4.3	208.2
L4 x T2	3	73.4	75.9	1	233.9	127.5	13.6	36.3	14	4.1	195.8
L5 x T2	3.6	69.4	70.8	1	197	102.7	13.6	33.4	11.2	3.9	190.9
L6 x T2	4.1	74	76.2	1	220.6	115.5	13.6	36.4	15	4.3	198.5
L7 x T2	3.5	68.9	71.4	0.8	205.1	105.3	14.1	35.4	13.6	4	205.2
L8 x T2	5	69	71	0.9	198.5	97.4	13.2	36.8	14.3	3.9	253.3
L9 x T2	3	73.5	76.8	0.8	218.3	113	13.6	33.9	13	4.4	245.7
L10 x T2	4.5	73	75.2	1	208.2	107.6	15.4	36.1	14.3	4.2	244.7
L11 x T2	4.5	70.5	73.7	0.9	225.8	125.6	14.4	33	13.6	4.1	244.2
L12 x T2	4.7	70.5	72.6	1.3	209.7	112.2	13.2	34.9	11.8	3.9	187.2
L13 x T2	4.2	72.9	74.8	1.2	234.9	122.2	14.8	35.1	14.6	4.4	219.4
L14 x T2	3.2	76	78.1	0.9	214.2	124.7	14.4	33.4	12.5	4.3	212
L15 x T2	3.7	73.4	75	0.9	223.6	130	13.8	35.9	13.2	4	225.9
L16 x T2	3.7	73	75.1	0.9	225.5	122.2	14.8	33.5	13.1	4.2	303
L17 x T2	3.4	74.6	75.7	0.9	218.9	124.7	14.2	33	12.5	4.5	246
L18 x T2	3.8	73	74.9	1	211.7	115	14.2	38.2	14.4	4.3	247.8
L19 x T2	4.6	70	71.9	1.2	232.9	132.4	14	34.6	13.6	4.4	263.3
L20 x T2	4.5	70.5	73.7	1	215	122.6	14.2	34.8	14.6	4.4	295.2
L21 x T2	4.7	70.4	73.4	1.1	220	125.3	13.8	29.4	11.1	4.4	224.6
L22 x T2	4.7	68.9	69.9	0.9	210	119.9	13.6	30.3	12	4.5	271.9
L23 x T2	5.2	74.1	75.4	1	205.8	105.4	14.2	36.4	12.8	4.3	208.3
L24 x T2	5.8	75.5	76.8	1.1	226.7	112.7	13.8	38.1	14.9	4.2	232.6
L25 x T2	4.3	75.1	76.1	1.1	218.1	110.2	13.2	39.5	14.7	4.3	211.4
L26 x T2	4	72.6	74.4	1	203.4	114.7	15	36.7	13	4.6	250

Appendix Table 7 (Continued)

L27 x T2	5.7	73	75.8	0.9	216.5	102.2	13.2	34.8	12.4	4.3	208
L28 x T2	4	73.9	75.3	1.4	218.3	114.9	13.6	30.6	11.8	4.2	247.5
L29 x T2	4.8	75	75.5	1.3	216.2	119.8	14	35.4	13.5	4.1	240.3
L30 x T2	3.4	76	78.5	1	226.4	125.3	13.2	36.1	13.8	4.1	216
L31 x T2	4	73	74.1	0.9	213.5	112.8	13.4	34.4	13.2	4.3	219.6
L32 x T2	4	73	75	1.1	225.6	117.3	15.4	35.9	14.5	4.5	230.7
L33 x T2	5.5	73	75.2	0.9	227.4	112.6	14.6	39.5	15.6	4.3	255.7
L34 x T2	4.2	75.5	78.6	0.9	221.9	115	13.2	36.9	15.9	4	215.9
L35 x T2	3.2	75	77.3	0.8	216.7	109.7	13.8	38.6	16.4	4	236.6
L36 x T2	5.6	73.1	74.8	1.1	228.5	117.1	14.6	38.6	15.4	4.4	207
L37 x T2	4.7	72.5	73.7	1.1	202.2	105	13.2	37.7	15	4	224.7
L38 x T2	3.6	75.5	75.9	1.5	206.7	114.4	13.6	35.9	13	4	231.9
L39 x T2	6.4	75.5	77.3	1.5	216.2	119.6	14.4	40.3	16.8	4.2	241.8
L40 x T2	3.1	76	76.9	1	213.2	119.9	14.2	33.3	13.2	4.1	251.4
L41 x T2	4.1	74.1	74.8	0.9	218.5	112.2	13.2	35.6	14	4.1	289.1
L42 x T2	3.8	74.4	75	0.9	218.1	135.4	13.6	36.6	13.4	3.9	172.3
L43 x T2	5	70.1	71.3	1	225.2	125	13.4	39.8	15.1	4.2	236.4
L1 x T1	5.1	69.6	71.1	1.3	199.7	109.8	14.6	28.3	10.5	4.1	179.6
L2 x T1	4.9	69.4	71.8	1	219	97.1	13.2	31.4	12.3	4.3	260.6
L3 x T1	3.4	69.5	71.8	0.8	205.3	109.9	16	35.5	13.3	4.1	202.6
L4 x T1	5.9	68.6	71	0.9	218.6	109.9	10.8	34.9	13.5	4	233.4
L5 x T1	3.7	68	69.1	1	175.4	85.1	12.2	37	13.4	4.2	247.1
L6 x T1	3.5	74.9	76.5	1	222.3	140.2	14.8	33.9	12.8	4.3	199.9
L7 x T1	5.3	67.5	70.5	0.9	197.4	102.4	13.6	39.7	16.9	4.5	265.2
L8 x T1	4	68	69	1.1	197.5	87.5	14	35.4	14.5	4.1	245.6
L9 x T1	4.4	69.9	74.7	1.1	221.5	115.2	14.2	35.6	14.1	4.3	234.2
L10 x T1	4.6	71.6	73.9	1	225.9	125.5	14.8	34.4	11.8	4.3	230.8
L11 x T1	4.4	70	71.1	1	215.2	117.7	14.8	34.7	13.6	4.2	263.4

Appendix Table 7 (Continued)

L12 x T1	4	76	76.9	0.9	216.4	114.8	14	30.7	11.5	4	217.4
L13 x T1	5	70.4	73	1	229.2	112.4	15	37.7	14.1	4.4	198.3
L14 x T1	3.8	75	73.9	0.8	215.4	105.4	13.8	34.4	12.8	4.4	240.6
L15 x T1	5.3	70.5	73.9	1.3	213.7	117.5	12.8	38.5	13.1	4.1	241.1
L16 x T1	2.8	70.5	73.6	0.8	200.6	102.3	14.4	30.7	12.5	4.3	267.4
L17 x T1	4.7	73	74.8	1	230.9	137.5	13.8	32	11.2	4.4	269.3
L18 x T1	5.3	70	72.1	1	206.7	99.9	13.2	37.7	14.6	4.4	251
L19 x T1	3.9	72.9	73.5	1.1	231.5	127.6	13.2	30.6	12.6	4.3	268.7
L20 x T1	2.7	73	75.3	0.9	204	105.2	14.2	30.2	12	4.5	230.5
L21 x T1	4.8	71.1	73.4	0.9	227.3	122.5	14.4	37.4	13.8	4.6	231.5
L22 x T1	3.8	69.6	71.3	0.9	227.3	137.5	13.6	33.9	12.9	4.7	264.7
L23 x T1	5.3	78.9	79.7	1	243.4	129.5	13.4	36.7	14	4.3	233.7
L24 x T1	5.6	74	75.2	1.2	216.7	119.9	13.4	35.2	13.7	4.3	258.5
L25 x T1	3.1	77	79.5	0.9	233.5	117.9	13.2	30.5	11.2	3.7	179.5
L26 x T1	5.5	70	72	1	207.9	112.8	15.6	37.1	13.6	4.9	235.3
L27 x T1	4.6	72.9	75	1	212.8	107.5	13.4	35.1	12.6	4.2	236
L28 x T1	4.1	70.6	72.7	0.9	226.8	127.2	13	35.4	13.2	4.2	246.7
L29 x T1	4.8	72.9	74.9	1	234.6	127.3	14.2	34.4	13.7	4.4	239.3
L30 x T1	5.5	74	76.5	1.1	230.2	127.2	14	37.1	15	4.4	272.2
L31 x T1	4.7	70	72	0.9	193.5	90.3	13.8	35.1	13.1	4.4	258
L32 x T1	2.8	75.5	78	0.9	200.8	102.8	15	30.7	11.8	4.2	194.2
L33 x T1	3	74	77	0.9	205.4	97.5	13.4	33.3	12.6	4	211.1
L34 x T1	4.2	73.5	75.2	1.2	223.5	120.6	14	41.2	16.2	4	200.8
L35 x T1	4.2	73	76	1.1	199.8	107.4	14.8	36.5	13.8	4.1	205.2
L36 x T1	3.7	72.6	74.3	1.1	209.1	107.6	14.4	35.3	13.8	4.4	206.7
L37 x T1	4.4	70.1	72.3	1.1	191.8	100.2	14.2	36.3	14.3	4.3	226
L38 x T1	3.1	73	73.3	0.9	211.9	112.1	13.6	32.2	12.7	4.1	237.7
L39 x T1	4.3	73.6	74.3	1.2	229.3	142.1	13.6	34.6	13.5	4	272.6

Appendix Table 7 (Continued)

L40 x T1	4.9	73.5	74.5	0.9	212.8	117.3	14.6	32.1	12	4.3	233.8
L41 x T1	5.9	71.1	73.3	1.1	227.9	119.9	13.4	30.5	13.5	4.5	308.3
L42 x T1	6	72.6	73.3	1	217.8	118	14.8	39.3	15.8	4.3	239.8
L43 x T1	2.8	74.4	75.5	1	216.5	110.5	13.2	32	12.3	4.1	217.5
BH-543	4.1	75.9	76.8	1	209.7	119.7	14.6	38.1	13.9	4.1	265.4
Melkasa-2	2.7	72	73.8	0.9	217.2	117.5	14.2	31.3	12.3	3.9	198.8
Cr mean	4.3	72.4	74.2	1	215.8	114.9	14	35.1	13.5	4.3	234.5
Ck mean	3.4	74	75.3	1	213.5	118.6	14.4	34.7	13.1	4	232.1
Mean	4.3	72.4	74.2	1	215.8	114.9	14	35.1	13.5	4.2	234.5
LSD (5%)	1.9	2.1	3.2	0.3	26.5	24.8	1.8	6.3	2.7	0.4	68.2
CV	22.5	1.5	2.1	16	6.2	10.8	6.5	8.9	9.9	4.6	14.6
Min	2.7	67.5	69	0.8	175.4	85.1	10.8	28.3	10.5	3.7	172.3
Max	6.4	78.9	79.7	1.5	243.4	142.1	16	41.2	16.9	4.9	308.3

AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH=plant height, RPE= Number of rows per ear, SD= number of days to silking, TKWT= thousand kernels weight

Appendix Table 8. Estimates of mean values for grain yield and related traits at Dhera

Genotypes	GY(t/ha)	AD(days)	SD(days)	EPP(#)	PH(cm)	EH(cm)	RPE(#)	KPR(#)	EL(cm)	ED(cm)	TKWT(gm)
L1 x T2	3	76.6	78.7	1	180.6	96.3	15	29.2	12.1	4.4	199.9
L2 x T2	4	73.1	75	1.5	196.9	93.3	14	31	13.3	4.7	190
L3 x T2	3.5	75.9	78.3	1.1	198.2	110.9	16	34.2	14.6	4.6	152.6
L4 x T2	2.1	78.4	84	0.9	192.8	92.1	14.2	31.3	12.6	4	210.8
L5 x T2	2.9	75	77.9	1	182.5	95.3	12.4	28.7	11.1	4	156.3
L6 x T2	2.5	80.2	83.2	1	208	109.1	14.4	32.4	12.2	4.1	205.6
L7 x T2	2.1	76.1	77	0.9	200.2	90.4	13.8	32	12.7	4.5	284.8
L8 x T2	3	73.8	77.1	1	186.2	81.9	13.6	26.3	11.4	4	219.8
L9 x T2	3	73.4	75.4	1	189.8	90.1	14.2	30.4	13.1	4.2	185.6
L10 x T2	2.8	80.2	82	1	202.4	120.1	13.8	33.2	12.6	4.3	159
L11 x T2	3	77.8	81.8	1	187.5	97.5	14.6	31.5	14.1	4.3	194.7
L12 x T2	1.8	78.9	81.2	1.1	187.6	94.8	12.8	32.5	13.3	4.2	148.9
L13 x T2	2.6	78.9	79.8	1	198.5	101.7	13.8	28.4	12.6	4.7	194.1
L14 x T2	1.6	83.9	86	0.8	194.3	102.5	13.2	23	10.6	4.1	199.8
L15 x T2	2.9	79.7	80.9	1.1	194	112.5	13.2	35.7	13.1	3.9	136.8
L16 x T2	1.9	81.8	83.7	1.1	182.8	85.1	14.5	26.2	11.7	4.3	222.9
L17 x T2	2.6	81.3	82.3	1	187.7	96.4	13.5	33.9	15	5.1	261.5
L18 x T2	2.5	79	82.1	1	197	95.8	14	27	11.7	4.4	189.9
L19 x T2	2.5	79.4	81.6	1	206.9	111	13.4	30.4	12.7	4.3	178.4
L20 x T2	3	80	82.4	0.9	208.9	114	14.6	28.2	12.7	4.6	215.2
L21 x T2	2.5	79.3	83.3	0.9	193	94.9	13.9	24.7	10.3	4.4	235.3
L22 x T2	3.1	76.8	78.7	1	202.8	110.6	13.6	28.2	11.9	4.8	219.5
L23 x T2	2.5	82.3	84.6	0.9	200.1	95.2	13.2	30.1	12.7	4.5	215.6
L24 x T2	2.4	82.2	84.1	1	202.1	115.9	13.1	30	12.6	4.3	192.6
L25 x T2	2.4	82	83.5	1	193.2	102.8	13.6	36	13.9	4.3	168.7
L26 x T2	2.3	81.2	83.1	1	190.7	85.3	15	22.6	10.3	4.2	185

Appendix Table 8 (Continued)

L27 x T2	2.8	80.7	82.9	0.9	205.4	103.2	13.8	32.8	13.4	4.5	213.4
L28 x T2	1.6	79.8	82.4	0.9	188.3	96.2	13.4	27	11.5	4.2	196.4
L29 x T2	2.2	82.7	84.7	1.1	204.7	109.4	14.2	27.4	11.1	4	162.2
L30 x T2	2.6	80.2	84.6	1.1	205.3	126.3	13.8	34.8	14.9	4.6	140.9
L31 x T2	2.6	79.9	82.7	0.9	192.1	97.7	14.2	33.5	13.6	4.3	256.7
L32 x T2	1.6	82.8	84.9	0.8	209.5	98.1	15	28.6	11.9	4.5	211.7
L33 x T2	2.4	80	83.5	1	194.6	100.3	13.8	33.6	13.1	4.4	209.9
L34 x T2	1.3	83.4	85.4	0.9	178.6	89.6	13.2	26.4	11.4	3.5	146.4
L35 x T2	2	84	85.8	0.9	192.7	94.7	13.4	32	14.3	3.7	128.5
L36 x T2	2.3	81.2	83.8	0.8	184	84.6	16.4	28.7	12.9	4.8	180.1
L37 x T2	3.9	79.4	80.7	1	196.9	107.6	14.4	36.7	16.2	4.3	193
L38 x T2	1.7	81.7	84	0.8	205.9	105.6	14.8	24.8	10.2	4.1	205.3
L39 x T2	3	82.8	84.6	0.9	202.7	96.6	13.3	29.6	13.4	4.3	279.9
L40 x T2	2.1	82.6	84.8	0.9	195.1	110.9	13.2	30.6	12.2	4.1	215.7
L41 x T2	2	81.2	83.9	0.9	183.8	88.2	13.1	37.3	17.4	4.5	295.4
L42 x T2	2.6	79.7	83.7	1	203.8	102.7	13.8	33	12.9	4	151.7
L43 x T2	2.8	80.5	84	1	186.6	96.7	13.8	29.4	12.7	4.6	195.5
L1 x T1	3	77.5	80.1	1	200.2	110.1	14.8	33.3	14.1	4.5	185.3
L2 x T1	3.7	77.1	78.4	1	193.1	80.5	14.4	32.5	15.1	4.6	290.6
L3 x T1	2.4	76.6	79.1	1	189.8	109.5	14.8	31.8	12.7	4.2	144.8
L4 x T1	2.9	77.7	81.6	0.8	185.2	75.3	14.1	33.5	15.8	4.5	305.5
L5 x T1	3.3	75.6	77.8	1	164.3	77.9	11.8	27.4	10.9	4.1	222.5
L6 x T1	2.1	79.8	82.2	1	202.8	103.4	15.2	29.8	12	4.3	161.2
L7 x T1	3.2	76.2	78.2	0.8	195.4	105.2	13.2	33.6	15.3	4.4	219.2
L8 x T1	2.4	73.6	77.3	1.1	165.4	72.6	12.4	29	13.7	3.7	161.8
L9 x T1	3.2	81.3	83.6	1	181.2	100.9	13	28.3	13.1	4.4	202.4
L10 x T1	3.3	83.8	84.9	1	193.8	109.2	14.1	33.6	13.8	4.7	207.7
L11 x T1	3.3	76.6	78.4	1	196.6	97.6	14	30.5	13.8	4.2	271.2

Appendix Table 8 (Continued)

L12 x T1	2.3	81.6	83.2	1	190.2	108.1	13.8	29.4	11.5	4.4	195.4
L13 x T1	3.1	78.7	80.4	1.1	197.4	103.3	16.6	27.6	12.4	4.4	183.9
L14 x T1	3.1	82.5	83.4	1	211.6	112.1	13.9	28.5	12.1	4.4	183.7
L15 x T1	2.9	78.1	80.2	1	186.5	98.9	13.6	35.6	14.1	4.4	184.5
L16 x T1	3.5	80.4	82.6	1	191.7	102.3	14	30.8	12.7	4.7	213.5
L17 x T1	3.8	80.5	83	1	200.3	94.6	14.1	32.9	12.2	4.9	278.2
L18 x T1	2.9	77.6	80.1	0.9	184.3	87.4	14.8	31.2	13.1	4.5	213.4
L19 x T1	3.2	79	83	0.9	192.5	92.7	13.8	25.7	12.5	4.6	166.1
L20 x T1	2.7	79.4	80	1	204.3	112.7	14	28.8	12.3	4.5	236.2
L21 x T1	2.2	82	83.9	0.9	194.6	98.2	13.8	23.4	9.9	4.2	199.2
L22 x T1	1.9	77.9	82.5	1.2	180.7	93.8	12.6	21.5	10.2	4	199.1
L23 x T1	2.7	82.5	85.4	0.9	196.6	91.3	13.8	32.7	13.8	4.8	219.2
L24 x T1	3.1	82	83.9	1	200.7	95.1	13.4	34	14.8	4.5	263.3
L25 x T1	2	83.4	85.8	1	211.2	109.2	12.6	25.6	10.4	3.7	175.3
L26 x T1	3.5	76.7	79.1	0.9	194.7	86.4	14	29.9	11.8	4.6	174.7
L27 x T1	3.2	79	80.6	1	191.1	91.4	12.8	32.8	13	4.6	243.8
L28 x T1	3.1	79.3	80.9	1	196.2	103.4	14.4	30.5	12.9	4.3	210.2
L29 x T1	3.8	79.9	81.4	1	200.9	103.6	16.6	33.8	14.3	5	218
L30 x T1	2.5	83	84.5	1	192.7	105.1	13.8	31.9	13.4	4.5	219.1
L31 x T1	2.6	77.3	79.5	1	188.2	90.8	13.8	30.4	12.8	4.2	188.1
L32 x T1	1.3	83.1	85.7	0.8	170.6	85.7	14.6	23.1	10.5	4	209.1
L33 x T1	1.6	80.9	83	0.9	177.6	71	14	28.3	12.4	4	180.1
L34 x T1	3.1	81.7	82.6	1.1	193	109.9	13.5	39.5	17.6	4.4	279.1
L35 x T1	2.9	80.9	82.9	1	198.2	100.7	14.2	33.5	14	4.2	203
L36 x T1	2.1	81.1	83.8	0.8	174	79.4	14	25.3	11.2	4.4	228
L37 x T1	3.2	77.1	79.9	0.8	147.5	68.9	12.5	25.3	11.5	3.8	168.6
L38 x T1	2.1	80	81.4	0.9	196	103.4	14.6	30.4	12.6	4.5	216.9
L39 x T1	2.3	80	82.1	1.1	205.7	115.6	14.2	29.2	13.2	3.9	176.1

Appendix Table 8 (Continued)

L40 x T1	2.5	79.8	82.1	1	202.1	101.8	13.6	28.5	12	4.6	177.3
L41 x T1	3	79.6	81.9	1	208.1	104.2	13.8	31.3	13.5	4.2	184.1
L42 x T1	1.3	82.2	85	1	172.4	78.2	12.5	31.5	13.6	3.8	211.2
L43 x T1	2.3	80.3	82	1	196.3	102.2	13.8	28.2	12.1	4.2	226.2
BH-543	1.7	83.3	85.1	0.7	190.4	87.8	14.6	30.9	13.8	4.2	208.2
Melkasa-2	2.2	75	77.5	1	197.8	90	14	33.4	12.6	4	208.7
Cr mean	2.6	79.7	82	1	193.1	98.2	13.9	30.2	12.8	4.3	203.5
Ck mean	2	79.2	81.3	0.9	194.1	88.9	14.3	32.2	13.2	4.1	208.5
Mean	2.6	79.7	82	1	193.2	98	13.9	30.3	12.8	4.3	203.6
LSD (5%)	1.2	3.4	3.6	0.3	21.6	26.2	1.5	7.9	3.4	0.6	75.4
CV	23.3	2.2	2.2	14.6	5.6	13.4	5.5	13	13.3	7	18.5
Min	1.3	73.1	75	0.7	147.5	68.9	11.8	21.5	9.9	3.5	128.5
Max	4	84	86	1.5	211.6	126.3	16.6	39.5	17.6	5.1	305.5

AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH=plant height, RPE= Number of rows per ear, SD= number of days to silking, TKWT= thousand kernels weigh

Appendix Table 9. Estimates of mean values for grain yield and related traits at Mieso

Genotypes	GY(t/ha)	AD(days)	SD(days)	EPP(#)	PH(cm)	EH(cm)	RPE(#)	KPR(#)	EL(cm)	ED(cm)	TKWT(gm)
L1 x T2	3.89	61.7	63	0.9	141.4	70.7	13.6	34.8	14	4.1	198.4
L2 x T2	4.21	60.4	60.7	0.9	152.6	77.1	14	35.9	14.5	4.3	339.9
L3 x T2	3.42	60.9	62.3	0.8	130.9	74.1	14.2	27.3	12.1	3.8	185.9
L4 x T2	3.24	67.5	69.8	0.7	138.5	93.3	13.8	29.4	11.3	4.4	153.2
L5 x T2	3.1	58.6	59.3	1	131.4	76.3	13	32	12.8	4	236.3
L6 x T2	4.04	65.3	66.9	0.8	138.8	89.2	12.6	32.2	12.8	4	257.7
L7 x T2	3.58	65.7	67.4	0.9	145.3	70.8	13.8	30.9	14.4	4.2	231.6
L8 x T2	3.83	61.6	61.9	1.1	147.7	83.1	13	29.8	13.2	3.8	216.9
L9 x T2	3.72	62	63	1	138.1	83.6	13	28.5	12.7	3.8	261.6
L10 x T2	4.13	64.7	66.5	1.1	112.8	81.5	14	29	13	4	251.4
L11 x T2	3.94	62.3	63.8	1	118.4	89.2	14.4	30.8	13.6	4	230.6
L12 x T2	4.16	68	69	1.1	122.7	69.8	12.7	30.3	12.9	4.1	222.1
L13 x T2	4.99	61.9	63.1	1.1	135.4	80.5	14.4	33.4	13.2	4	274.9
L14 x T2	3.16	67.8	69	0.9	124.3	94.4	12.4	39.7	17.7	4.4	431.4
L15 x T2	4.11	61.6	63.4	0.9	136.9	92.5	12.4	33	12.1	3.7	183.7
L16 x T2	4.07	66.1	67.5	1.2	132.9	78.6	14	32.3	13.5	4.1	260.6
L17 x T2	2.85	67.6	69.3	0.9	118.6	93.6	13.2	32	13	4.1	235.9
L18 x T2	3.19	63.9	64.2	1	123.2	73.5	12.4	34.6	14.7	3.8	212.9
L19 x T2	3.46	65.8	67.2	1	132.4	89.1	13.2	31	13.6	4.1	207.8
L20 x T2	3.36	69.2	70.4	0.9	140.3	71.5	14	27.6	12.1	4.1	247.9
L21 x T2	4.12	66.6	67	1	146.3	100.6	13.8	24.8	10.3	4.1	177.8
L22 x T2	3.99	61.8	62.3	1	122.2	86	14.2	36.7	15.7	4.1	304.2
L23 x T2	4.03	68.5	70	1.1	128.9	103.8	11.8	37.7	15.9	4.2	289.4
L24 x T2	3.47	68.2	68.8	0.9	132.5	77.5	13.2	31.6	12.2	3.7	180.4
L25 x T2	3.75	66.8	67.7	1	138.6	84.4	12	30.5	12.8	4.1	221.3
L26 x T2	4.08	62.9	63.9	0.9	131	89.3	14	32.3	13.9	4.5	249.3

Appendix Table 9 (Continued)

L27 x T2	3.66	66.7	68.3	0.9	148.3	78	13	32.3	12.7	3.9	226
L28 x T2	3.59	65.9	67.2	0.9	152.6	82.2	13.2	30.6	13.1	4.1	286.1
L29 x T2	4.81	66.4	66.7	1.2	142.5	92.2	13.4	33.4	14.9	4.1	230.7
L30 x T2	3.21	68.8	71	1	123.3	106.8	13	32.1	13.6	4	226.7
L31 x T2	2.95	69.7	70.5	0.8	142.6	80.6	13.2	35.4	14.9	4	250.6
L32 x T2	4.65	66	68.9	0.8	124.4	83.3	13.2	32.4	14	4	223
L33 x T2	3.72	68.2	69.8	1	128.6	85.6	12.8	34	15.6	4	246.1
L34 x T2	2.21	72	74.2	1	114.1	82.5	13.4	33.4	14.5	3.7	226.8
L35 x T2	3.07	69	69.6	0.9	129	83.5	13.2	34.4	16.2	3.5	291.2
L36 x T2	5.07	63.8	64.2	1	152.9	92.3	14	35.7	16.8	4.5	307.6
L37 x T2	3.89	65.1	67.3	0.9	111.6	71.8	13.6	37.5	16	4	290
L38 x T2	2.81	68.5	69.8	0.8	128.4	90.8	14.2	27.6	12	3.9	262.7
L39 x T2	3.36	66.4	67.8	0.9	132	87.2	14.2	32.4	14.7	4.1	241.6
L40 x T2	2.75	65	64.9	0.9	122.5	99.9	14.4	37.4	16.6	4.2	182.4
L41 x T2	4.92	62.8	63.5	1.1	142.2	69	13.2	38.2	17.3	4.3	298.3
L42 x T2	4.02	62.2	63	0.9	128.4	79.9	14.8	34.8	14.3	4.2	279.5
L43 x T2	3.73	65.4	66.1	1	134.3	82.5	13.6	32.9	13.5	4	187.6
L1 x T1	2.43	64.4	65.6	1.1	114.8	71.8	14.2	31.8	12.8	4.1	195.2
L2 x T1	4.75	60.3	61	1	145.7	88.5	14	33.4	15.5	4.2	238.9
L3 x T1	4	59.9	60.4	1.1	123.9	88.3	14.2	35.9	15.8	4.2	285.3
L4 x T1	3.13	63.9	64.9	0.8	148.8	82.8	14	30.5	11.9	4.1	175.7
L5 x T1	3.55	62.2	63	0.9	138.1	74.2	13.2	28.4	12.4	3.9	214.7
L6 x T1	3.79	65.9	65.9	0.9	146.8	93.1	14.8	33.5	13.4	4	255.6
L7 x T1	4.48	64.3	64.7	0.9	125.9	72.4	14	35.4	14.1	4.1	283.8
L8 x T1	4.25	66.4	67.8	0.9	122.8	67.8	12.4	31.1	13.5	3.9	267.5
L9 x T1	3.32	67.6	69.2	0.9	141.6	85.7	13.8	30	11.8	3.9	186.4
L10 x T1	3.79	63.2	64.1	0.9	142.5	95.6	13.8	34.7	14.4	3.9	200.4
L11 x T1	1.86	67.3	69.7	1.1	138.5	86.8	13	35.5	14.2	4	250

Appendix Table 9 (Continued)

L12 x T1	5.09	62.3	62.7	1.2	139.4	69.6	13.2	29	11.8	4.1	318.2
L13 x T1	5.64	59.3	60.4	1	155.9	80.8	15	38.2	15.6	4.4	210.2
L14 x T1	2.92	64.8	64.7	0.9	147.6	99.3	15.2	25.7	12.3	4.2	184.7
L15 x T1	2.78	66	67.2	1.1	131.8	85	13.4	35.9	14.1	3.9	187.4
L16 x T1	2.9	66.1	66.8	1	155.3	90.5	14.2	33.6	12.4	4.1	193.9
L17 x T1	5.32	61.9	61.8	1.1	141.9	94.6	13.6	33.9	14.9	4.3	181.3
L18 x T1	4.05	65	66.6	0.9	135.7	74.7	13.6	33.9	13.4	4.2	236.3
L19 x T1	3.62	66.6	68.6	1	143.6	78.8	14	28	11.8	4.2	189
L20 x T1	2.85	69.1	70	1	130.1	85.9	13.6	27.2	12.4	3.4	177.8
L21 x T1	4.85	61.2	62	1.1	128.8	91.1	13.2	30.3	13.4	4.3	262.8
L22 x T1	2.72	64.1	65.9	1	130.7	101.3	14.4	29.6	15	3.7	187.2
L23 x T1	3.07	65	67.4	0.8	136.8	87.6	13	31.9	13.5	4.2	215.5
L24 x T1	3.36	68.3	68	1	156.1	72.5	13.8	32.4	14.4	4.3	230
L25 x T1	3.27	68.9	70.4	1	129.4	102.1	12.3	34	13.5	4.2	231.4
L26 x T1	3.57	66.5	67.2	0.9	131.9	85	14	35.3	14.1	4.3	271.3
L27 x T1	3.24	66.5	68	1	136.7	91.5	14	35.4	15.9	4.2	158.9
L28 x T1	3.68	64	64.7	1	133.6	84.8	14.2	29.8	12.6	4.2	245
L29 x T1	3.79	66.9	67.8	1	133.3	95.1	14	30.2	14.2	4	211.9
L30 x T1	3.13	65.3	65.7	0.7	134.6	87	12.8	30.5	12.5	4.2	206.7
L31 x T1	3.32	64.9	65.5	0.9	142	75.3	13.6	33.1	13.7	3.9	253
L32 x T1	2.5	68.4	70.2	1.1	136	77.9	13.6	28.1	12.4	3.8	164.5
L33 x T1	3.48	66.6	68	0.9	150.1	72.7	13.8	26.9	11.7	4	226.9
L34 x T1	4.39	69	70	0.8	147	75.7	12.6	34.3	14.5	3.7	217.2
L35 x T1	3.24	68.7	71.2	1.1	143.6	84.5	14	35	15	3.7	176.5
L36 x T1	3.83	65.1	67.1	1	134.2	72.2	14	33.5	13.2	4.1	220.8
L37 x T1	3.56	63.5	64.2	1.1	138.5	72.7	14.2	32.8	14.3	4	185
L38 x T1	2.93	66.9	69.3	1.1	140.2	92.3	14	36.2	15.9	4.2	278.2
L39 x T1	3.37	69.4	71	1	139.2	95.9	12.4	34.9	16.4	4	344.6

Appendix Table 9 (Continued)

L40 x T1	3.38	66.9	67.8	1	134.3	79.9	13.8	31.6	12.9	4.2	233
L41 x T1	5.51	65	66.2	1.1	144.3	85.7	13.4	31.1	12.8	4	265
L42 x T1	3.83	66.8	69.1	1	119.3	95.4	13.2	32.5	13.6	4	222
L43 x T1	3.81	64.6	65.4	1	135.3	70.4	12	30.4	12.3	4.2	238
BH-543	3.75	62	62.5	1	127.2	88.5	14	36.4	15.5	4.3	243.3
Melkasa-2	3.57	59.6	60.6	1	129	84	13.8	33.3	15	4.6	343.4
Cr mean	3.68	65.3	66.5	1	135.4	84.2	13.6	32.4	13.8	4.1	234.9
Ck mean	3.66	60.8	61.6	1	128.1	86.3	13.9	34.9	15.3	4.5	293.4
Mean	3.68	65.2	66.4	1	135.3	84.2	13.6	32.5	13.8	4.1	236.2
LSD (5%)	1.57	3.7	3.7	0.2	23.3	21.6	1.5	6.6	3.2	0.5	92.8
CV	21.37	2.8	2.8	12.4	8.6	12.9	5.7	10.1	11.7	6.1	19.6
Min	1.86	58.6	59.3	0.7	111.6	67.8	11.8	24.8	10.3	3.4	153.2
Max	5.64	72	74.2	1.2	156.1	106.8	15.2	39.7	17.7	4.6	431.4

AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH=plant height, RPE= Number of rows per ear, SD= number of days to silking, TKWT= thousand kernels weigh

Appendix Table 10. Estimates of mean values for grain yield and related traits at Pawe

Genotypes	GY(t/ha)	AD(days)	SD(days)	EPP(#)	PH(cm)	EH(cm)	RPE(#)	KPR(#)	EL(cm)	ED(cm)	TKWT(gm)
L1 x T2	5.99	64	66.1	1.2	171.2	78.1	14.2	37.5	15.4	4.6	262.6
L2 x T2	6.08	63.2	65.8	1.2	188.7	76.4	12.8	36.1	15.6	4.4	318.1
L3 x T2	5.17	62.7	64.6	1.1	204.5	90.6	15	39.8	17.5	4.7	296.4
L4 x T2	7.29	65.9	68.5	1.2	217.3	83.3	13.8	45.8	18.6	4.8	341.2
L5 x T2	5.28	61.5	64.1	1.3	183.5	80.9	12.2	39.1	14.9	4.4	283
L6 x T2	6.06	68	69.9	1.1	216.7	100.3	13.4	41.2	17.6	4.7	295.1
L7 x T2	6.02	65.4	68.5	0.9	217.7	89.6	14.2	35.8	18.3	4.9	247.4
L8 x T2	6.09	64.4	67.4	1.1	185.7	72.4	13.6	36.6	16.2	4.6	334.7
L9 x T2	5.84	59.2	61.6	1.3	193.1	81.4	12.8	37.5	17.4	4.5	313.8
L10 x T2	7.18	67.9	70	1.1	215.8	87.8	14	39.8	18.2	4.6	295.7
L11 x T2	8.06	63.1	65.1	1.3	209	101.9	14	39	17.5	4.8	352.8
L12 x T2	4.56	68	70	1.3	204.6	87.1	13.2	38.8	15.5	4.3	265.5
L13 x T2	9.08	63.3	65.2	1.2	214.5	94.9	14.4	42.3	18.7	4.8	306.8
L14 x T2	4.2	69.1	71	1.1	193.6	90.7	12.8	34.8	15.3	4.6	280.4
L15 x T2	6.44	67	69	1.4	194.5	86.3	13	41.8	16.8	4.7	291.5
L16 x T2	7	65.2	67.1	1.3	197.8	94.9	14	42.5	18	4.9	356.9
L17 x T2	6.09	68.4	70.5	1.2	207.2	100.3	12.8	39.7	17.1	5	360.9
L18 x T2	5.85	65	68	1.2	192.6	87.3	13.6	39.2	16	4.6	307.5
L19 x T2	7.94	65	66.4	1.3	218.4	97	12.6	36.5	17.2	4.9	390.1
L20 x T2	6.23	66.5	69	1	211.5	98.4	14.2	36.1	16.2	5.1	300.9
L21 x T2	7.78	65.4	67.5	1	205.8	100.4	13.8	37.6	16.5	5.3	381.7
L22 x T2	8.44	63	65	1.3	192.3	80.4	13.6	40.2	16	4.9	309.2
L23 x T2	9.35	68.9	71.2	1.2	214	97.5	13.2	40.5	18.7	4.9	361.6
L24 x T2	8.58	70	71.9	1.1	222.6	86	13	42.6	18.7	5.1	394.8
L25 x T2	9.85	66.7	68.6	1.2	216.2	96.5	13.4	41.5	18.1	4.9	297
L26 x T2	6.97	67.3	69.5	1.1	187.1	85	14.4	40	17.4	4.9	291.2

Appendix Table 10 (Continued)

L27 x T2	8.05	66.2	68.6	1.2	224	100.9	11.6	43.2	19	4.8	380.4
L28 x T2	8.91	62.9	64.9	1	214.9	99.1	13.4	43.1	19.8	5	369.1
L29 x T2	6.4	67.5	69.6	1.2	208.8	99.9	13.6	40.2	18.6	4.7	302.5
L30 x T2	10.77	67.6	69.5	1	216.8	111.4	13	45	20.1	4.7	377.7
L31 x T2	7.83	65	67.5	1.3	198.5	86.7	14.4	42.1	18	4.8	287.1
L32 x T2	7.16	61	63.4	1.3	204.5	91.9	13.6	41.4	18.5	4.8	318.7
L33 x T2	6.72	66	68.5	1	209.7	93.9	14	42.2	19.7	4.9	282.7
L34 x T2	5.92	68.6	70.5	1	190.9	85.6	11.8	40.8	19	4.3	372.8
L35 x T2	6.29	68.5	70.6	1.2	190.5	89.8	13.4	41.9	19.3	4.7	323.9
L36 x T2	6.77	67	70.5	0.9	213.9	91.5	15.2	40.3	18.2	5.1	246.2
L37 x T2	6.67	64.9	67	1.2	189.4	85.8	13.6	40.8	17.4	4.7	275
L38 x T2	8.4	67.4	70	1.2	193.4	79.4	13.4	41.5	17.6	4.7	349
L39 x T2	5.84	67	69.5	0.9	189.9	84.7	13.4	41.3	19.6	4.6	287
L40 x T2	7.5	67	69.5	1	207	101.5	14.4	41	17.8	4.7	271.5
L41 x T2	7.5	67.4	69	1.1	209	86.5	12.4	41.4	19.5	4.9	349
L42 x T2	7.83	65.9	67.9	1.2	197	94.3	13.2	41.8	18.6	4.6	334.3
L43 x T2	8.44	64.6	66.6	1.1	202.5	86.5	13.4	39.7	17.6	4.8	314
L1 x T1	7.7	63	65	1.2	187.1	83.2	14.1	36.8	17.2	5	306.2
L2 x T1	6.04	61.1	63.5	1.2	206.4	74.6	15	35.7	16.4	5	299.8
L3 x T1	7.46	62.3	64.4	1.1	195.1	77.2	14.6	40.6	18.1	4.7	287.9
L4 x T1	7.16	64.7	66.6	1	223.4	92.7	12.8	47	19.9	4.8	297.8
L5 x T1	5.87	59.4	61.5	1.1	182.6	79.8	12	40.7	15.5	4.6	320.3
L6 x T1	8.07	67.3	69.3	1	215.5	95.1	14.8	39.3	17.5	5.1	330.7
L7 x T1	7.53	61.9	64	1.1	192.4	72.1	13.2	39.1	17	4.9	332
L8 x T1	5.48	61.1	63	1	176	70.9	13.6	38.7	16.9	4.4	308.1
L9 x T1	7.28	65.6	67.5	1.1	200.3	90.3	13.8	40.9	17.7	5.1	340.7
L10 x T1	7.76	68.8	70.9	1.2	209.3	93	14.6	42.6	18.2	4.8	276.5
L11 x T1	6.98	62.1	64	1	211.3	102.1	14.4	38.7	17.7	4.6	298.2

Appendix Table 10 (Continued)

L12 x T1	4.62	67.3	69.4	1.1	186	68.1	13	38.7	15.6	4.5	266
L13 x T1	9.19	63.5	65.5	1.3	220.8	94.4	15	39.4	18.6	5.2	327.9
L14 x T1	9.2	66.1	68	1	206.1	80.5	13.6	39.4	18.7	5.3	388.4
L15 x T1	6.23	64.6	67	1.2	207.3	94.6	13.2	43.1	17.7	4.7	261.4
L16 x T1	6.73	65	67.5	1.3	213.6	88	14.6	43.8	17.7	4.8	315.8
L17 x T1	7.46	66.8	68.9	1	203.2	84.9	12.2	39.1	16.9	5	332.6
L18 x T1	6.29	64.1	66.1	1.1	182.4	75.6	13.8	36.5	14.9	4.7	323.4
L19 x T1	5.89	66.8	68.9	1	210	83.3	12.6	36	17.1	5	326.7
L20 x T1	7.85	66.5	68.6	1.1	208.3	83	13.2	37.5	16.8	4.9	366.4
L21 x T1	6.65	64.9	67	1	213.8	108	13.8	36.4	15.7	5.1	338.8
L22 x T1	5.99	64.2	66.1	1.1	206.2	90.7	13.6	39.7	16.8	5.1	320.4
L23 x T1	10.88	67.9	70	1.3	227.9	103.1	13.2	42.3	19.9	5	360.5
L24 x T1	8.98	67.8	69.6	1.2	223.8	97.8	12.3	42.5	18.7	5	401.7
L25 x T1	10.41	68	70	1.2	224.5	102.9	13	43.6	19	5.1	375.1
L26 x T1	8.48	66	68	1.1	195.6	85.3	14	42.6	18.4	5.2	309.7
L27 x T1	9.74	66	68.5	1.1	218.2	92.1	12.2	42.7	19.5	5.1	417.1
L28 x T1	8.33	63.8	65.9	1.2	191.9	80.5	12.8	43.7	18.6	4.9	355.6
L29 x T1	8.28	66.5	69	1	231.2	108.6	15	37.8	18.2	5.1	265.3
L30 x T1	10.61	66.7	68.6	1.1	222.2	105.3	13.4	40.8	19.3	5	396.7
L31 x T1	9.2	63.9	66.4	1.2	204.3	81.5	13.6	42.4	18.2	5	351.6
L32 x T1	5.06	66.9	69	0.8	206.6	76.6	13.6	36.7	16.5	4.7	291.2
L33 x T1	4.4	67.8	69.9	1.1	200.3	89.3	14.2	37.4	16.9	4.6	299.2
L34 x T1	7.58	64.4	66.5	1.2	195.9	75.6	14	42.6	18.8	4.8	288
L35 x T1	6	67.4	69.5	0.9	198	81.5	13.8	41.1	19.1	4.9	370
L36 x T1	6.33	65.1	68	1.1	215.5	104.3	13.6	38.2	17.3	4.8	280.6
L37 x T1	6.19	64	66.5	1.2	193.6	78.7	13.6	40.3	17.8	4.7	285.1
L38 x T1	8.83	67.9	70	1	213.1	99	14	42.7	18.3	5	362.5
L39 x T1	6.52	68	70	1	198.3	94.1	13.4	40.5	20	5	361.9

Appendix Table 10 (Continued)

L40 x T1	7.46	66.7	68.6	1.1	219.6	104.6	14.4	40.3	16.4	4.8	337.2
L41 x T1	7.41	65.9	68.5	1.1	208.8	87.8	14	38.3	18.5	5	356.6
L42 x T1	9.75	63.1	65	1.1	201.3	94.5	13.2	41.8	18.6	4.9	313.1
L43 x T1	7.88	64.2	66.1	1.2	200.4	83.5	12.8	41.5	17.9	5	372.8
BH-543	8.43	66.8	69.4	1.1	227.7	113.7	14.4	40.7	22.4	4.9	370.7
Melkasa-2	4.51	61	63.5	1.3	186.3	77.4	13.6	33.3	15.1	4.5	310
Cr mean	7.28	65.5	67.7	1.1	204.5	89.6	13.6	40.2	17.8	4.8	323.2
Ck mean	6.47	63.9	66.5	1.2	207	95.6	14	37	18.8	4.7	340.4
Mean	7.26	65.5	67.7	1.1	204.5	89.7	13.6	40.2	17.8	4.8	323.6
LSD (5%)	1.97	2.1	2.3	0.3	17	15.4	1.3	4.1	2.2	0.3	80.8
CV	13.57	1.6	1.7	14.1	4.2	8.6	4.8	5.1	6.2	2.9	12.5
Min	4.2	59.2	61.5	0.8	171.2	68.1	11.6	33.3	14.9	4.3	246.2
Max	10.88	70	71.9	1.4	231.2	113.7	15.2	47	22.4	5.3	417.1

AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH=plant height, RPE= Number of rows per ear, SD= number of days to silking, TKWT= thousand kernels wei

Appendix Table 11. Estimates of general combining ability effects (GCA) of 43 inbred lines and two testers for grain yield at Melkasa, 2010

Lines	GY(t/ha)	AD(days)	SD(days)	EPP(#)	PH(cm)	RPE(#)	KPR(#)	EL(cm)	ED(cm)	TKWT(gm)
L1	-0.49	-2.68**	-2.71**	-0.01	-29.05**	0.78*	-1.18	-1.20	0.09	-38.07
L2	0.65	-4.63**	-4.81**	-0.06	2.00	0.58	-1.63	-0.60	-0.01	-11.27
L3	-0.80	-2.68**	-2.96**	-0.16*	-19.75*	1.98**	-1.28	-1.55*	-0.06	-67.12*
L4	0.05	-0.33	0.24	-0.11	15.50*	-0.22	5.02**	1.50*	0.04	23.69
L5	-0.76	-4.18**	-4.46**	-0.16*	-25.45**	-0.52	1.17	-0.95	-0.06	5.09
L6	-1.39**	1.47**	1.24*	-0.06	13.50	-0.02	0.42	-0.25	0.04	-104.62**
L7	0.83	-2.83**	-3.01**	-0.21**	-22.70**	0.18	1.62	2.10**	0.24**	113.69**
L8	-0.76	-2.73**	-2.96**	-0.11	-14.75	-0.12	-0.83	1.15	-0.06	10.99
L9	-1.07*	-0.48	0.29	-0.16*	-0.50	-0.32	-1.13	-0.95	-0.01	14.19
L10	0.18	0.77	0.89	-0.01	3.90	0.28	0.67	0.25	-0.16*	-58.52
L11	0.98	-3.23**	-3.16**	0.04	2.95	0.38	-1.23	1.10	0.04	21.94
L12	-0.58	1.22*	0.94	0.39**	-18.70*	-0.72*	-2.23	-1.60*	-0.41**	-14.32
L13	-0.73	0.92	1.14	-0.06	2.70	0.58	-0.83	-0.90	-0.11	-48.12
L14	-1.65**	2.37**	3.39**	-0.16*	5.50	0.18	-2.78*	-0.50	0.04	26.64
L15	-0.45	0.42	0.54	0.09	7.45	-0.52	1.27	-0.10	-0.06	-31.92
L16	-1.13*	1.07	0.99	-0.16*	-17.15*	0.18	0.72	-0.55	-0.11	-28.32
L17	0.14	1.02	0.29	-0.01	11.50	-0.02	-2.38	-1.10	0.34**	51.64
L18	-0.80	-1.18*	-0.51	-0.01	-5.15	-0.42	1.62	-0.50	-0.06	33.89
L19	-0.02	-0.88	-1.16	0.04	15.95*	-0.92**	-4.63**	-1.50*	-0.01	77.84*
L20	-0.02	-0.68	-0.46	-0.11	-7.40	0.28	-4.68**	-0.75	0.24**	15.29

Appendix Table 11 (Continued)

L21	1.44*	-1.43*	-1.31*	0.14*	12.25	-0.12	-0.93	-0.85	0.39**	64.09*
L22	0.48	-2.23**	-2.61**	-0.01	10.45	0.18	1.72	0.05	0.24**	13.74
L23	1.96**	1.72**	1.69**	0.34**	20.10*	-0.02	0.52	-0.65	-0.06	-40.62
L24	1.56**	1.77**	1.39*	0.24**	8.95	-0.62	-0.68	-0.30	-0.16*	-32.42
L25	0.89	1.97**	1.69**	0.34**	7.75	-1.12**	2.72*	-0.30	-0.16*	-65.32*
L26	-0.31	0.42	0.44	-0.11	-5.35	0.28	1.27	-0.95	0.09	26.44
L27	0.39	0.72	0.84	-0.11	17.45*	-0.32	3.32*	0.40	0.24**	-62.77
L28	-0.25	-0.58	-0.41	0.04	-4.30	-0.22	1.27	-0.10	-0.06	-8.62
L29	0.80	0.97	0.94	0.14*	3.45	1.08**	1.82	0.55	0.04	31.09
L30	0.69	2.42**	2.49**	-0.06	16.15*	-0.32	1.82	1.50*	-0.01	-30.67
L31	-0.34	-1.23*	-1.26*	-0.11	1.15	-0.32	0.67	-0.30	-0.06	-2.92
L32	-0.30	1.92**	1.54*	-0.01	2.60	0.58	-0.63	0.30	0.14	-55.97
L33	0.78	0.92	1.44*	0.04	-1.30	-0.22	1.67	1.65*	-0.06	-60.47
L34	-0.27	1.12*	0.79	0.19**	-1.60	0.08	1.87	2.10**	-0.26**	-11.22
L35	-0.78	2.37**	2.34**	0.09	-8.50	-0.42	1.27	1.50*	-0.31**	27.09
L36	-0.82	1.67**	1.69**	0.04	4.65	1.08**	-1.53	-0.05	-0.01	-49.92
L37	1.28*	-1.58**	-1.71**	-0.11	-3.45	-0.02	-0.63	0.95	0.14	134.34**
L38	-0.65	1.77**	1.89**	-0.01	3.30	0.48	-2.13	-1.15	0.04	-8.22
L39	-0.25	1.22*	1.79**	0.04	0.55	-0.62	1.27	1.50*	-0.16*	15.44
L40	-0.14	0.47	0.34	-0.06	-11.75	0.18	1.22	0.00	0.19*	48.64
L41	1.64**	1.32*	0.89	0.09	14.50	-0.92**	-4.23**	0.40	-0.01	62.79
L42	-0.07	0.32	-0.01	-0.06	-10.85	-0.42	3.12*	1.50*	-0.31**	28.29

Appendix Table 11 (Continued)

L43	0.15	1.37*	1.29*	-0.11	3.60	-0.02	-2.33	-0.85	-0.01	-15.42
SE	0.52	0.55	0.6	0.07	7.64	0.33	1.29	0.65	0.08	31.53
SED	0.73	0.78	0.85	0.09	10.80	0.46	1.83	0.91	0.11	44.58

** = Significant at $P<0.01$ level of probability, * = Significant at $P<0.05$ Level of probability, AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, RPE = Number of rows per ear, SD = number of days to silking, SE= standard error, TKWT = thousand kernels weight

Appendix Table 12. Estimates of general combining ability effects (GCA) of 43 inbred lines and two testers for agronomic traits at Ziway, 2010

Lines	AD(days)	SD(days)	PH(cm)	EH(cm)	RPE(#)	EL(cm)	ED(cm)	KPR(#)
L1	-2.58**	-3.54**	-20.74**	-12.16	0.83	-2.03**	0.05	-2.67
L2	-3.43**	-3.09**	6.16	-12.81*	-0.17	-0.13	0.15	-1.57
L3	-3.13**	-3.59**	-7.79	-4.91	2.03**	0.72	-0.05	1.48
L4	-1.38*	-0.74	10.41	3.84	-1.77**	0.22	-0.20*	0.48
L5	-3.68**	-4.24**	-29.64**	-20.96**	-1.07*	-1.23	-0.20*	0.08
L6	2.07**	2.16**	5.61	12.99*	0.23	0.37	0.05	0.03
L7	-4.18**	-3.24**	-14.59*	-11.01	-0.12	1.72*	0.00	2.43
L8	-3.88**	-4.19**	-17.84**	-22.41**	-0.37	0.87	-0.25*	0.98
L9	-0.68	1.56	4.06	-0.76	-0.07	0.02	0.10	-0.37
L10	-0.08	0.36	1.21	1.69	1.13*	-0.48	0.00	0.13
L11	-2.13**	-1.79*	4.66	6.79	0.63	0.07	-0.10	-1.27
L12	0.87	0.56	-2.79	-1.36	-0.37	-1.88**	-0.30**	-2.32
L13	-0.73	-0.29	16.21*	2.44	0.93*	0.82	0.15	1.28
L14	3.12**	1.81*	-1.04	0.19	0.13	-0.88	0.10	-1.22
L15	-0.43	0.26	2.81	8.89	-0.67	-0.38	-0.20*	2.08
L16	-0.63	0.16	-2.79	-2.61	0.63	-0.73	0.00	-3.02
L17	1.42**	1.06	9.06	16.24*	0.03	-1.68*	0.20*	-2.62
L18	-0.88	-0.69	-6.64	-7.41	-0.27	0.97	0.10	2.83
L19	-0.93	-1.49	16.36*	15.14*	-0.37	-0.43	0.10	-2.52
L20	-0.63	0.31	-6.34	-0.96	0.23	-0.23	0.20*	-2.62
L21	-1.63**	-0.79	7.81	9.04	0.13	-1.08	0.25*	-1.72
L22	-3.13**	-3.59**	2.81	13.84*	-0.37	-1.08	0.35**	-3.02
L23	4.12**	3.36**	8.76	2.59	-0.17	-0.13	0.05	1.43
L24	2.37**	1.81*	5.86	1.44	-0.37	0.77	0.00	1.53
L25	3.67**	3.61**	9.96	-0.81	-0.77	-0.58	-0.25*	-0.12
L26	-1.08*	-0.99	-10.19	-1.11	1.33**	-0.23	0.50**	1.78
L27	0.57	1.21	-1.19	-10.01	-0.67	-1.03	0.00	-0.17
L28	-0.13	-0.19	6.71	6.19	-0.67	-1.03	-0.05	-2.12
L29	1.57**	1.01	9.56	8.69	0.13	0.07	0.00	-0.22
L30	2.62**	3.31**	12.46	11.39	-0.37	0.87	0.00	1.48
L31	-0.88	-1.14	-12.34	-13.31*	-0.37	-0.38	0.10	-0.37
L32	1.87**	2.31**	-2.64	-4.81	1.23**	-0.38	0.10	-1.82
L33	1.12*	1.91*	0.56	-9.81	0.03	0.57	-0.10	1.28

Appendix Table 12 (Continued)

L34	2.12**	2.71**	6.86	2.94	-0.37	2.52**	-0.25*	3.93*
L35	1.62**	2.46**	-7.59	-6.31	0.33	1.57*	-0.20*	2.43
L36	0.47	0.36	2.96	-2.51	0.53	1.07	0.15	1.83
L37	-1.08*	-1.19	-18.84**	-12.26	-0.27	1.12	-0.10	1.88
L38	1.87**	0.41	-6.54	-1.61	-0.37	-0.68	-0.20*	-1.07
L39	2.17**	1.61*	6.91	15.99*	0.03	1.62*	-0.15	2.33
L40	2.37**	1.51	-2.84	3.74	0.43	-0.93	-0.05	-2.42
L41	0.22	-0.14	7.36	1.19	-0.67	0.22	0.05	-2.07
L42	1.12*	-0.04	2.11	11.84	0.23	1.07	-0.15	2.83
L43	-0.13	-0.79	5.01	2.89	-0.67	0.17	-0.10	0.78
SE	0.53	0.79	6.69	6.28	0.46	0.67	0.10	1.54
SED	0.75	1.12	9.46	8.88	0.64	0.95	0.14	2.17

** = Significant at $P<0.01$ level of probability, * = Significant at $P<0.05$ Level of probability, AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, RPE = Number of rows per ear, SD = number of days to silking, SE= standard error, TKWT = thousand kernelsweight

Appendix Table 13. Estimates of general combining ability effects (GCA) of 43 inbred lines and two testers for grain yield and related traits at Dhera, 2010

Lines	Gy(t/ha)	AD(days)	SD(days)	PH(cm)	EH(cm)	RPE(#)	KPR(#)	EL(cm)	ED(cm)	TKWT(gm)
L1	0.37	-2.64**	-2.59**	-2.74	4.97	0.99*	1.04	0.28	0.12	-10.92
L2	1.22**	-4.59**	-5.29**	1.86	-11.33	0.29	1.54	1.38	0.32*	36.78*
L3	0.32	-3.44**	-3.29**	0.86	11.97*	1.49**	2.79	0.83	0.07	-54.82**
L4	-0.13	-1.64	0.81	-4.14	-14.53*	0.24	2.19	1.38	-0.08	54.63**
L5	0.47	-4.39**	-4.14**	-19.74**	-11.63	-1.81**	-2.16	-1.82*	-0.28	-14.12
L6	-0.33	0.31	0.71	12.26*	8.02	0.89*	0.89	-0.72	-0.13	-20.12
L7	0.02	-3.54**	-4.39**	4.66	-0.43	-0.41	2.59	1.18	0.12	48.48**
L8	0.07	-5.99**	-4.79**	-17.34**	-20.98**	-0.91*	-2.56	-0.27	-0.48*	-12.72
L9	0.47	-2.34**	-2.49**	-7.64	-2.73	-0.31	-0.86	0.28	-0.03	-9.52
L10	0.42	2.31**	1.46	4.96	16.42**	0.04	3.19	0.38	0.17	-20.17
L11	0.52	-2.49**	-1.89*	-1.09	-0.68	0.39	0.79	1.13	-0.08	29.43
L12	-0.58	0.56	0.21	-4.24	3.22	-0.61	0.74	-0.42	-0.03	-31.37
L13	0.22	-0.89	-1.89*	4.81	4.27	1.29**	-2.21	-0.32	0.22	-14.52
L14	-0.28	3.51**	2.71**	9.81	9.07	-0.36	-4.46*	-1.47	-0.08	-11.77
L15	0.27	-0.79	-1.44	-2.89	7.47	-0.51	5.44**	0.78	-0.18	-42.87*
L16	0.07	1.41	1.16	-5.89	-4.53	0.34	-1.71	-0.62	0.17	14.68
L17	0.57	1.21	0.66	0.86	-2.73	-0.11	3.19	0.78	0.67**	66.33**
L18	0.07	-1.39	-0.89	-2.49	-6.63	0.49	-1.11	-0.42	0.12	-1.87
L19	0.22	-0.49	0.31	6.56	3.62	-0.31	-2.16	-0.22	0.12	-31.27
L20	0.22	0.01	-0.79	13.46*	15.12*	0.39	-1.71	-0.32	0.22	22.18

Appendix Table 13 (Continued)

L21	-0.28	0.96	1.61	0.66	-1.68	-0.06	-6.16**	-2.72**	-0.03	13.73
L22	-0.13	-2.34**	-1.39	-1.39	3.97	-0.81*	-5.36**	-1.77*	0.07	5.78
L23	-0.03	2.71**	3.01**	5.21	-4.98	-0.41	1.19	0.43	0.32*	13.88
L24	0.12	2.41**	2.01*	8.26	7.27	-0.66	1.79	0.88	0.07	24.43
L25	-0.43	3.01**	2.66**	9.06	7.77	-0.81*	0.59	-0.67	-0.33*	-31.52
L26	0.27	-0.74	-0.89	-0.44	-12.38*	0.59	-3.96	-1.77*	0.07	-23.67
L27	0.37	0.16	-0.24	5.11	-0.93	-0.61	2.59	0.38	0.22	25.08
L28	-0.28	-0.14	-0.34	-0.89	1.57	-0.01	-1.46	-0.62	-0.08	-0.22
L29	0.37	1.61	1.06	9.66	8.27	1.49**	0.39	-0.12	0.17	-13.42
L30	-0.08	1.91*	2.56**	5.86	17.47**	-0.11	3.14	1.33	0.22	-23.52
L31	-0.03	-1.09	-0.89	-2.99	-3.98	0.09	1.74	0.38	-0.08	18.88
L32	-1.18**	3.26**	3.31**	-3.09	-6.33	0.89*	-4.36*	-1.62	-0.08	6.88
L33	-0.63*	0.76	1.26	-7.04	-12.58*	-0.01	0.74	-0.07	-0.13	-8.52
L34	-0.43	2.86**	2.01*	-7.34	1.52	-0.56	2.74	1.68*	-0.38*	9.23
L35	-0.18	2.76**	2.36*	2.31	-0.53	-0.11	2.54	1.33	-0.38*	-37.77*
L36	-0.43	1.46	1.81*	-14.14*	-16.23**	1.29**	-3.21	-0.77	0.27	0.53
L37	0.92**	-1.44	-1.69	-20.94**	-9.98	-0.46	0.79	1.03	-0.28	-22.72
L38	-0.73*	1.16	0.71	7.81	6.27	0.79*	-2.61	-1.42	-0.03	7.58
L39	0.02	1.71*	1.36	11.06*	7.87	-0.16	-0.81	0.48	-0.23	24.48
L40	-0.33	1.51	1.46	5.46	8.12	-0.51	-0.66	-0.72	0.02	-7.02
L41	-0.13	0.71	0.91	2.81	-2.03	-0.46	4.09*	2.63**	0.02	36.23
L42	-0.68*	1.26	2.36*	-5.04	-7.78	-0.76*	2.04	0.43	-0.43**	-22.07

Appendix Table 13 (Continued)

L43	-0.08	0.71	1.01	-1.69	1.22	-0.11	-1.41	-0.42	0.07	7.33
SE	0.3	0.83	0.89	5.39	5.93	0.38	1.99	0.84	0.15	18.2
SED	0.43	1.18	1.27	7.63	8.39	0.54	2.81	1.19	0.21	25.74

** = Significant at $P<0.01$ level of probability, * = Significant at $P<0.05$ Level of probability, AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, RPE = Number of rows per ear, SD=number of days to silking, SE=standard error, TKWT = thousand-kernels weight

Appendix Table 14. Estimates of general combining ability effects (GCA) of 43 inbred lines and two testers for grain yield and related traits at Mieso, 2010

Line	GY(t/ha)	AD (days)	SD(days)	EH(days)	RPE(days)	EL(days)	TKWT(gm)
L1	-0.52	-2.28*	-2.18*	-12.90*	0.35	-0.38	-38.06
L2	0.80*	-4.98**	-5.63**	-1.35	0.45	1.22	54.54*
L3	0.03	-4.93**	-5.13**	-2.95	0.65	0.17	0.74
L4	-0.5	0.37	0.87	3.90	0.35	-2.18**	-70.41**
L5	-0.36	-4.93**	-5.33**	-8.90	-0.45	-1.18	-9.36
L6	0.23	0.27	-0.08	7.00	0.15	-0.68	21.79
L7	0.35	-0.33	-0.43	-12.55*	0.35	0.47	22.84
L8	0.36	-1.33	-1.63	-8.70	-0.85*	-0.43	7.34
L9	-0.16	-0.53	-0.38	0.50	-0.15	-1.53	-10.86
L10	0.28	-1.38	-1.18	4.40	0.35	-0.08	-8.96
L11	-0.78*	-0.53	0.27	3.85	0.15	0.12	5.44
L12	0.94	-0.18	-0.63	-14.45**	-0.6	-1.43	35.29
L13	1.63**	-4.73**	-4.73**	-3.50	1.15**	0.62	7.69
L14	-0.64	0.97	0.37	12.70*	0.25	1.22	73.19**
L15	-0.24	-1.53	-1.18	4.60	-0.65	-0.68	-49.31*
L16	-0.2	0.77	0.67	0.40	0.55	-0.83	-7.61
L17	0.4	-0.58	-0.93	9.95	-0.15	0.17	-26.26
L18	-0.06	-0.88	-1.08	-10.05	-0.55	0.27	-10.26
L19	-0.14	0.87	1.42	-0.20	0.05	-1.08	-36.46
L20	-0.58	3.82**	3.72**	-5.45	0.25	-1.53	-22.01
L21	0.80*	-1.43	-1.98*	11.70*	-0.05	-1.93*	-14.56
L22	-0.33	-2.38*	-2.38	9.50	0.75	1.57	10.84
L23	-0.13	1.42	2.22	11.55*	-1.15**	0.92	17.59
L24	-0.27	2.92**	1.92*	-9.15	-0.05	-0.48	-29.66
L25	-0.17	2.52**	2.57**	9.10	-1.40**	-0.63	-8.51
L26	0.14	-0.63	-0.93	3.00	0.45	0.22	25.44
L27	-0.23	1.27	1.67	0.60	-0.05	0.52	-42.41
L28	-0.05	-0.38	-0.53	-0.65	0.15	-0.93	30.69
L29	0.62	1.32	0.77	9.50	0.15	0.77	-13.56
L30	-0.51	1.72	1.87*	12.75*	-0.65	-0.73	-18.16
L31	-0.55	1.97	1.52	-6.20	-0.15	0.52	16.94
L32	-0.11	1.87	3.07**	-3.55	-0.15	-0.58	-41.11
L33	-0.08	2.07	2.42*	-5.00	-0.25	-0.13	1.64

Appendix Table 14 (Continued)

L34	-0.38	5.17**	5.62**	-5.05	-0.55	0.72	-12.86
L35	-0.53	3.52**	3.92**	-0.15	0.05	1.82*	-1.01
L36	0.77	-0.88	-0.83	-1.90	0.45	1.22	29.34
L37	0.04	-1.03	-0.73	-11.90*	0.35	1.37	2.64
L38	-0.81*	2.37*	3.07**	7.40	0.55	0.17	35.59
L39	-0.32	2.57**	2.92**	7.40	-0.25	1.77*	58.24*
L40	-0.62	0.62	-0.13	5.75	0.55	0.97	-27.16
L41	1.53**	-1.43	-1.63	-6.80	-0.25	1.27	46.79
L42	0.24	-0.83	-0.43	3.50	0.45	0.17	15.89
L43	0.09	-0.33	-0.73	-7.70	-0.75	-0.88	-22.06
S.E	0.39	0.9	0.93	5.43	0.39	0.81	23.44
SED	0.55	1.27	1.32	7.68	0.55	1.15	33.16

** = Significant at P<0.01 level of probability, * = Significant at P<0.05 Level of probability, AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, RPE = Number of rows per ear, SD = number of days to silking, SE= standard error, TKWT = thousand kernels weight

Appendix Table 15. Estimates of general combining ability effects (GCA) of 43 inbred lines and two testers for grain yield at Pawe, 2010

Lines	GY(t/ha)	AD(days)	SD(days)	PH(cm)	EH(cm)	RPE(#))	KPR(#)	EL(cm)	ED(cm)	TKWT(gm)
L1	-0.44	-2.01**	-2.13**	-25.32**	-8.93**	0.6	-3.08**	-1.45*	-0.03	-38.80
L2	-1.22*	-3.36**	-3.03**	-6.92**	-14.08**	0.35	-4.33**	-1.75**	-0.13	-14.25
L3	-0.97	-3.01**	-3.18**	-4.67*	-5.68**	1.25**	-0.03	0.05	-0.13	-31.05
L4	-0.06	-0.21	-0.13	15.88**	-1.58	-0.25	6.17**	1.50**	-0.03	-3.70
L5	-1.71**	-5.06**	-4.88**	-21.42**	-9.23**	-1.45**	-0.33	-2.55**	-0.33**	-21.55
L6	-0.22	2.14**	1.92**	11.63**	8.12**	0.55	0.02	-0.20	0.07	-10.30
L7	-0.51	-1.86**	-1.43**	0.58	-8.73**	0.15	-2.78**	-0.10	0.07	-33.50
L8	-1.50**	-2.76**	-2.48**	-23.62**	-17.93**	0.05	-2.58*	-1.20*	-0.33**	-1.80
L9	-0.72	-3.11**	-3.13**	-7.77**	-3.73	-0.25	-1.03	-0.20	-0.03	4.05
L10	0.19	2.84**	2.77**	8.08**	0.82	0.75*	0.97	0.45	-0.13	-37.10
L11	0.24	-2.91**	-3.13**	5.68*	12.42**	0.65*	-1.38	-0.15	-0.13	2.30
L12	-2.69**	2.14**	2.02**	-9.17**	-11.98**	-0.45	-1.48	-2.20**	-0.43**	-57.45**
L13	1.85**	-2.11**	-2.33**	13.18*	5.07*	1.15**	0.62	0.90	0.17*	-5.85
L14	-0.58	2.09**	1.82**	-4.62*	-3.98*	-0.35	-3.13**	-0.75	0.12	11.20
L15	-0.95	0.29	0.32	-3.57	0.87	-0.45	2.22*	-0.50	-0.13	-46.75*
L16	-0.42	-0.41	-0.38	1.23	1.87	0.75*	2.92**	0.10	0.02	13.15
L17	-0.51	2.09**	2.02**	0.73	3.02	-1.05**	-0.83	-0.75	0.17*	23.55
L18	-1.21*	-0.96	-0.63*	-16.97**	-8.13**	0.15	-2.38*	-2.30**	-0.18*	-7.75
L19	-0.37	0.39	-0.03	9.73**	0.57	-0.95**	-3.98**	-0.60	0.12	35.20

Appendix Table 15 (Continued)

L20	-0.24	0.99	1.12**	5.43*	1.12	0.15	-3.43**	-1.25*	0.17*	10.45
L21	-0.07	-0.36	-0.43	5.33*	14.62**	0.25	-3.23**	-1.65*	0.37**	37.05
L22	-0.07	-1.91**	-2.13**	-5.22*	-4.03*	0.05	-0.28	-1.35*	0.17*	-8.40
L23	2.83**	2.89**	2.92**	16.48**	10.72**	-0.35	1.17	1.55**	0.12	37.85
L24	1.50**	3.39**	3.07**	18.73**	2.32	-0.90**	2.32*	0.95	0.22**	75.05**
L25	2.85**	1.84**	1.62**	15.88**	10.12**	-0.35	2.32*	0.80	0.17	12.85
L26	0.44	1.14*	1.07**	-13.12**	-4.43*	0.65*	1.07	0.15	0.22**	-22.75
L27	1.61**	0.59	0.87**	16.63**	6.92**	-1.65**	2.72*	1.50**	0.12	75.55**
L28	1.34**	-2.16**	-2.28**	-1.07	0.22	-0.45	3.17**	1.45*	0.12	39.15
L29	0.06	1.49**	1.62**	15.53**	14.67**	0.75*	-1.23	0.65	0.07	-39.3
L30	3.41**	1.64**	1.37**	15.03**	18.77**	-0.35	2.67*	1.95**	0.02	64.00**
L31	1.23*	-1.06*	-0.73*	-3.07	-5.48**	0.45	2.02	0.35	0.07	-3.85
L32	-1.17*	-1.56**	-1.48**	1.08	-5.33*	0.05	-1.18	-0.25	-0.08	-18.25
L33	-1.72**	1.39*	1.52**	0.53	2.02	0.55	-0.43	0.55	-0.08	-32.25
L34	-0.53	0.99	0.82**	-11.07**	-8.98**	-0.65*	1.47	1.15*	-0.28**	7.20
L35	-1.14*	2.44**	2.37**	-10.22**	-3.93*	0.05	1.27	1.45*	-0.03	23.75
L36	-0.73	0.54	1.57**	10.23**	8.32**	0.85**	-0.98	0.00	0.12	-59.80**
L37	-0.85	-1.06*	-0.93**	-12.97**	-7.33**	0.05	0.32	-0.15	-0.13	-43.15*
L38	1.33**	2.14**	2.32**	-1.22	-0.38	0.15	1.87	0.20	0.02	32.55
L39	-1.10*	1.99**	2.07**	-10.37**	-0.18	-0.15	0.67	2.05**	-0.03	1.25
L40	0.2	1.34*	1.37**	8.83**	13.47**	0.85**	0.42	-0.65	-0.08	-18.85
L41	0.17	1.14*	1.07**	4.43*	-2.43	-0.35	-0.38	1.25*	0.12	29.60

Appendix Table 15 (Continued)

L42	1.51**	-1.01	-1.23**	-5.32*	4.82*	-0.35	1.57	0.85	-0.08	0.50
L43	0.88	-1.11*	-1.33**	-3.02	-4.58*	-0.45	0.37	0.00	0.07	20.20
S.E	0.49	0.53	0.58	4.21	3.9	0.31	1.03	0.55	0.07	20.37
SED	0.69	0.74	0.81	5.95	5.51	0.44	1.46	0.78	0.1	28.81

** = Significant at P<0.01 level of probability, * = Significant at P<0.05 Level of probability, AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, RPE = Number of rows per ear, SD = number of days to silking, SE= standard error, TKWT = thousand kernels weight

Appendix Table 16. Estimates of specific combining ability effects (SCA) for line by tester crosses of maize inbred lines evaluated at Melkasa, 2010

crosses	GY(t/ha)	AD(days)	SD(days)	ED(cm)	KPR(#)
L1 x T1	0.61	-1.03	-0.98	-0.19	-2.36
L1 x T2	-0.61	1.03	0.98	0.19	2.36
L2 x T1	0.22	0.32	0.32	0.01	-3.01
L2 x T2	-0.22	-0.32	-0.32	-0.01	3.01
L3 x T1	0.45	0.67	0.67	0.06	4.04*
L3 x T2	-0.45	-0.67	-0.67	-0.06	-4.04*
L4 x T1	0.47	-0.18	-0.03	-0.14	-0.06
L4 x T2	-0.47	0.18	0.03	0.14	0.06
L5 x T1	1.03	-0.73	-0.93	0.06	0.39
L5 x T2	-1.03	0.73	0.93	-0.06	-0.39
L6 x T1	0.11	0.62	0.67	0.06	-1.96
L6 x T2	-0.11	-0.62	-0.67	-0.06	1.96
L7 x T1	0.58	-0.78	-0.08	-0.04	-0.16
L7 x T2	-0.58	0.78	0.08	0.04	0.16
L8 x T1	-0.49	0.02	0.07	0.06	1.99
L8 x T2	0.49	-0.02	-0.07	-0.06	-1.99
L9 x T1	-0.31	-0.53	0.22	-0.19	-1.91
L9 x T2	0.31	0.53	-0.22	0.19	1.91
L10 x T1	0.19	-0.28	0.02	-0.04	-0.81
L10 x T2	-0.19	0.28	-0.02	0.04	0.81
L11 x T1	0.59	-0.18	0.07	-0.14	1.59
L11 x T2	-0.59	0.18	-0.07	0.14	-1.59
L12 x T1	-0.64	0.27	0.37	0.01	-0.81
L12 x T2	0.64	-0.27	-0.37	-0.01	0.81
L13 x T1	0.67	-0.43	-0.23	0.11	0.09
L13 x T2	-0.67	0.43	0.23	-0.11	-0.09
L14 x T1	0.96	-0.58	-0.68	0.06	0.64
L14 x T2	-0.96	0.58	0.68	-0.06	-0.64
L15 x T1	-0.09	0.27	0.37	-0.04	-0.01
L15 x T2	0.09	-0.27	-0.37	0.04	0.01
L16 x T1	-0.36	0.22	0.12	0.11	3.84*
L16 x T2	0.36	-0.22	-0.12	-0.11	-3.84*
L17 x T1	1.11	-1.13	-0.98	0.06	0.74

Appendix Table 16 (Continued)

L17 x T2	-1.11	1.13	0.98	-0.06	-0.74
L18 x T1	0.72	0.07	-0.18	0.16	1.04
L18 x T2	-0.72	-0.07	0.18	-0.16	-1.04
L19 x T1	-0.71	-0.43	0.17	-0.09	-1.81
L19 x T2	0.71	0.43	-0.17	0.09	1.81
L20 x T1	0.15	0.67	-0.33	-0.04	-1.86
L20 x T2	-0.15	-0.67	0.33	0.04	1.86
L21 x T1	0.88	0.72	-0.38	0.21	1.29
L21 x T2	-0.88	-0.72	0.38	-0.21	-1.29
L22 x T1	0.16	0.82	0.92	0.06	0.14
L22 x T2	-0.16	-0.82	-0.92	-0.06	-0.14
L23 x T1	-1.32*	0.47	0.82	-0.24*	-2.56
L23 x T2	1.32*	-0.47	-0.82	0.24*	2.56
L24 x T1	-1.97**	-0.18	0.12	-0.14	-0.06
L24 x T2	1.97**	0.18	-0.12	0.14	0.06
L25 x T1	-0.67	0.42	0.42	-0.04	-0.66
L25 x T2	0.67	-0.42	-0.42	0.04	0.66
L26 x T1	0.22	0.07	-0.23	0.11	1.09
L26 x T2	-0.22	-0.07	0.23	-0.11	-1.09
L27 x T1	0.44	-0.03	0.07	-0.04	-0.36
L27 x T2	-0.44	0.03	-0.07	0.04	0.36
L28 x T1	-0.16	0.27	-0.08	0.06	0.49
L28 x T2	0.16	-0.27	0.08	-0.06	-0.49
L29 x T1	-0.04	1.52*	1.17	-0.14	-0.56
L29 x T2	0.04	-1.52*	-1.17	0.14	0.56
L30 x T1	0.24	-0.33	-0.88	-0.09	0.64
L30 x T2	-0.24	0.33	0.88	0.09	-0.64
L31 x T1	-0.76	0.12	-0.63	0.16	0.89
L31 x T2	0.76	-0.12	0.63	-0.16	-0.89
L32 x T1	-0.83	0.47	0.27	-0.14	-2.01
L32 x T2	0.83	-0.47	-0.27	0.14	2.01
L33 x T1	-2.27**	1.57*	1.97*	-0.14	-3.01
L33 x T2	2.27**	-1.57*	-1.97*	0.14	3.01
L34 x T1	0.91	-1.63*	-1.98*	0.26*	1.89
L34 x T2	-0.91	1.63*	1.98*	-0.26*	-1.89

Appendix Table 16 (Continued)

L35 x T1	0.82	-1.08	-1.23	0.01	0.29
L35 x T2	-0.82	1.08	1.23	-0.01	-0.29
L36 x T1	-1.16	0.62	1.02	-0.19	-2.11
L36 x T2	1.16	-0.62	-1.02	0.19	2.11
L37 x T1	-0.48	0.77	0.92	-0.04	0.09
L37 x T2	0.48	-0.77	-0.92	0.04	-0.09
L38 x T1	0.87	-0.38	-0.88	0.16	2.29
L38 x T2	-0.87	0.38	0.88	-0.16	-2.29
L39 x T1	-0.05	-0.23	0.62	0.16	1.79
L39 x T2	0.05	0.23	-0.62	-0.16	-1.79
L40 x T1	0.22	0.12	-0.53	0.11	-0.26
L40 x T2	-0.22	-0.12	0.53	-0.11	0.26
L41 x T1	0.34	-0.33	0.12	0.11	1.79
L41 x T2	-0.34	0.33	-0.12	-0.11	-1.79
L42 x T1	-0.29	-1.13	-0.98	0.11	2.04
L42 x T2	0.29	1.13	0.98	-0.11	-2.04
L43 x T1	-0.31	0.62	0.72	-0.09	-2.61
L43 x T2	0.31	-0.62	-0.72	0.09	2.61
SE	0.73	0.78	0.85	0.11	1.83
SED	1.04	1.10	1.20	0.16	2.59

** = Significant at P<0.01 level of probability, * = Significant at P<0.05 Level of probability, AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, RPE = Number of rows per ear, SD=number of days to silking, SE=standard error, TKWT = thousand-kernels weight

Appendix Table 17. Estimates of specific combining ability effects (SCA) for line by tester crosses of maize inbred lines evaluated at Ziway, 2010

crosses	GY(t/ha)	AD(days)	SD(days)
L1 x T1	0.26	0.17	0.77
L1 x T2	-0.26	-0.17	-0.77
L2 x T1	0.16	0.82	1.02
L2 x T2	-0.16	-0.82	-1.02
L3 x T1	-0.59	0.62	1.52
L3 x T2	0.59	-0.62	-1.52
L4 x T1	1.41*	-2.03**	-2.13
L4 x T2	-1.41*	2.03**	2.13
L5 x T1	0.01	-0.33	-0.53
L5 x T2	-0.01	0.33	0.53
L6 x T1	-0.34	0.82	0.47
L6 x T2	0.34	-0.82	-0.47
L7 x T1	0.86	-0.33	-0.13
L7 x T2	-0.86	0.33	0.13
L8 x T1	-0.54	-0.13	-0.68
L8 x T2	0.54	0.13	0.68
L9 x T1	0.66	-1.43	-0.73
L9 x T2	-0.66	1.43	0.73
L10 x T1	0.01	-0.33	-0.33
L10 x T2	-0.01	0.33	0.33
L11 x T1	-0.09	0.12	-0.98
L11 x T2	0.09	-0.12	0.98
L12 x T1	-0.39	3.12**	2.47*
L12 x T2	0.39	-3.12**	-2.47*
L13 x T1	0.36	-0.88	-0.58
L13 x T2	-0.36	0.88	0.58
L14 x T1	0.26	-0.13	-1.78
L14 x T2	-0.26	0.13	1.78
L15 x T1	0.76	-1.08	-0.23
L15 x T2	-0.76	1.08	0.23
L16 x T1	-0.49	-0.88	-0.43
L16 x T2	0.49	0.88	0.43
L17 x T1	0.61	-0.43	-0.13

Appendix Table 17 (Continued)

L17 x T2	-0.61	0.43	0.13
L18 x T1	0.71	-1.13	-1.08
L18 x T2	-0.71	1.13	1.08
L19 x T1	-0.39	1.82*	1.12
L19 x T2	0.39	-1.82*	-1.12
L20 x T1	-0.94	1.62*	1.12
L20 x T2	0.94	-1.62*	-1.12
L21 x T1	0.01	0.72	0.32
L21 x T2	-0.01	-0.72	-0.32
L22 x T1	-0.49	0.72	1.02
L22 x T2	0.49	-0.72	-1.02
L23 x T1	0.01	2.77**	2.47*
L23 x T2	-0.01	-2.77**	-2.47*
L24 x T1	-0.14	-0.38	-0.48
L24 x T2	0.14	0.38	0.48
L25 x T1	-0.64	1.32	2.02
L25 x T2	0.64	-1.32	-2.02
L26 x T1	0.71	-0.93	-0.88
L26 x T2	-0.71	0.93	0.88
L27 x T1	-0.59	0.32	-0.08
L27 x T2	0.59	-0.32	0.08
L28 x T1	0.01	-1.28	-0.98
L28 x T2	-0.01	1.28	0.98
L29 x T1	-0.04	-0.68	0.02
L29 x T2	0.04	0.68	-0.02
L30 x T1	1.01	-0.63	-0.68
L30 x T2	-1.01	0.63	0.68
L31 x T1	0.31	-1.13	-0.73
L31 x T2	-0.31	1.13	0.73
L32 x T1	-0.64	1.62*	1.82
L32 x T2	0.64	-1.62*	-1.82
L33 x T1	-1.29*	0.87	1.22
L33 x T2	1.29*	-0.87	-1.22
L34 x T1	-0.04	-0.63	-1.38
L34 x T2	0.04	0.63	1.38

Appendix Table 17 (Continued)

L35 x T1	0.46	-0.63	-0.33
L35 x T2	-0.46	0.63	0.33
L36 x T1	-0.99	0.12	0.07
L36 x T2	0.99	-0.12	-0.07
L37 x T1	-0.19	-0.83	-0.38
L37 x T2	0.19	0.83	0.38
L38 x T1	-0.29	-0.88	-0.98
L38 x T2	0.29	0.88	0.98
L39 x T1	-1.09	-0.58	-1.18
L39 x T2	1.09	0.58	1.18
L40 x T1	0.86	-0.88	-0.88
L40 x T2	-0.86	0.88	0.88
L41 x T1	0.86	-1.13	-0.43
L41 x T2	-0.86	1.13	0.43
L42 x T1	1.06	-0.53	-0.53
L42 x T2	-1.06	0.53	0.53
L43 x T1	-1.14	2.52**	2.42*
L43 x T2	1.14	-2.52**	-2.42*
SE	0.69	0.75	1.12
SED	0.98	1.06	1.59

** = Significant at P<0.01 level of probability, * = Significant at P<0.05 Level of probability, AD = number of days to anthesis, GY= grain yield, SD=number of days to silking, SE=standard error

Appendix Table 18. Estimates of specific combining ability effects (SCA) for line by tester crosses of maize inbred lines evaluated at Dhera, 2010

Crosses	GY(t/ha)	AD(days)	SD(days)	PH(cm)	RPE(#)	ED(cm)	TKWT(gm)
L1 x T1	-0.12	0.53	0.89	11.88	-0.08	0.04	-13.01
L1 x T2	0.12	-0.53	-0.89	-11.88	0.08	-0.04	13.01
L2 x T1	-0.27	2.08	1.89	0.18	0.22	-0.06	44.59
L2 x T2	0.27	-2.08	-1.89	-0.18	-0.22	0.06	-44.59
L3 x T1	-0.67	0.43	0.59	-2.12	-0.58	-0.21	-9.61
L3 x T2	0.67	-0.43	-0.59	2.12	0.58	0.21	9.61
L4 x T1	0.28	-0.27	-1.01	-1.72	-0.03	0.24	41.64
L4 x T2	-0.28	0.27	1.01	1.72	0.03	-0.24	-41.64
L5 x T1	0.08	0.38	0.14	-7.02	-0.28	0.04	27.39
L5 x T2	-0.08	-0.38	-0.14	7.02	0.28	-0.04	-27.39
L6 x T1	-0.32	-0.12	-0.31	-0.52	0.42	0.09	-27.91
L6 x T2	0.32	0.12	0.31	0.52	-0.42	-0.09	27.91
L7 x T1	0.43	0.13	0.79	-0.32	-0.28	-0.06	-38.51
L7 x T2	-0.43	-0.13	-0.79	0.32	0.28	0.06	38.51
L8 x T1	-0.42	-0.02	0.29	-8.32	-0.58	-0.16	-34.71
L8 x T2	0.42	0.02	-0.29	8.32	0.58	0.16	34.71
L9 x T1	-0.02	4.03**	4.29**	-2.22	-0.58	0.09	2.69
L9 x T2	0.02	-4.03**	-4.29**	2.22	0.58	-0.09	-2.69
L10 x T1	0.13	1.88	1.64	-2.22	0.17	0.19	18.64
L10 x T2	-0.13	-1.88	-1.64	2.22	-0.17	-0.19	-18.64
L11 x T1	0.03	-0.52	-1.51	6.63	-0.28	-0.06	32.54
L11 x T2	-0.03	0.52	1.51	-6.63	0.28	0.06	-32.54
L12 x T1	0.13	1.43	1.19	3.38	0.52	0.09	17.54
L12 x T2	-0.13	-1.43	-1.19	-3.38	-0.52	-0.09	-17.54
L13 x T1	0.13	-0.02	0.49	1.53	1.42*	-0.16	-10.81
L13 x T2	-0.13	0.02	-0.49	-1.53	-1.42*	0.16	10.81
L14 x T1	0.63	-0.62	-1.11	10.73	0.37	0.14	-13.76
L14 x T2	-0.63	0.62	1.11	-10.73	-0.37	-0.14	13.76
L15 x T1	-0.12	-0.72	-0.16	-1.67	0.22	0.24	18.14
L15 x T2	0.12	0.72	0.16	1.67	-0.22	-0.24	-18.14
L16 x T1	0.68	-0.62	-0.36	6.53	-0.23	0.19	-10.41
L16 x T2	-0.68	0.62	0.36	-6.53	0.23	-0.19	10.41
L17 x T1	0.48	-0.32	0.54	8.38	0.32	-0.11	2.64

Appendix Table 18 (Continued)

L17 x T2	-0.48	0.32	-0.54	-8.38	-0.32	0.11	-2.64
L18 x T1	0.08	-0.62	-0.81	-4.27	0.42	0.04	6.04
L18 x T2	-0.08	0.62	0.81	4.27	-0.42	-0.04	-6.04
L19 x T1	0.23	-0.12	0.89	-5.12	0.22	0.14	-11.86
L19 x T2	-0.23	0.12	-0.89	5.12	-0.22	-0.14	11.86
L20 x T1	-0.27	-0.22	-1.01	-0.22	-0.28	-0.06	4.79
L20 x T2	0.27	0.22	1.01	0.22	0.28	0.06	-4.79
L21 x T1	-0.27	1.43	0.49	2.88	-0.03	-0.11	-23.76
L21 x T2	0.27	-1.43	-0.49	-2.88	0.03	0.11	23.76
L22 x T1	-0.72	0.63	2.09	-8.97	-0.48	-0.41	-15.91
L22 x T2	0.72	-0.63	-2.09	8.97	0.48	0.41	15.91
L23 x T1	-0.02	0.18	0.59	0.33	0.32	0.14	-3.91
L23 x T2	0.02	-0.18	-0.59	-0.33	-0.32	-0.14	3.91
L24 x T1	0.23	-0.02	0.09	1.38	0.17	0.09	29.64
L24 x T2	-0.23	0.02	-0.09	-1.38	-0.17	-0.09	-29.64
L25 x T1	-0.32	0.78	1.34	11.08	-0.48	-0.31	-2.41
L25 x T2	0.32	-0.78	-1.34	-11.08	0.48	0.31	2.41
L26 x T1	0.48	-2.17	-1.81	4.08	-0.48	0.19	-10.86
L26 x T2	-0.48	2.17	1.81	-4.08	0.48	-0.19	10.86
L27 x T1	0.08	-0.77	-0.96	-5.07	-0.48	0.04	9.49
L27 x T2	-0.08	0.77	0.96	5.07	0.48	-0.04	-9.49
L28 x T1	0.63	-0.17	-0.56	6.03	0.52	0.04	1.19
L28 x T2	-0.63	0.17	0.56	-6.03	-0.52	-0.04	-1.19
L29 x T1	0.68	-1.32	-1.46	0.18	1.22*	0.49*	22.19
L29 x T2	-0.68	1.32	1.46	-0.18	-1.22*	-0.49*	-22.19
L30 x T1	-0.17	1.48	0.14	-4.22	0.02	-0.06	33.39
L30 x T2	0.17	-1.48	-0.14	4.22	-0.02	0.06	-33.39
L31 x T1	-0.12	-1.22	-1.41	0.13	-0.18	-0.06	-40.01
L31 x T2	0.12	1.22	1.41	-0.13	0.18	0.06	40.01
L32 x T1	-0.27	0.23	0.59	-17.37*	-0.18	-0.26	-7.01
L32 x T2	0.27	-0.23	-0.59	17.37*	0.18	0.26	7.01
L33 x T1	-0.52	0.53	-0.06	-6.42	0.12	-0.21	-20.61
L33 x T2	0.52	-0.53	0.06	6.42	-0.12	0.21	20.61
L34 x T1	0.78	-0.77	-1.21	9.28	0.17	0.44*	60.64*
L34 x T2	-0.78	0.77	1.21	-9.28	-0.17	-0.44*	-60.64*

Appendix Table 18(Continued)

L35 x T1	0.33	-1.47	-1.26	4.83	0.42	0.24	31.54
L35 x T2	-0.33	1.47	1.26	-4.83	-0.42	-0.24	-31.54
L36 x T1	-0.22	0.03	0.19	-2.92	-1.18	-0.21	18.24
L36 x T2	0.22	-0.03	-0.19	2.92	1.18	0.21	-18.24
L37 x T1	-0.47	-1.07	-0.21	-22.62**	-0.93	-0.26	-17.91
L37 x T2	0.47	1.07	0.21	22.62**	0.93	0.26	17.91
L38 x T1	0.08	-0.77	-1.11	-2.87	-0.08	0.19	0.09
L38 x T2	-0.08	0.77	1.11	2.87	0.08	-0.19	-0.09
L39 x T1	-0.47	-1.32	-1.06	3.58	0.47	-0.21	-57.61*
L39 x T2	0.47	1.32	1.06	-3.58	-0.47	0.21	57.61*
L40 x T1	0.08	-1.32	-1.16	5.58	0.22	0.24	-24.91
L40 x T2	-0.08	1.32	1.16	-5.58	-0.22	-0.24	24.91
L41 x T1	0.38	-0.72	-0.81	14.23	0.37	-0.16	-61.36*
L41 x T2	-0.38	0.72	0.81	-14.23	-0.37	0.16	61.36*
L42 x T1	-0.77	1.33	0.84	-13.62	-0.63	-0.11	24.04
L42 x T2	0.77	-1.33	-0.84	13.62	0.63	0.11	-24.04
L43 x T1	-0.37	-0.02	-0.81	6.93	0.02	-0.21	9.64
L43 x T2	0.37	0.02	0.81	-6.93	-0.02	0.21	-9.64
SE	0.43	1.18	1.27	8.39	0.54	0.21	25.74
SED	0.61	1.67	1.79	11.87	0.76	0.3	36.4

** = Significant at P<0.01 level of probability, * = Significant at P<0.05 Level of probability, AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, RPE = Number of rows per ear, SD=number of days to silking, SE=standard error, TKWT = thousand-kernels weight

Appendix Table 19. Estimates of specific combining ability effects (SCA) for line by tester crosses of maize inbred lines evaluated at Mieso, 2010

Crosses	AD(days)	SD(days)	PH(cm)	KPR(#)	EL(cm)	TKWT(gm)
L1 x T1	1.35	1.33	-15.7	-1.3	-0.46	8.19
L1 x T2	-1.35	-1.33	15.7	1.3	0.46	-8.19
L2 x T1	-0.05	0.18	-5.85	-1.05	0.64	-40.71
L2 x T2	0.05	-0.18	5.85	1.05	-0.64	40.71
L3 x T1	-0.5	-0.92	-5.9	4.5	1.99	59.49
L3 x T2	0.5	0.92	5.9	-4.5	-1.99	-59.49
L4 x T1	-1.8	-2.42	2.75	0.75	0.44	21.04
L4 x T2	1.8	2.42	-2.75	-0.75	-0.44	-21.04
L5 x T1	1.8	1.88	0.95	-1.6	-0.06	-1.01
L5 x T2	-1.8	-1.88	-0.95	1.6	0.06	1.01
L6 x T1	0.3	-0.47	1.6	0.85	0.44	8.74
L6 x T2	-0.3	0.47	-1.6	-0.85	-0.44	-8.74
L7 x T1	-0.7	-1.32	-12.1	2.45	-0.01	35.89
L7 x T2	0.7	1.32	12.1	-2.45	0.01	-35.89
L8 x T1	2.4	2.98*	-14.85	0.85	0.29	35.09
L8 x T2	-2.4	-2.98*	14.85	-0.85	-0.29	-35.09
L9 x T1	2.80*	3.13*	-0.65	0.95	-0.31	-27.81
L9 x T2	-2.80*	-3.13*	0.65	-0.95	0.31	27.81
L10 x T1	-0.75	-1.17	12.45	3.05	0.84	-15.71
L10 x T2	0.75	1.17	-12.45	-3.05	-0.84	15.71
L11 x T1	2.5	2.98*	7.65	2.55	0.44	19.49
L11 x T2	-2.5	-2.98*	-7.65	-2.55	-0.44	-19.49
L12 x T1	-2.85*	-3.12*	5.95	-0.45	-0.41	57.84
L12 x T2	2.85*	3.12*	-5.95	0.45	0.41	-57.84
L13 x T1	-1.3	-1.32	7.85	2.6	1.34	-22.56
L13 x T2	1.3	1.32	-7.85	-2.6	-1.34	22.56
L14 x T1	-1.5	-2.12	9.25	-6.80**	-2.56*	-113.56**
L14 x T2	1.5	2.12	-9.25	6.80**	2.56*	113.56**
L15 x T1	2.2	1.93	-4.95	1.65	1.14	11.64
L15 x T2	-2.2	-1.93	4.95	-1.65	-1.14	-11.64
L16 x T1	0	-0.32	8.8	0.85	-0.41	-23.56
L16 x T2	0	0.32	-8.8	-0.85	0.41	23.56
L17 x T1	-2.85*	-3.72**	9.25	1.15	1.09	-17.51

Appendix Table 19 (Continued)

L17 x T2	2.85*	3.72**	-9.25	-1.15	-1.09	17.51
L18 x T1	0.55	1.23	3.85	-0.15	-0.51	21.49
L18 x T2	-0.55	-1.23	-3.85	0.15	0.51	-21.49
L19 x T1	0.4	0.73	3.2	-1.3	-0.76	0.39
L19 x T2	-0.4	-0.73	-3.2	1.3	0.76	-0.39
L20 x T1	-0.05	-0.17	-7.5	0	0.29	-25.26
L20 x T2	0.05	0.17	7.5	0	-0.29	25.26
L21 x T1	-2.70*	-2.47	-11.15	2.95	1.69	52.29
L21 x T2	2.70*	2.47	11.15	-2.95	-1.69	-52.29
L22 x T1	1.15	1.83	1.85	-3.35	-0.21	-48.71
L22 x T2	-1.15	-1.83	-1.85	3.35	0.21	48.71
L23 x T1	-1.75	-1.27	1.55	-2.7	-1.06	-27.16
L23 x T2	1.75	1.27	-1.55	2.7	1.06	27.16
L24 x T1	0.05	-0.37	9.4	0.6	1.24	34.59
L24 x T2	-0.05	0.37	-9.4	-0.6	-1.24	-34.59
L25 x T1	1.05	1.38	-7	1.95	0.49	14.84
L25 x T2	-1.05	-1.38	7	-1.95	-0.49	-14.84
L26 x T1	1.8	1.68	-1.95	1.7	0.24	20.79
L26 x T2	-1.8	-1.68	1.95	-1.7	-0.24	-20.79
L27 x T1	-0.1	-0.12	-8.2	1.75	1.74	-23.76
L27 x T2	0.1	0.12	8.2	-1.75	-1.74	23.76
L28 x T1	-0.95	-1.22	-11.9	-0.2	-0.11	-10.76
L28 x T2	0.95	1.22	11.9	0.2	0.11	10.76
L29 x T1	0.25	0.58	-7	-1.4	-0.21	0.39
L29 x T2	-0.25	-0.58	7	1.4	0.21	-0.39
L30 x T1	-1.75	-2.62	3.25	-0.6	-0.41	-0.21
L30 x T2	1.75	2.62	-3.25	0.6	0.41	0.21
L31 x T1	-2.4	-2.47	-2.7	-0.95	-0.46	10.99
L31 x T2	2.4	2.47	2.7	0.95	0.46	-10.99
L32 x T1	1.2	0.68	3.4	-1.95	-0.66	-19.46
L32 x T2	-1.2	-0.68	-3.4	1.95	0.66	19.46
L33 x T1	-0.8	-0.87	8.35	-3.35	-1.81	0.19
L33 x T2	0.8	0.87	-8.35	3.35	1.81	-0.19
L34 x T1	-1.5	-2.07	14.05	0.65	0.14	4.99
L34 x T2	1.5	2.07	-14.05	-0.65	-0.14	-4.99

Appendix Table 19 (Continued)

L35 x T1	-0.15	0.83	4.9	0.5	-0.46	-47.56
L35 x T2	0.15	-0.83	-4.9	-0.5	0.46	47.56
L36 x T1	0.65	1.48	-11.75	-0.9	-1.66	-33.61
L36 x T2	-0.65	-1.48	11.75	0.9	1.66	33.61
L37 x T1	-0.8	-1.52	11.05	-2.15	-0.71	-42.71
L37 x T2	0.8	1.52	-11.05	2.15	0.71	42.71
L38 x T1	-0.8	-0.22	3.5	4.5	2.09	17.54
L38 x T2	0.8	0.22	-3.5	-4.5	-2.09	-17.54
L39 x T1	1.5	1.63	1.2	1.45	0.99	61.29
L39 x T2	-1.5	-1.63	-1.2	-1.45	-0.99	-61.29
L40 x T1	0.95	1.48	3.5	-2.7	-1.71	35.09
L40 x T2	-0.95	-1.48	-3.5	2.7	1.71	-35.09
L41 x T1	1.1	1.38	-1.35	-3.35	-2.11	-6.86
L41 x T2	-1.1	-1.38	1.35	3.35	2.11	6.86
L42 x T1	2.3	3.08*	-6.95	-0.95	-0.21	-18.96
L42 x T2	-2.3	-3.08*	6.95	0.95	0.21	18.96
L43 x T1	-0.4	-0.32	-1.9	-1.05	-0.46	34.99
L43 x T2	0.4	0.32	1.9	1.05	0.46	-34.99
SE	1.27	1.32	8.34	2.35	1.15	33.16
SED	1.80	1.86	11.80	3.33	1.63	46.90

** = Significant at P<0.01 level of probability, * = Significant at P<0.05 Level of probability, AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, RPE = Number of rows per ear, SD=number of days to silking, SE=standard error, TKWT = thousand-kernels weig

Appendix Table 20. Estimates of specific combining ability effects (SCA) for line by tester crosses of maize inbred lines evaluated at Pawe, 2010

Crosses	GY(t/ha)	AD(days)	SD(days)	PH(cm)	EH(cm)	RPE(#)	ED(cm)
L1 x T1	0.65	-0.23	-0.22	6.65	3.55	-0.12	0.13
L1 x T2	-0.65	0.23	0.22	-6.65	-3.55	0.12	-0.13
L2 x T1	-0.22	-0.78	-0.82	7.55	0.10	1.03*	0.23*
L2 x T2	0.22	0.78	0.82	-7.55	-0.10	-1.03*	-0.23*
L3 x T1	0.94	0.07	0.23	-6.00	-5.70	-0.27	-0.07
L3 x T2	-0.94	-0.07	-0.23	6.00	5.70	0.27	0.07
L4 x T1	-0.27	-0.33	-0.62	1.75	5.70	-0.57	-0.07
L4 x T2	0.27	0.33	0.62	-1.75	-5.70	0.57	0.07
L5 x T1	0.09	-0.78	-0.97	-1.75	0.45	-0.17	0.03
L5 x T2	-0.09	0.78	0.97	1.75	-0.45	0.17	-0.03
L6 x T1	0.80	-0.08	0.03	-1.90	-1.60	0.63	0.13
L6 x T2	-0.80	0.08	-0.03	1.90	1.60	-0.63	-0.13
L7 x T1	0.55	-1.48*	-1.92*	-13.95*	-7.75	-0.57	-0.07
L7 x T2	-0.55	1.48*	1.92*	13.95*	7.75	0.57	0.07
L8 x T1	-0.51	-1.38	-1.87*	-6.15	0.25	-0.07	-0.17
L8 x T2	0.51	1.38	1.87*	6.15	-0.25	0.07	0.17
L9 x T1	0.52	3.47**	3.28**	2.30	5.45	0.43	0.23*
L9 x T2	-0.52	-3.47**	-3.28**	-2.30	-5.45	-0.43	-0.23*
L10 x T1	0.09	0.72	0.78	-4.55	3.60	0.23	0.03
L10 x T2	-0.09	-0.72	-0.78	4.55	-3.60	-0.23	-0.03
L11 x T1	-0.74	-0.23	-0.22	-0.15	1.10	0.13	-0.17
L11 x T2	0.74	0.23	0.22	0.15	-1.10	-0.13	0.17
L12 x T1	-0.17	-0.08	0.03	-10.60	-8.50	-0.17	0.03
L12 x T2	0.17	0.08	-0.03	10.60	8.50	0.17	-0.03
L13 x T1	-0.15	0.37	0.48	1.85	0.75	0.23	0.13
L13 x T2	0.15	-0.37	-0.48	-1.85	-0.75	-0.23	-0.13
L14 x T1	2.30**	-1.23	-1.17	4.95	-4.10	0.33	0.28**
L14 x T2	-2.30**	1.23	1.17	-4.95	4.10	-0.33	-0.28**
L15 x T1	-0.31	-0.93	-0.67	5.10	5.15	0.03	-0.07
L15 x T2	0.31	0.93	0.67	-5.10	-5.15	-0.03	0.07
L16 x T1	-0.34	0.17	0.53	6.60	-2.45	0.23	-0.12
L16 x T2	0.34	-0.17	-0.53	-6.60	2.45	-0.23	0.12
L17 x T1	0.48	-0.53	-0.47	-3.30	-6.70	-0.37	-0.07

Appendix Table 20 (Continued)

L17 x T2	-0.48	0.53	0.47	3.30	6.70	0.37	0.07
L18 x T1	0.02	-0.18	-0.62	-6.40	-4.85	0.03	-0.02
L18 x T2	-0.02	0.18	0.62	6.40	4.85	-0.03	0.02
L19 x T1	-1.23	1.17	1.58	-5.50	-5.85	-0.07	-0.02
L19 x T2	1.23	-1.17	-1.58	5.50	5.85	0.07	0.02
L20 x T1	0.61	0.27	0.13	-2.90	-6.70	-0.57	-0.17
L20 x T2	-0.61	-0.27	-0.13	2.90	6.70	0.57	0.17
L21 x T1	-0.77	0.02	0.08	2.70	4.80	-0.07	-0.17
L21 x T2	0.77	-0.02	-0.08	-2.70	-4.80	0.07	0.17
L22 x T1	-1.43*	0.87	0.88	5.65	6.15	-0.07	0.03
L22 x T2	1.43*	-0.87	-0.88	-5.65	-6.15	0.07	-0.03
L23 x T1	0.56	-0.23	-0.27	5.65	3.80	-0.07	-0.02
L23 x T2	-0.56	0.23	0.27	-5.65	-3.80	0.07	0.02
L24 x T1	0.00	-0.83	-0.82	-0.70	6.90	-0.42	-0.12
L24 x T2	0.00	0.83	0.82	0.70	-6.90	0.42	0.12
L25 x T1	0.08	0.92	1.03	2.85	4.20	-0.27	0.03
L25 x T2	-0.08	-0.92	-1.03	-2.85	-4.20	0.27	-0.03
L26 x T1	0.55	-0.38	-0.42	2.95	1.15	-0.27	0.08
L26 x T2	-0.55	0.38	0.42	-2.95	-1.15	0.27	-0.08
L27 x T1	0.64	0.17	0.28	-4.20	-3.40	0.23	0.08
L27 x T2	-0.64	-0.17	-0.28	4.20	3.40	-0.23	-0.08
L28 x T1	-0.49	0.72	0.83	-12.80*	-8.30	-0.37	-0.12
L28 x T2	0.49	-0.72	-0.83	12.80*	8.30	0.37	0.12
L29 x T1	0.74	-0.23	0.03	9.90	5.35	0.63	0.13
L29 x T2	-0.74	0.23	-0.03	-9.90	-5.35	-0.63	-0.13
L30 x T1	-0.28	-0.18	-0.12	1.40	-2.05	0.13	0.08
L30 x T2	0.28	0.18	0.12	-1.40	2.05	-0.13	-0.08
L31 x T1	0.48	-0.28	-0.22	1.60	-1.60	-0.47	0.03
L31 x T2	-0.48	0.28	0.22	-1.60	1.60	0.47	-0.03
L32 x T1	-1.25	3.22**	3.13**	-0.25	-6.65	-0.07	-0.12
L32 x T2	1.25	-3.22**	-3.13**	0.25	6.65	0.07	0.12
L33 x T1	-1.36*	1.17	1.03	-6.00	-1.30	0.03	-0.22*
L33 x T2	1.36*	-1.17	-1.03	6.00	1.30	-0.03	0.22*
L34 x T1	0.63	-1.83*	-1.67*	1.20	-4.00	1.03*	0.18
L34 x T2	-0.63	1.83*	1.67*	-1.20	4.00	-1.03*	-0.18

Appendix Table 20 (Continued)

L35 x T1	-0.35	-0.28	-0.22	2.45	-3.15	0.13	0.03
L35 x T2	0.35	0.28	0.22	-2.45	3.15	-0.13	-0.03
L36 x T1	-0.42	-0.68	-0.92	-0.50	7.40	-0.87	-0.22*
L36 x T2	0.42	0.68	0.92	0.50	-7.40	0.87	0.22*
L37 x T1	-0.44	-0.18	0.08	0.80	-2.55	-0.07	-0.07
L37 x T2	0.44	0.18	-0.08	-0.80	2.55	0.07	0.07
L38 x T1	0.01	0.52	0.33	8.55	10.80	0.23	0.08
L38 x T2	-0.01	-0.52	-0.33	-8.55	-10.80	-0.23	-0.08
L39 x T1	0.14	0.77	0.58	2.90	5.70	-0.07	0.13
L39 x T2	-0.14	-0.77	-0.58	-2.90	-5.70	0.07	-0.13
L40 x T1	-0.22	0.12	-0.12	5.00	2.55	-0.07	-0.02
L40 x T2	0.22	-0.12	0.12	-5.00	-2.55	0.07	0.02
L41 x T1	-0.25	-0.48	0.08	-1.40	1.65	0.73	-0.02
L41 x T2	0.25	0.48	-0.08	1.40	-1.65	-0.73	0.02
L42 x T1	0.76	-1.13	-1.12	0.85	1.10	-0.07	0.08
L42 x T2	-0.76	1.13	1.12	-0.85	-1.10	0.07	-0.08
L43 x T1	-0.48	0.07	0.08	-2.35	-0.50	-0.37	0.03
L43 x T2	0.48	-0.07	-0.08	2.35	0.50	0.37	-0.03
SE	0.69	0.74	0.81	5.95	5.51	0.44	0.1
SED	0.98	1.05	1.15	8.42	7.80	0.62	0.14

** = Significant at P<0.01 level of probability, * = Significant at P<0.05 Level of probability, AD = number of days to anthesis, ED = ear diameter, EH = ear height, EL = ear length, EPP= number of ears per plant, GY= grain yield, KPR = number of kernels per row, PH = plant height, RPE = Number of rows per ear, SD=number of days to silking, SE=standard error, TKWT = thousand-kernels weight