COMBINING ABILITY AND HETEROSIS ESTIMATION IN ELITE SORGHUM [*Sorghum bicolor* (L) Moench] INBRED LINES UNDER MOISTURE STRESS CONDITIONS

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COMBINING ABILITY AND HETEROSIS ESTIMATION IN ELITE SORGHUM [*Sorghum bicolor* (L) Moench] INBRED LINES UNDER MOISTURE STRESS CONDITIONS

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DEDICATION

I dedicate this thesis manuscript to both my mother W/ro Nadi Ayana and My father Ato Begna Chimdessa, who were committed to encourage and support me throughout my education efforts and grew me up by providing me all the necessary treatments.

STATEMENT OF THE AUTHOR

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

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BIOGRAPHICAL SKETCH

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LIST OF ABBREVIATIONS AND ACRONYMS

BP	Better Parent
BPH	Better Parent Heterosis
CMS	Cytoplasmic Male Sterile
DAP	Di-Ammonium Phosphate
GCA	General Combining Ability
GLM	General Linear Model
EBI	Ethiopian Biodiversity Institute
KB	Kobo
LSD	Least Significance Difference
MARC	Melkassa Agricultural Research Center
Me	Mean square error
MI	Mieso
MoA	Ministry of Agriculture
MP	Mid-parent
MPH	Mid Parent Heterosis
SAS	Stastical Analysis of software
SC	Standard Check
SCA	Specific Combining Ability
SD	Standard Deviation
SE GCA	Standard error for General Combining Ability
SE SCA	Standard error for Specific Combining Ability
SH	Standard Heterosis
SV	Source of Variation
WARC	Werer Agricultural Research Center

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ABSTRACT

The most important prerequisite in crop improvement is the selection of suitable parents, which could combine well and produce desirable hybrids. However, lack of potential parents and hybrids, limited genetic variation, narrow genetic base and information on the genetic components are the most important limiting factors for sorghum yield improvement under moisture stress. Therefore, the present study was conducted to determine the combining abilities, heterosis, mean yield performance and gene action governing the quantitative traits for yield and its components using line x tester mating design. The experimental materials consisted of fifteen parents along with their twenty six hybrids and one standard check. The experiment was laid out using alpha lattice design with two replications at Mieso and Kobo during the cropping season of 2018/19. Combined analysis of variance revealed highly significant differences due to genotypes for all studied traits over locations, which indicates the availability of substation genetic variation among genotypes. Based on general combining ability analysis, inbred line 3 and 4 were identified as best general combiners for both days to flowering and plant height traits whereas inbred line 2 and 7 were identified as best general combiners for stay green traits. Thousand seed weight showed best general combiners in inbred line 6, 10 and 12. The hybrid crosses 4x14, 8x15 and 11x14 were identified as best specific combiners for grain yield while hybrid 1x15 was best specific combiner for days to flowering, days to maturity, panicle length, panicle width and thousand seed weight. The estimates of general and specific combining ability revealed the preponderance of non-additive gene action since the ratio of general combining ability to specific combining ability was less than unity for all the traits under study except for plant height. The maximum grain yield was obtained from a hybrid 4x14 (6.32 t/ha) followed by hybrid 8x15(5.92 t/ha), 1x15 (5.88 t/ha), 13x14 (5.78 t/ha) and 6x15 (5.57 t/ha) with the average value of 5.0 tones/ha which had higher mean value than the mean of the parents and the check. Among the hybrids, 8x15 recorded maximum heterosis (112.41%) over the mid parents, hybrid 1x15 revealed maximum heterosis (68.71%) over the better parent whereas 4x14 recorded maximum grain yield with (30.71%) heterosis over the standard check for grain yield. The two heterotic groups were identified based on their specific combining ability effects and also three heterotic groups were identified based on their general combining ability effects to develop superior hybrids from broad base and suitable parents. Finally, based on mean yield performance, heterotic response, combining ability estimates and nature of gene action for grain yield and its components, inbred lines 4, 9, 10, 11, 12, 13 and the hybrid crosses 4x14, 8x15, 1x15, *11x14, 11x15,* 13x14, 6x15 *were found to be the most promising and potential varieties which could be exploited commercially after critical evaluation for their superiority and yield stability across the locations over years.*

Key words: Combining ability, Heterosis, Sorghum, Hybrid, Drought

1 INTRODUCTION

Sorghum *(Sorghum bicolor (L.) Moench)* is self-pollinated, diploid (2n=2x =20) crop species and belongs to the *poaceae* family with a genome size of 730 Mb (Paterson *et al.,* 2009). Sorghum is a C4 plant with higher photosynthetic efficiency and higher abiotic stress tolerance (Reddy *et al*., 2009). The origin and the early domestication of sorghum took place in northeaster Africa approximately 5000 years ago (Mann *et al*., 1983). Ethiopia is the center of origin and diversity for sorghum where large variability in wild and cultivated forms remains (Doggett, 1988). It is widely grown in the arid and semi-arid tropics, because of its unique adaptation to harsh and drought prone environments (Adugna, 2007).

Sorghum is the fifth leading cereal crop in the world after wheat, maize, rice and barley with area coverage of about 42.70 million ha and total production of 62.3 million tons (FAO, 2017). In Africa, the area under sorghum production is about 26.14 million ha and total production and average yield being 42.35 million tons and 1.62 ton/ha, respectively (FAO, 2017). Ethiopia is the second largest sorghum producing country in Eastern Africa next to Sudan and it stands third in Ethiopia in terms of area coverage after teff and maize and second next to maize in terms of productivity (2.7 t/ha) (CSA, 2018).

Sorghum is grown globally for food and feed purposes in dry land agriculture because of its wider adaptability to drought prone areas (Reddy *et al*., 2004). It has a short growth period and is relatively drought tolerant, which makes sorghum a preferred cereal in arid and semi-arid regions (Funnell-Harris *et al*., 2013). Sorghum is used for biofuel production (Dutra *et al*., 2013), beer production (Smith & Frederiksen, 2000) and silage (Pinho *et al*., 2015). As food-grade, special attention is given to sorghum because it is gluten-free and contains high levels of health-promoting phytochemicals (Asif *et al*., 2010). In developing countries, sorghum is primarily used as a food crop (Bawazir, 2009), and has been improved to a great extent for grain yield (Adebo *et al*., 2017). More than 500 million people consume sorghum as their principal food source in developing countries (Burke *et al*., 2013).

There is a potential to increase sorghum productivity from 3 to 6 ton/ha using improved varieties and production technologies (Asfaw *et al*., 2005). In spite of its importance, sorghum yield is low in Ethiopia as compared to its potential (7 to 9 ton/ha) mainly because of the use of low yielding cultivars, biotic and abiotic stresses.

Combining ability studies provide useful information regarding the selection of suitable parents for effective hybridization programs and indicate the nature and magnitude of various types of gene action involved in the expression of quantitative characters (Sprague and Tatum, 1942). General combining ability (GCA) is the mean performance of a genotype when crossed with a series of other genotypes whereas specific combining ability is the deviation of the performance of crosses from the average general combining ability of two parental lines. Combining ability analysis is an important method to realize gene actions and it is frequently used by crop breeders to select parents with a high general combining ability (GCA) and hybrids with high specific combining ability (SCA) effects (Yingzhong, 1999). The information on the nature and magnitude of gene action is important in understanding the genetic potential of a population and deciding the breeding procedure to be adopted in a given population (Ingle *et al.*, 2018).

Efficient transmission of desirable genes from selected parents to their progeny needs firm knowledge about gene action (Falconer & Mackay, 1996). For improvement in crop, the most important prerequisite is the selection of suitable parents, which could combine well and produce desirable hybrids. Heterosis is the superiority of hybrids over their parents in terms of productivity, growth, development and resistance (Shull, 1914). The exploitation of heterosis through hybrid breeding is one of the landmark achievements in plant breeding (Duvick, 2001). Stephens and Holland (1954) reported for the first time, breeding for heterosis in sorghum can be accomplished by identification of stable cytoplasmic male sterile lines, maintainer and restorer lines having high GCA for desirable characters. Potential of sorghum hybrids is estimated from the percentage increase or decrease of their performance over the mid parent (average heterosis) and better parent (heterobeltiosis) (Ringo *et al.*, 2015).

The national and regional sorghum improvement programs have released a number of open pollinated sorghum varieties for the moisture deficit lowland areas of Ethiopia. However, hybrids have been found to be better suited than open pollinated varieties to such stress environments as a result of earliness, better adaptation and stability (EIAR, 2014). Therefore, there is still need for development of more acceptable varieties/hybrids, which are high yielding, drought escaping, and able to tolerate low soil fertility, pests and diseases in the moisture stress areas. Over 80% of the sorghum in Ethiopia is produced under severe to moderate drought stress conditions (EIAR, 2014).

The extent of yield loss due to drought is high and complete yield loss was observed in some parts of the country, such as Mehoni area (EIAR, 2014) and causes significant yield loss during vegetative (36%) and reproductive stages (55%) (Assefa *et al*., 2010). Therefore, the sorghum crops which are high yielding, early maturing and drought tolerant are the great interest to the farmers (Geremew *et al*., 2004). In addition to the superiority in grain yield performance, adaptation of the varieties to local environments and improvement of farmers' preferred traits, including earliness, greenness, plant height and grain size are vital for varieties to be adopted by farmers (Geremew *et al*., 2004).

During the main cropping season of 2005, a total of 21 genotypes (15F1s and 6 parents) were evaluated in half diallel mating design for heterosis and combining ability in Ethiopian sorghum landrace at Bako Research Center (Girma *et al*., 2010). Fifty four F1 hybrids were evaluated for combining ability effects of major morpho-agronomic traits of introduced parental lines (18 pollinators and 3 A-lines) in 2005 at two droughts prone areas, which were Melkassa and Shewarobit (Tadesse *et al*., 2008). Mengistu *et al*., (2010) evaluate the combining ability of five landraces and one advanced line in half diallel mating design. So far one hundred eight F1 hybrids were assessed for their combining ability performance derived from six female A-lines and eighteen pollinator lines at three locations *viz*. Melkassa, Babillie and Mieso (Egu *et al*., 2009). In addition to this, a total of 139 F1 hybrids derived from twenty-six lines of eighteen male and eight female lines were evaluated for heterosis and combining ability study in 2013 main season at three testing sites *viz*. Arsinegelie, Bako and Mieso (Mindaye *et al*., 2016).

As explained above, numbers of studies have investigated the utility of developing varieties in sorghum for adoption in the lowland areas of Ethiopia. These studies consistently identified varieties that produced more grain yield than the already existing varieties (EIAR, 2014). However, the improved varieties lacked the adaptive traits for diverse local environments and had lower grain size. The development of locally adapted improved hybrid varieties to a particular environment is one solution to overcome the challenges of both local adaptation and local farmers end use requirements. The current study focused on investigating the effectiveness of developing the potential hybrids and parents that also address the adaptation issue and multiple trait demands of farmers.

Therefore, this study was conducted with following objectives.

General objective

- To investigate the magnitude of heterosis and combining ability of sorghum inbred lines in line x tester mating design and to identify potential parents and crosses for further sorghum breeding programme.

Specific objectives

- ✓ To estimate general and specific combining abilities of sorghum inbred lines under line x tester mating design for yield and yield related traits.
- ✓ To identify good combining parents and hybrids to use in future breeding programme
- ✓ To determine the type of gene actions involved in controlling yield and yield related traits.
- ✓ To estimate the magnitude of heterosis and classify the elite sorghum inbred lines into different heterotic groups.

2 LITERATURE REVIEW

2.1 Origin, Diversity and Domestication of Sorghum

The center of origin and domestication for cultivated sorghum is considered to be the north-eastern part of Africa, most likely in the modern Ethiopia and Sudan countries. Hence, Ethiopia is a centre of diversity for sorghum, and the extremely diverse sorghum types found in the country are of global significance (Ayana *et al.*, 2000). Sorghum appears to have been domesticated in Ethiopia about 5000 years ago (Dillon *et al*., 2007). Sorghum has a large genetic diversity (Billot *et al*., 2013), derived from farmers selection over years, under a wide range of environments. This adaptation to diverse agro-climatic conditions is a source of favourable alleles that could be used in breeding (Morris *et al*., 2013).

Given the diversity of sorghum, studying genetic diversity (Ayana, 2001) and biochemical composition of sorghum germplasm from Ethiopia is very important for several reasons. The presence of wild and cultivated sorghums in Ethiopia reveals that Ethiopia is the primary center of origin and center of diversity (Asfaw, 2009). Being sorghum is an indigenous crop, tremendous amount of variability exists in the country. The subspecies bicolor includes the domesticated sorghum used for grain and it is divided based on floral morphology into five interfertile races including, Bicolor, Kafir, Caudatum, Durra, and Guinea that can produce 10 intermediate races (Brown *et al*., 2011, Morris *et al*., 2013).

In addition to disruptive selection, geographic isolation and recombination in different environments led to the creation of a large number of types, varieties and races of sorghum. As a result, three broad groups of Sorghum bicolor were generated; cultivated and improved types, wild types and intermediate types (Kimber, 2000). These improved sorghum types were speeded via the movement of people and trade routes into other regions of Africa, India, and Middle East and eventually into the Far East. By the time sorghum was transported to America during the late 1800s to early 1900s, the diversity of new sorghum types, varieties and races created through the movement of people, disruptive selection, geographic isolation and recombination of these types in different environments would have been large (Dillon *et al*., 2007). Early domestication of sorghum was associated with changing the small-seeded, shattering and open panicles toward improved types with larger, non-shattering seeds and more compact panicles.

Stable, high-yielding sorghum varieties have been recently developed through breeding or improvement programmes utilizing sorghum landrace varieties from Africa, India and China. This has involved selecting traits such as photoperiod insensitivity, reduced height (to reduce lodging), drought tolerance, pest and disease resistance (Reddy *et al*., 2006). Domesticated sorghum is drought tolerant with an extensive root system, a waxy bloom on the leaves that reduces water loss, and the ability to stop growth in periods of drought and resume growth under suitable environmental conditions. Sorghum requires rainfall of 500 to 800 mm throughout the growing season and can withstand temporary water logging (Balole and Legwaila, 2006). Domesticated sorghum tolerates a range of soil types including heavy Vertisols, light sandy soils, loams, and sandy loams and soil p^H levels from 5.0 to 8.5 (AERC, 2008; Balole and Legwaila, 2006).

2.2 Drought Constraint to Sorghum Production

Drought is a major constraint in sorghum production worldwide and is considered as the most important cause of yield reduction in crop plants (Sabadin *et al*., 2012; Besufekad and Bantte, 2013), especially in water-limited areas of the world including parts of eastern and southern Africa. The crop growth and development are constantly influenced by environmental conditions such as stresses which are the most important yield reducing factors in the world (Dennis, 2000). Drought is the most important abiotic factor limiting growth, adversely affect growth and crop production and one of the most important environmental stresses, especially in warm and dry areas of crop yield are limited (Porudad and Beg, 2003).

Drought is actually a meteorological event which implies the absence of rainfall for a period of time, long enough to cause moisture-depletion in soil and water deficit with a decrease of water potential in plant tissues. But from agricultural point of view, drought is the inadequacy of water availability, including precipitation and soil-moisture storage capacity, in quantity and distribution during the life cycle of a crop plant, which restricts the expression of full genetic potential of the plant. It acts as a serious limiting factor in agricultural production by preventing a crop from reaching the genetically determined theoretical maximum yield. Increased crop yield is required to meet the needs of future population growth, but drought causes significant yield reductions for rainfed and irrigated crops. Climate changes will increase the frequency of droughts, particularly in many countries in Africa that are already drought-prone.

For instance, by 2050, water shortages are expected to affect 67% of the world's population (Ceccarelli *et al*., 2004). Climate extremes are expected to increase with climate change, which may negatively affect crop production (Troy et al., 2015). In most areas where crop production is dependent on rainfall there is always risk of crop failure or yield loss due to moisture stress. In the semi-arid tropic areas, moisture is always inadequate for crop growth because of low precipitation and erratic distribution and poor soil moisture storage capacity of soils. In severe cases the stress could lead to total crop loss (Sinha, 1986). Drought is the major limiting factors for yield stability in the semi-arid tropics, where rainfall is inadequate, non-uniform and erratic in distribution (Hamblin *et al*., 2005). Worldwide, the yield loss each year due to drought was estimated to be around USD 10 billion (Mutava, 2009).

There is wide genetic variation for physiological and yield traits associated with tolerance to limited moisture stress within sorghum genotypes and these traits can be used for identifying drought tolerant genotypes of sorghum (Mutava *et al*.,2011). Agricultural drought, namely water deficiency, adversely affect plant and crop production by reducing leaf size, stem extension and root proliferation, disturbing plant water and nutrient relations, and inhibiting water-use efficiency. During periods of severe drought, these losses can be much higher and can potentially result in complete crop failure. Obviously, drought is currently the leading threat to the world's food security. At the same time, it is a big challenge to achieve an average annual increase in cereal production of 44 million metric tons per year for meeting the demand of 9 billion people by 2050.

2.3 Mechanisms of Drought Resistance of Sorghum

Drought stress is a serious agronomic problem contributing to severe yield losses worldwide. This agricultural constraint may nevertheless be addressed by developing crops that are well adapted to drought prone environments. The mechanisms that enable this crop to survive under these harsh conditions are complex and not well understood. Previous researches suggest three general strategies for plant survival in drought environments (Ludlow and Muchow, 1990). These strategies are drought escape, avoidance and tolerance. However, crop plants use more than one mechanism at a time to resist drought. Drought tolerance is the ability to withstand water-deficit with low tissue water potential. To improve drought tolerance trait, breeding requires fundamental changes in the set of relevant attributes, finally emerging as something named drought tolerance (Maleki *et al.*, 2013).

Drought tolerance depends on the plant developmental stage at the onset of the stress syndrome, which in sorghum may happen during the early vegetative seedling stage, during panicle development and in post-flowering, in the period between grain filling and physiological maturity (Rosenow *et al*., 1996). In particular, post-flowering drought stress can result in significant reductions in crop yield (Rosenow *et al*., 1996). Drought escape is the ability of a plant to complete its life cycle before serious soil and plant water deficits develop. This mechanism involves rapid phenological development (early flowering and early maturity), developmental plasticity (variation in duration of growth period depending on the extent of water-deficit) and remobilization of parenthesis assimilates to grain.

Drought avoidance is the ability of plants to maintain relatively high tissue water potential despite a shortage of soil-moisture. Mechanisms for improving water uptake, storing in plant cell and reducing water loss confer drought avoidance. Drought avoidance is performed by maintenance of turgor through increased rooting depth, efficient root system and by reduction of water loss through reduced epidermal (stomatal and lenticular) conductance, reduced absorption of radiation by leaf rolling or folding, and reduced evaporation surface (leaf area). The mechanisms that confer drought resistance by reducing water loss (such as stomatal closure and reduced leaf area) usually result in reduced assimilation of carbon dioxide. Consequently, crop adaptation must reflect a balance among escape, avoidance and tolerance while maintaining adequate productivity.

Drought resistance is a complex trait, expression of which depends on action and interaction of different morphological (earliness, reduced leaf area, leaf rolling, wax content, efficient rooting system, awn, stability in yield and reduced tillering), physiological (reduced transpiration, high water-use efficiency, stomatal closure and osmotic adjustment) and biochemical (accumulation of proline, polyamine, trehalose, etc., increased nitrate reductase activity and increased storage of carbohydrate) characters. Due to its inherent nature, sorghum has drought resistant mechanisms that make it better fit in moisture stressed areas and less competition from other crops. Sorghum is the single most important cereal in drought prone areas and the climate-resilient crops that can better adapt to climate changes (Reddy *et al*., 2011). Sorghum is one of the most drought tolerant crop species and is an important model system for studying physiological and molecular mechanisms underlying drought tolerance (Mullet *et al.*, 2001; Sanchez *et al*., 2002).

Post-flowering drought adaptation in sorghum is associated with the stay green phenotype, which is characterized by the maintenance of green stems and upper leaves under water limitation after flowering (Subudhi *et al*., 2000). Stay green (SG) is the general term given to a variant in which senescence (normally apparent to the eye as loss of chlorophyll) is delayed compared with a standard reference genotype (Thomas and Howarth 2000). Drought due to climate change is favouring sorghum production even in areas that were originally favorable for other crop production. Sorghum is the dominant crop in the arid and semi-arid tropics, where drought seriously affects its production.

The use of improved cultivars, particularly hybrids, was found to be the major component of the integrated approach of mitigating the drastic effect of drought. Several factors such as low soil fertility, poor pest and disease control and low yielding potential of local varieties contributed to low yield, much of the reduction in yield is thought to be due to severe drought stress (Boyer, 1982). Efforts have been underway to mitigate the effect of recurrent drought through soil and moisture conservation and tillage practices and development of varieties adapted to the dry land condition. Previous reports indicated that significant morphological and genetic variability attributes to drought tolerance were detected among African sorghums (Doggett, 1988).

2.4 Genetics of Drought Resistance in Sorghum

Drought resistance is of enormous importance in crop production. The identification of genetic factors involved in plant response to drought stress provides a strong foundation for improving drought tolerance. Stay-green is a drought resistance trait in sorghum that gives plants resistance to premature senescence under severe soil moisture stress during the post-flowering stage. There is different morphological and physiological mechanisms contribute to overcome the effect of drought in crop plants (Mitra, 2001). Plants have evolved a series of mechanisms at the morphological, physiological, biochemical, cellular, and molecular levels to overcome water deficit or drought stress conditions. Various drought-related traits, including root traits, leaf traits, osmotic adjustment capabilities, water potential, ABA content, and stability of the cell membrane, have been used as indicators to evaluate the drought resistance of plants. Stay-green sorghum plants exhibit greener leaves and stems during the grain-filling period under water-limited conditions compared with their senescent counterparts, resulting in increased grain yield, grain mass, and lodging resistance (Borrel *et al*., 2014).

Stay-green has been mapped to a number of key chromosomal regions, including Stg1, Stg2, Stg3, and Stg4, but the functions of these individual quantitative trait loci (QTLs) remain unclear. The stay-green trait is positively correlated with sorghum grain yield in field conditions under terminal drought (Jordan *et al*., 2003, 2012). Stay-green is one form of drought resistance mechanism, which gives sorghum resistance to premature senescence under soil moisture stress during the post-flowering period. Drought is a serious agronomic problem and the single greatest factor contributing to crop yield loss in the world today. This problem may be alleviated by developing crops that are well adapted to dry-land environments.

Sorghum is one of the most drought-tolerant grain crops and is an excellent crop model for evaluating mechanisms of drought tolerance. Tremendous genetic variability has been reported among sorghum germplasm for their reaction to drought. Genotypes expressing various degree of stay green trait have been identified (Ducan *et al*, 1981; Rosenow and Clark, 1981). However, the heritability of this trait from different genotypes was not consistent. In some backgrounds it appeared to be regulated by dominant genes (e.g., B35), whereas in the others it appears to be recessive (e.g., R9188) (Rosenow, 1984). In a diallel study conducted to estimate the inheritance of the stay green trait, by dissecting into two components which determine the occurrence of the trait, suggested that inheritance of the onset of senescence was additive, whereas for the rate of senescence slow rate was completely dominant over the fast rate (Van Oosteron *et al*., 1996).

Another study on the genetic basis of osmotic regulation revealed the existence of significant variation among different sorghum genotypes (Blum and Sullivan, 1986). A biparental progeny genetic study revealed that two independent major genes (oal and OA2), were involved in the regulation of osmotic adjustment in sorghum (Basnayake *et al*., 1995). But in another study conducted using a different set of population a monogenic inheritance has also been reported to control the trait (Moigan, 1991). In a population derived from TX7078 x B35 six QTL associated with pre-flowering tolerance and eight additional QTL associated with yield and yield components were identified (Ejeta *et al*., 1997).

2.5 Concept of Combining Ability

The concept of combining ability was first used by maize breeders in the USA in the 1930s to predict parental breeding value from their progenies (Simmonds and Smartt, 1999). Combining ability in crosses is defined as the ability of parents to combine amongst each other during the process of fertilization to transmit superior performance and favourable genes to their progenies. Combining ability studies of germplasm facilitates its exploitation in breeding and the choice of suitable parents for superior hybrid combinations (Akinwale *et al*., 2014). In a classical breeding program, it is necessary to identify superior parents for hybridization and crosses to expand the genetic variability for selection of superior genotypes (Hallauer and Miranda, 1988).

Knowledge of combining ability is essential for selection of suitable parents for hybridization and identification of promising hybrids in breeding program. Line × tester is useful in deciding the relative ability of female and male lines to produce desirable hybrid combinations. It provides information on gene effects in controlling inheritance of traits of interest and helps in selecting the parents to be included in cultivar improvement or hybridization programs. It is the best way to test the value of a germplasm and identify the best parents to produce superior hybrids (Kanawade *et al*., 2001; Kenga *et al*., 2004; Mindaye *et al*., 2016). Combining ability studies provide information on the genetic mechanisms controlling the inheritance of quantitative traits and enable the breeders to select suitable parents for further improvement or use in hybrid breeding for commercial purposes.

Combining ability is necessary in identification of good parental lines in hybrid breeding programs (Kambal and Webster, 1965). Plant breeders can take advantage from such information on combining ability for developing high yielding lines and hybrids. Combining ability is used in understanding the nature of gene action involved in the expression of quantitative traits and to predict the performance of the progenies. Combining ability plays a significant role in crop improvement because it helps the breeder to determine the nature and magnitude of gene action involved in the inheritance traits. Combining ability is useful in selection of desirable parents for exploitation of hybrids and transgressive expressions and also to assess the ability of parents to generate potential hybrids with a reasonable level of stability (Mehmet Coban., 2015).

Combining ability is useful for plant breeders to better understand genetic variance and inbred lines to identify desirable parents to use in commercial hybrid production. Plant breeders use results of research on combining ability to help select the best parents for development of hybrids or varieties (Hallauer and Miranda, 1988). Breeding method for the improvement of a crop depends primarily on the nature and magnitude of gene action involved in the expression of quantitative and qualitative traits. Combining ability analysis helps in the identification of parents with high general combining ability (GCA) effects and cross combinations with high specific combining ability (SCA) effects. Additive and non-additive gene actions in the parents estimated through combining ability analysis may be useful in determining the possibility for commercial exploitation of heterosis and isolation of pure lines among the progenies of the heterotic F1.

In addition, information on combining ability would be used to define the gene effects in the expression of quantitative traits (Goyal and Kumar, 1991). Combining ability is an estimation of the value of genotypes on the basis of their offspring performance in some definite mating design. Generally parents are selected based on their combining ability for the traits of interest (House, 1985). Parents that have high genetic variance components have high breeding value and impart large effects on their hybrids (Falconer and Mackay, 1996). Heritability and combining ability estimates are required for efficient identification of good parents (Kambal and Webster, 1965; Falconer and Mackay, 1996). The success of any breeding programme largely depends upon the choice of parents for hybridization.

The ability of the parents to combine well depends upon the complex interaction among genes which cannot be judged by mere yield performance. Combining ability analysis is a powerful tool to estimate combining ability effects and helps in selecting desirable parents and crosses for exploitation of heterosis and involving them in production of desirable hybrids and segregates (Sarker *et al*., 2002; Rashid *et al*., 2007). Information on combining ability and heterosis is a valuable tool in determining superior parents and hybrid combinations in a hybrid breeding program. Combining ability estimation are important genetic attributes for sorghum breeders in anticipating improvement in productivity *via* hybridization and selection.

2.5.1 General and Specific Combining Abilities

The concept of general and specific combining ability was given by Sprague and Tatum (1942), who were the first to define the performance of parents and crosses in terms of combining ability. Accordingly, they coined the term 'general combining ability (GCA) for average performance of the lines in a series of hybrid combinations while specific combining ability (SCA) was referred to those cases in which certain combinations performed relatively better or worse that would be reported on the basis of general combining ability of the parents. A high GCA estimate indicates higher heritability and less environmental effects and higher achievement in selection. GCA effects represent the fixable and heritable component of genetic variance and have direct association with narrow sense heritability and homozygosity. Selection is effective for achieving maximum genetic gain and it's due to additive effect of genes, whereas SCA represents the non-fixable and non-heritable component of genetic variation. Specific combining ability is an indicative of heterosis and heterozygosity. Maximum genetic gain achieved through heterosis breeding rather than selection and SCA was the result of dominance and epistasis (Fasahat *et al*., 2016)

Griffing (1956) applied the concept of gca and sca in relation to diallel crossing system while Kempthorne (1957) proposed the concept of gca and sca in line × tester analysis. Line x tester is basically an extension of top cross design in the sense that instead of one tester as used in top cross, more than ones testers are used under L x T mating design. This design involves hybridization between lines (f) and wide based testers (t) in one to one fashion generating f x m = fm hybrids (Sharma, 2006). Line × tester analysis is one of the most powerful tools for predicting the general combining ability (GCA) of parents and selecting of suitable parents and crosses with high specific combining ability (SCA) (Rashid *et al*., 2007).

The line x tester mating design for combining ability suggested by Kempthorne (1957) is an appropriate method to identify superior parents and hybrids based on GCA and SCA respectively. It is also helpful for estimating the nature and magnitude of gene action controlling quantitative traits (Muthuswamy *et al*., 2003). GCA is calculated for a specific trait as the (positive or negative) deviation of the mean offspring performance of a genotype from the grand mean of all offsprings included in the particular mating design. Therefore, inbred lines are selected as parental lines based on the highest SCA.

Successful and sound breeding program depends on the correct understanding of gene action involved in determining the different characters. It is claimed that if the gca variance is greater, it implies preponderance of additive gene action for the trait and if sca variance is greater, then the particular character is mostly under the control of non-additive gene action. If the ratio of gca to sca variances was less than unity for all the traits indicating the pre-dominant role of non-additive gene action and recommended to utilize non-additive variance through heterosis breeding (Machado *et al.*, 2002). Combining ability analysis helps in the identification of parents with high general combining ability (gca) effects and cross combinations with high specific combining effects (sca) for commercial exploitation of heterosis and isolation of pure lines among the progenies of the heterotic hybrids.

Specific combining ability represents the non-fixable component of genetic variation and it is important to provide information on hybrid performance. The criterion for selection is by considering general combining ability effects (gca) of the parents. Since the parents with high mean values may not necessarily be able to transmit their superior traits into their progenies, it become necessary to access their compatibility to express their own high performance to the hybrids involving them. As a general rule, GCA is the result of additive gene effects, while SCA is the result of deviations from the additive gene action caused by dominance and epistasis (Bernardo, 2014). In statistical terms, the GCA is the main effect while the SCA is an interaction (Bernardo, 2014).

Kambal and Webster (1965) used the ratios of male GCA to the sum male GCA plus male GCA x location interaction and female GCA to the sum female GCA plus female GCA x location interaction to express stability of GCA of males and GCA of females over locations. The general combining ability variance provides estimate of additive genetic variance which is required for the estimation of narrow sense heritability (Griffing, 1956). High SCA effects resulting from crosses where both parents are good general combiners (i.e., good GCA × good GCA) may be ascribed to additive × additive gene action. The high SCA effects derived from crosses including good × poor general combiner parents may be attributed to favourable additive effects of the good general combiner parent and epistatic effects of poor general combiner, which fulfils the favourable plant attribute. High SCA effects manifested by low × low crosses may be due to dominance × dominance type of non-allelic gene interaction producing over dominance thus being non-fixable.

A number of previous studies have shown that both GCA and SCA effects were significant for yield and yield components (Jagadeshwar and Shinde, 1992), which implies that both additive and non-additive gene actions are determining these traits. Days to flowering was noted to be regulated by additive gene action alone, whereas both additive and non-additive gene effects were important for plant height. For head and grain weight, non-additive effects were more important than additive (Subbarao *et al*., 1976). The other study conducted in the semi-arid Kenya showed significant GCA effect for all the traits studied (Haussmann *et al*., 1999), which indicated the predominance of additive genetic effects for grain yield components, plant height and leaf rolling score.

In a recent study conducted by Kenga *et al*., (2004) significant effects were detected for both GCA and SCA for yield and various yield components including days to anthesis, plant height, threshing percentage and seed mass, whereas only GCA effect was significant for inflorescence length. An investigation conducted at Akola and Agricultural Research Station, Washim to assess magnitude of heterosis and combining ability revealed the importance of non-additive gene action for several traits (viz., days to 50 per cent flowering, days to maturity, plant height, panicle weight, fodder yield plant-1, grain yield plant-1, leaf area index and harvest index except panicle length, number of grains panicle-1 and 100 seed weight for which additive gene action was found to be important (Jadhav and Deshmukh, 2017).

In a line x tester experiment conducted by, Harer and Bapta (1983) additive gene action was observed to be more important for plant height, number of leaves, leaf length, total leaf area, days to flowering, panicle length and 1000- kernel weight, whereas non additive gene action was predominant for leaf width, weight of panicle and total grain yield per plant. Moreover, additive gene action was also reported for days to flowering and maturity (Senthil and Palanisamy, 1994). Tadesse *et al*., (2008) was reported the predominance of additive gene for plant height and panicle exertion traits which implied the importance of general combining ability over specific combining ability for those traits. Girma *et al*., (2010) was observed the preponderance of additive gene action over the non-addtive gene action for plant height and thousand seed weight which is very important in the improvement through effective selection.

2.6 Concept of Heterosis

Heterosis or hybrid vigor is a phenomenon where hybrid progeny have superior performance compared to their parental inbred lines (Ghaderi *et al.,* 1984). An understanding of the fundamental nature of gene action or genetic basis of heterosis and combining ability of parents are of primary interest to plant breeders (Barh *et al*., 2016). The magnitude of heterosis provides information on the extent of genetic diversity of parents in developing superior F1s so as to exploit hybrid vigour (Shull, 1952). Heterosis is superiority of the hybrids over their parents in terms of yield performance, growth, reproductive ability, adaptability, disease and insect resistance, general vigour, quality, size, fruitfulness, speed of development, or to climatic rigors of any kind manifested by cross bred organisms as compared with corresponding inbreds (Shull, 1952). Heterosis represents percentage increase or decrease in the mean values of the F1 over their mid-parental value (Meena, 2017).

The terms heterosis and hybrid vigor are synonymous and often used interchangeably (Ghaderi *et al.,* 1984). Heterosis was demonstrated as early as 1927 in sorghum (Conner and Karper, 1927) and its commercial exploitation was possible only after the discovery of a stable and heritable cytoplasmic-nuclear male sterility (CMS) mechanism (Stephens and Holland 1954). Exploitation of heterosis began in the United States in the 1950s, resulting in large increases in yields of sorghum and maize (USDA, 2007; Troyer and Wellin, 2009). Breeding for heterosis in sorghum can be accomplished by identification of stable cytoplasmic male sterile lines, maintainer and restorer lines having high GCA for desirable character.

Heterosis breeding has received much attention in several crop plants including sorghum. A large degree of heterosis occurs when the parents are genetically divergent or unrelated, resulting in a heterozygous hybrid. Therefore, development of superior high-yielding sorghum hybrids requires a system by which genotypes can be crossed on the basis of the degree of ‘unrelatedness’ between them. Exploitation of hybrid vigour is considered to be one of the outstanding achievements in plant breeding. The characteristically superior performance of hybrid sorghums was because of a phenomenon known as heterosis or hybrid vigor in which hybrids demonstrated markedly vigorous growth and yield when compared with their parents (Bernardo, 2014).

Hybrid vigour is the manifest effect of heterosis, denotes the increase in value of the characters noticed in the hybrids over the parents, checks etc. The utilization of heterosis in various crops throughout the world has tremendously increased the production of human food and livestock feed. Some investigators prefer to use the term hybrid vigor in referring to the developed superiority of hybrids, and use heterosis only for reference to the mechanism by which the superiority is developed. Heterosis is a situation whereby the hybrid is superior to the open pollinated variety parents (Fasoulas, 2000). Depending upon breeding objectives, both positive and negative heterosis is useful for crop improvement. In general, positive heterosis is desired for yield and negative heterosis for early maturity (Shiva *et al.*, 2016).

For most of the characters, the desirable heterosis is positive. But for some characters like earliness, height in cereals and toxic substances are negative heterosis. Research result showed that yield increment over the parental mean in the F1 generation reduces by 50% in the F2 generation (Quinby *et al*., 1958). If F1 hybrid will be selfed over further generations inbreeding depression will appear, the genes of the parental lines will be recombined and new combinations could be selected. The success in the development of superior hybrids or varieties depends on the choice of parents for hybridization and amount and type of genetic variability present in the base population to be improved. Verma and Kumar (1974) and Joshi (1979) emphasized that greater attention should be paid on the choice of parents for hybridization.

Selection of parents for hybridization can be made with the help of combining ability analysis (Sprague and Tatum, 1942). Sorghum exhibits hybrid vigor and more than 95% of sorghum varieties grown for grain in the United States are F1 hybrid varieties (Axtell *et al*., 1999). Heterosis is expressed in three ways, depending on the criteria used to compare the performance of a hybrid. From the plant breeder's viewpoint, better parent and/or standard variety is more effective. From a practical point of view, standard heterosis is most important because it is aimed at developing desired hybrids superior to the existing high yielding commercial varieties. Expression of heterosis in population or line crosses requires two conditions: (i) dominance at loci controlling the trait of interest (ii) differing allele frequencies at those loci in the populations or lines involved in the crosses (Falconer and Mackay, 1996).

2.6.1 Average Heterosis

Mid-parent heterosis is the superiority of a hybrid over the mean of its parents and which is used in quantitative genetics (Bernardo, 2014). If the hybrid is superior to the mid -parent, it is regarded as heterosis (average heterosis or relative heterosis) (Hallauer *et al*., 2010). The estimates of heterosis in the crosses were expressed on the basis of the mid parents. It has been determined for various agronomic and physiological traits in sorghum by several investigators. Negative heterosis for days to 50% flowering, indicating earliness has been reported as the expression of hybrid vigor in sorghum by several investigators (Patil and Thombre, 1986). For instance, Toure *et al*. (1996) and Rafiq *et al*. (2003) reported negative mid-parent heterosis -15.11, and -5.38 for days to flowering respectively. The highest mid-parent heterosis (57.10%) for plant height was reported by Rafiq *et al*. (2003). Mid-parent heterosis (207%) for plant was also reported by Rafiq *et al*. (2002). For instance, Haussmann *et al*. (1998) reported the relative superiority for grain yield sorghum hybrid over the mid-parent at 68%. Moreover, Osuna-Ortega *et al*. (2001) observed highest mid parent and better-parent heterosis 173% for grain yield.

2.6.2 Heterobeltiosis

Blum *et al*., (1977) defined heterosis as the advantage of the hybrid over the best parent and estimated over the superior or better parent. The superiority of hybrid over better parent resulted due to dominance or over dominance. Parent versus crosses performance is probably the most basic comparison in quantitative inheritance and the degree of heterosis provides the simplest and easiest measure of genetic diversity and gives preliminary idea about the probable gene action involved in determining a particular character (Fanseco and Peterson, 1968). Different authors reported heterosis over better parents for different characters of sorghum. Toure *et al*. (1996) reported highly significant positive heterosis over the best parent for grain yield ranging from -0.35 to 72.95%. Liang *et al*., 1973, Harer and Bapat, 1982 reported low to negative heterosis for leaf number per plant, While higher heterosis for leaf length and leaf area reported by Harer and Bapat, 1982 and Giriraj and Goud ,1984. Similarly, positive heterosis was reported for panicle length, panicle weight and kernel number per panicle by different author Rafiq *et al*. (2003) over better parents. Osuna-Ortega *et al*. (2001) observed highest better-parent heterosis 103% for grain yield.

2.6.3 Standard Heterosis

The superior performance of hybrid over the standard commercial hybrid variety in terms of desired traits is known as standard heterosis (Virmani, 1994). It has practical importance in plant breeding and it is also referred as economic heterosis. The commercial usefulness of a hybrid would primarily depend on its performance in comparison to the best commercial variety of the concerned crop species. From a practical point of view, standard heterosis is most important, because it is aimed at developing desired hybrids superior to the existing high yielding commercial varieties (Virmani, 1994).

2.7 Heterotic Grouping and Heterotic Pattern

Heterotic group is a group of related or unrelated genotypes from the same or different populations, which display similar combining ability and heterotic response when crossed with genotypes from other genetically distinct germplasm groups (Melchinger and Gumber, 1998). Heterotic grouping refers to the identification of groups that are genetically distinct from each other and that produce superior hybrids when crossed using morphological *per se* performance (Sawadogo *et al*., 2014) and genetic relationship (Zongo *et al*., 2005; Deu *et al.,* 2006; Billot *et al*., 2013). Heterotic grouping is using combining ability information in identifying suitable hybrid parents (Badu- Apraku *et al.*, 2013; Akinwale *et al*., 2014). This method of classify available germplasm into distinct heterotic groups and to identify suitable parents for crosses based on specific combining ability (SCA) effects of grain yield (Fan *et al*., 2009) and heterotic grouping based on general combining ability (GCA) of multiple traits (HGCAMT) (Akinwale *et al*., 2014; Badu-Apraku *et al*., 2013).

Identification of inbred lines with good combining ability is a prerequisite for the success of any breeding programme aimed at hybrid development (Dao *et al*., 2014; Nyaligwa *et al*., 2015). Thus, there is a need of information on combining ability based heterotic grouping help breeders when selecting parents to use in crosses. Assigning germplasm into different heterotic grouping is fundamental for the maximum exploitation of heterosis for hybrid cultivar development. Similarly, information on genetic diversity is also very important for hybrid breeding and population improvement programs for assessing the level of genetic diversity and assigning them into different heterotic groups (Reif *et al.,* 2003). For an efficient hybrid breeding program, it is desirable to organize the germplasm into heterotic groups (Reif *et al.,* 2007). In sorghum, heterosis for yield has been reported to range from 39 to 80%

(Quinby, 1962). Broadening the genetic base of heterotic pools is a key to ensure continued genetic gain in hybrid breeding. The selection of parents and breeding strategies for the successful hybrid production facilitated by heterotic grouping of parental lines and determination of combining abilities of them. Combining ability and heterotic grouping studies of germplasm, facilitates its exploitation in breeding and the choice of suitable parents for superior hybrid combinations (Akinwale *et al*., 2014). Crosses between inbred lines from groups with differing genetic backgrounds are expected to exhibit high levels of heterosis than those among lines from the more genetically related groups (Fato *et al*., 2012). Heterotic pattern is a specific pair of heterotic groups, which may be populations or lines that express in their crosses high heterosis and consequently high hybrid performance.

The concept of heterotic patterns is important in that it helps breeders in choosing parents of crosses for line development as well as testers to evaluate combining ability of newly developed inbred lines and therefore, simplifying germplasm management and organization (Reif *et al*., 2005; Nepir *et al*., 2015). Heterotic groups and patterns help 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. Assigning germplasm into different heterotic groups and patterns is fundamental for exploitation of heterosis for hybrid development. If once heterotic groups and their pattern are identified then large number of hybrid combination can be developed within short period of time because grouping of lines in different clusters would avoid the development of unnecessary hybrids from the heterotic patterns.

2.8 Genetic Basis of Heterosis

Genetic hypotheses are amongst the oldest but still most prevailing explanations for heterosis (Lamkey and Edwards, 1999). According to quantitative genetic theory, heterosis can result from dominance, over dominance, and epistasis. The relevance of the three hypotheses has been investigated intensively using phenotypic data and also through molecular marker-assisted QTL mapping (Reif *et al*., 2005). Davenport (1908) proposed the dominance theory and supported by Bruce (1910), Jones (1917) and Collins (1921) that cites the effect of dominant favorable alleles masking unfavourable recessive alleles as the reason for the superiority of a hybrid (Bernardo, 2014). The dominance hypothesis argues that the better performance of hybrids is caused by masking of deleterious recessive alleles.

In heterozygous state, the deleterious effects of recessive alleles are masked by their dominant alleles. Thus heterosis results from the masking of harmful effects of recessive alleles by their dominant alleles. Inbreeding depression, on the other hand, is produced by the harmful effects of recessive alleles, which become homozygous due to inbreeding. Therefore, according to the dominance hypotheses, heterosis is not the result of heterozygosity, but it is the result of prevention of expression of harmful recessives by their dominant alleles. Similarly, inbreeding depression does not result from homozygosity. But from the homozygosity of recessive alleles, which have harmful effects. East (1908) and Shull (1908) independently proposed the over dominance theory, which suggests that the heterozygous condition is responsible for heterosis and it is the inherent superiority of a heterozygote over either homozygote (Bernardo, 2014). Quinby (1974) proposed a complementary interaction between recessive and dominant alleles as a possible cause of heterosis. The effect of dominant favorable alleles masking unfavourable recessive alleles as the reason for the superiority of a hybrid (Bernardo, 2014).

Over dominance is the most important contributor to heterosis of yield, number of grains per panicle, and grain weight. According to over dominance hypothesis, heterozygotes at least some of the loci are superior to both the relevant homozygotes. Thus heterozygote Aa would be superior to both the homozygotes AA and aa. Consequently, heterozygosity is essential and the cause of heterosis, while homozygosity resulting from inbreeding produces inbreeding depression. The over dominance hypothesis argues that the heterozygous genotype has inherent superiority over either of the two homozygous genotypes. The epistasis hypothesis attributes the observed heterosis to the interaction between loci. In most cases, two or more mechanisms are involved in heterosis rather than a single unified theory (Kaeppler, 2012; Schnable and Springer, 2013).

2.9 Hybrid Development of Sorghum

Hybrid is the progeny (F1) as a result of cross between two or more distinct parents or genotypes (Ghaderi *et al.*, 1984). Sorghum improvement programme launched in 1961 by the Indian Council of Agricultural Research in collaboration with Rockefeller Foundation of U.S.A to find possibility of developing high yielding hybrids. First hybrid of sorghum CSH-1 was released in 1964. Since, then many hybrids such as CSH-5, CSH-9, CSH- 10, CSH-13, CSH-14, CSH-16 and CSH-23 have been developed and released for cultivation.

This hybrid was developed by All India Sorghum Crop Improvement Project, Indore in the year 1999. Many cytoplasmic genetic male sterile lines (CMS) and restorer lines have been developed at Indore and at other sorghum research centre of the country. The CMS in sorghum genotypes was developed by backcrossing chromosomes of kafir into the cytoplasm of milo. Similarly, genetic male sterility (ms) has been discovered in sorghum male sterile plants (Msms) (Acquaah, 2007). The discovery of cytoplasmic male sterility in sorghum facilitates the commercial utilization of hybrid vigor (Akata *et al*., 2017). Stephens and Holland (1954) reported for the first time, the use of cytoplasmic genetic male sterility for developing hybrids to increase sorghum production. Different male-sterility inducing systems, such as A2 and A3 cytoplasm, have been discovered in the last few decades, and hold promise for widening the genetic variability of elite lines.

The Sorghum Conversion Program continues to serve as a major source of new germplasm for many breeding programs throughout the world (Smith and Frederiksen, 2000). There was a report as sorghum hybrids can provide a 20 to 60% grain yield advantage over the open pollinated parents (Pfeiffer *et al*., 2010). Breeding for heterosis in sorghum accomplished by identification of stable cytoplasmic male sterile lines, maintainer and restorer lines having high GCA for desirable character. The genetic effects of various characters can be better understood through the application of biometrical principles. Biometrical models are available for getting information on the combining ability status of parental lines of which Lines x Tester approach (Kempthorne, 1957). This approach provides information on relative magnitude of fixable and non-fixable genetic variation available in the material.

The hybrid seed production involves a CMS line (A line), a maintainer line (B line) and a restorer line (R line). Scheme of Hybrid Seed Production using the CGMS involves two main steps. First is the production of A line (A x B) and second involves production of Hybrid Seed (A x R). The lines that produce fertile F1s when crossed with A-lines are called restorer lines or R-lines. The development of hybrid parents involves two steps: (1) identification of potential B- and R-lines; and (2) development of A-lines and R-lines. This is to need to develop alternative male sterility sources and fertility restoration systems. Research on sorghum hybrid development in Ethiopia began in the mid-seventies, with an objective of developing sorghum hybrids for the low altitude and moisture stress ecological zones. Series of A and B lines were introduced along with suitable restorers for hybrid development from

abroad. Best looking and agronomically suitable A and B lines were identified (Brhane 1980). He also mentioned that introduction of fertility restorer line (R-line) has been effected since 1977 and the best combiners have been identified. Hybrid parents need to be genetically complementary for vigor and yield associated traits, but not for other often recessive traits that would adversely affect height, maturity, grain qualities or resistance. In the recent efforts research aiming at studying the digestibility, drought and striga tolerance of the introduced hybrids are undertaking. Meanwhile, hybrid development activities using male sterile female lines found to have better adaptation and locally adapted and high yielding male parents are being conducting. So far four hybrids found to be better performing in the drier areas and farmers were producing the hybrids where the drought causes significant yield losses.

3 MATERIALS AND METHODS

3.1 Description of the Study Areas

The experiment was conducted across the two environments representing the dry lowlands areas of Ethiopia. These were Mieso from the Oromia Regional State and Kobo from the Amhara Regional State. In these target environments, drought is a serious challenge for sorghum production and they are considered as major testing sites for drought adaptation (EIAR, 2014). Mieso is 302 kilometers far away from Addis Abeba in the eastern part of the country in the Oromia Regional State. It is located at an altitude of 1470 meter above sea level. It is located at 8º30´N latitude and 39º21´E longitudes with an average minimum and maximum temperatures of 14.0^{o}C and 30.01^{o}C respectively. The average annual rainfall is 763mm and the dominant soil type is Vertisols with p^{H} 7.3-7.8 (MARC, 2007).

Kobo is 437 kilometres far away from Addis Abeba in the northern part of the country in the Amhara Regional State. It is located at an altitude of 1479 meter above sea level. It is situated at 12º09´N latitude and 39º38´E longitudes with an average minimum and maximum temperatures of 15.32^{o}C and 30.24^{o}C respectively. The average annual rainfall is 650mm and the dominant soil type is Vertisols with p^{H} 7.61 (EIAR, 2014).

3.2 Genetic Materials

The experiment consisted of two male parents and thirteen cytoplasmic male sterile lines as female parents along with their 26 hybrids and one standard check (ESH-4). These fifteen parents (2 males and 13 females) were crossed according to the line x tester mating design developed by Kempthorne (1957), by using irrigation during 2017 at Werer Agricultural Research Center (WARC). A total of fourty two genotypes, consisting the parents along with their hybrids and a check were used in this study. The seed parents were developed by back crossing of the new B lines with known B lines to introgress the cytoplasmic male sterile gene through recurrent selection. The seed parents TX-623B, P-9501B, P-9505B, P-9534B, P-851015B, P-850341B, P-9511B, B5 and B6 were introduced from Purdue University. They were tested for adaptation, performance and stability of male sterility and are being used for the hybrid development in the program. The seed parent, MARC1B, MARC2B, MARC3B, and MARC6B were developed and released by National Sorghum Research Program to use as CMS lines. ESH-4 is a hybrid which was released since 2016 by the National Sorghum

Research Program (MARC) for dry lowland areas. It has high yielding and drought tolerance merits and used as standard check. Melkam was developed and released by Melkassa Agricultural Research Center, whereas ICSR-14 was introduced from India (ICRISAT). They were used as restorer lines for low moisture stress areas and selected on the basis of their wider adaptability traits for drought stress environments and grain yield performance.

Table 2: Description of the genotypes included in the experiment at Mieso and Kobo in 2018/2019 cropping season

S.N	Lines	Pedigree	S.N	Hybrids	Pedigree
1	TX-623B	TX-623B	21	P-851015A X ICSR -14	P-851015A X ICSR-14
2	P-9501B	P-9501B	22	P-850341A X ICSR-14	P-850341A X ICSR-14
3	P-9505B	P-9505B	23	A5 X ICSR-14	A5 X ICSR-14
4	P-9534B	P-9534B	24	A6 X ICSR-14	A6 X ICSR-14
5	P-851015B	P-851015B	25	MARC1A X ICSR-14	MARC1A X ICSR-14
6	P-850341B	P-850341B	26	MARC2A X ICSR-14	MARC2A X ICSR-14
7	B5	B5	27	MARC3A X ICSR-14	MARC3A X ICSR-14
8	B6	B6	28	MARC6A X ICSR-14	MARC6A X ICSR-14
9	MARC1B	MARC1B	29	P9511A X ICSR-14	P9511A X ICSR-14
10	MARC2B	MARC2B	30	TX-623A X Melkam	TX-623A X Melkam
11	MARC3B	MARC3B	31	P-9501A X Melkam	P-9501A X Melkam
12	MARC6B	MARC6B	32	P-9505A X Melkam	P-9505A X Melkam
13	P9511B	P9511B	33	P-9534A X Melkam	P-9534A X Melkam
	Testers		34	P-851015A X Melkam	P-851015A X Melkam
14	Melkam	WSV387	35	P-850341A X Melkam	P-850341A X Melkam
15	ICSR-14	ICSR-14	36	A5 X Melkam	A5 X Melkam
	Check		37	A6 X Melkam	A6 X Melkam
16	ESH-4	PU20AXPU304	38	MARC1A X Melkam	MARC1A X Melkam
	Hybrids		39	MARC2A X Melkam	MARC2A X Melkam
17	TX-623A X ICSR-14	TX-623AX ICSR-14	40	MARC3A X Melkam	MARC3A X Melkam
18	P-9501A X ICSR-14	P-9501A X ICSR-14	41	MARC6A X Melkam	MARC6A X Melkam
19	P-9505A X ICSR-14	P-9505A X ICSR-14	42	P9511A X Melkam	P9511A X Melkam
20	P-9534A X ICSR-14	P-9534A X ICSR-14			

3.3 Experimental Design and Trial Management

The experiment was laid out using alpha lattice (0, 1) design with two replications at two locations in the cropping season of 2018/2019. Each genotype was planted in 2 rows of 5 m length with the row spacing of 75 cm which gives rise to plot area of 7.5 m^2. Each block was separated by 1 m length. The experiment accommodated seven plots per block and six blocks per replication.

The seeds were drilled in each row at the rates of 12 kg/ha. After three weeks of sowing, the seedlings were thinned to 0.20 m distance between plants. All the standard agronomic packages and fertilizer rates of 100 kg/ha DAP and 50 kg/ha Urea were applied to basal and Nitrogen (Urea) was applied after three weeks of sowing (African Soil health consortium, 2017). Weeds were controlled manually and Pests were controlled using insecticide karate.

3.4 Data Collection

Data were collected both on plot and plant basis by random sampling technique with the use of descriptors for sorghum (IBPGR/ICRISAT, 1993). The important yield and yield related traits and as well as drought tolerance associated traits were recorded using standard procedures as follows:

Data collected on the basis of individual plants

I. Plant height (PH in cm): The height of the plant from the bottom to the tip of the panicle during flowering on 5 randomly tagged plants.
II. Total number of leaves per plant: Recorded on five randomly tagged plants and averaged.
III. Panicle exertion (PE in cm): Panicle exertion measured between the bases of flag leaf to the bases of panicle from five randomly selected plants (Asfaw & Bekele, 2013).
IV. Panicle length (PL in cm): Distance from the panicle tip to the lowest panicle branch on five randomly tagged plants.
V. Panicle width (PW in cm): The average width of five randomly selected plants at the middle of the panicle (head).
VI. Leaf length (LL in cm): Average length of the fourth leaf from the flag leaf on five randomly selected plants.
VII. Leaf width (LW in cm): Average width of the fourth leaf from the flag leaf at the widest point of leaves on five randomly selected plants.
VIII. Total leaf area (LA in cm^2): Total leaf area computed as length × width of the fourth leaf from the flag leaf × 0.71 of randomly tagged five plants (Krishnamurthy *et al*., 1974).
IX. Panicle yield (PY in g): The weight of individual panicle measured using one randomly selected representative plant.

Data collected on the basis of plots

I. Days to flowering (DTF): Number of days from emergence till 50% of the plants in a plot showed flowering halfway down the panicle.

II. Days to maturity (DTM): The number of days from emergence to the date when 95% of the plants matured physiologically.

III. Stay green score (1-5): It was measured at maturity stage as a measure of stay green traits (Haussman *et al.*, 1999).

IV. Grain yield (GY): Grain yield obtained from total harvest of the plot and then converted to ton/ha after adjusting to optimum seed moisture content.

V. Number of productive tillers: The number productive of tillers counted that bear grains per plot.

VI. Thousands seed weight (TSW in g): The weight of 1000 grains sampled from a plot at 12.5% moisture content recorded in gram.

VII. Over all plant aspect (PAS): Over all agronomic performance of the observation based on the recorded traits using 1-5 scale, where 1 = excellent, 2 = very good, 3 = good, 4 = poor and 5 = very poor

3.5 Statistical Analyses

3.5.1 Analyses of Variances (ANOVA)

The analyses of variance was carried out using GLM procedure of SAS statistical version 9.4 (SAS, 2016) according to alpha lattice design for both separate and combined across locations. Prior to combining the data from the different environments, Bartlett's test for homogeneity of variance was done (Steel and Torrie, 1980) and checked by using F-test (ratio of the largest mean square error to the smallest mean square error is less than three or four) according to Gomez and Gomez, (1984) and the test indicated that the error means were homogeneous for all traits and the data were combined for further analyses. Mean comparisons among genotypes were done by the least significant difference (LSD) test at 1% and 5% levels of significance. In this regard, genotypes were used as fixed factor while locations, replications and incomplete blocks within replications were considered as random factors.

Analysis of variance for single location was done using the following model:-

$$Yijl = \mu + \tau i + \gamma j + \rho l\,(j) + \varepsilon ijl$$

Where; μ is the overall (grand) mean, τi is the effect due to the ith treatment, (i=1, 2, 3…, t), γj is the effect due to the jth replication, and, (j=1, 2…, r), ρl (j) is block within replicate effect, εijl is the error term where the error terms, are independent observations from an approximately Normal distribution with mean = 0 and constant variance σ^2 ε.

Table 3: Skeleton of analysis of variance table for individual location at Mieso and Kobo in 2018/2019

SV	DF	MS	F-Values
Replication(r)	r-1	MSr	MSr/Mse
Blocks(Rep)	r(b-1)	MSb	MSb/Mse
Genotypes(g)	g-1	MSg	MSg/Mse
Parents(p)	p-1	MSp	MSp/Mse
Lines	l-1	MSl	MSl/Mse
Testers	t-1	MSt	MSt/Mse
Hybrids	h-1	MSh	MSh/Mse
Check	c-1	MSc	MSc/Mse
Line x Tester	(l-1)(t-1)	MS(l x t)	MS(lxt)/Mse
Parents vs Hybrids	1	MS(p vs h)	MS(p vs h)/Mse
Hybrids vs Check	1	MS(h vs c)	MS(h vs c)/Mse
Parents vs check	1	MS(p vs c)	MS(p vs c)/Mse
Error	(r-1)(g-1)	MSE	
Total	rg-1	MST	

Source: Sharma *et al., (1999) and* Ceyhan *(2003).*

Key: DF = degree of freedom = number of replication, b = block, g = genotypes p = parents, h = hybrids, c = check, l = lines, t = testers, MS = mean squares, MSR = mean squares of replication, MSg = mean squares of genotypes, MSb = mean squares of blocks within replication, MSc = mean square of check, MSp = mean square of parents, MSh = mean square of hybrids, MSl = mean square of lines, MSt = mean square of testers, MS(lxt) = mean square of line x tester interaction, MS(p vs h) = mean square of parents vs hybrids, MS(h vs c) = mean square of hybrids vs check, MS(p vs c) = mean square of parents vs check, Mse = mean square of error, MST = mean square of total.

Table 4: ANOVA skeleton for combined analysis across location at Mieso and Kobo in 2018/2019

SV	DF	MS	F-Values
Location(L)	L – 1	MSL	
Rep (Location)	L(r − 1)	MSr	MSr/Mse
Genotypes	g − 1	MSg	MSg/Mse
Parents	p – 1	MSp	MSp/Mse
Lines	l− 1	MSl	MSl/Mse
Testers	t − 1	MSt	MSt/Mse
Line x Tester	(l-1)(t-1)	MS(lxt)	MS(lxt)/Mse
Hybrid	h − 1	MSh	MSh/Mse
Check	c − 1	MSc	MSc/Mse
Hybrid vs Check	1	MSh vs c	MSh vs c/Mse
Hybrid vs Parent	1	MSh vs p	MSh vs p/Mse
Parent vs Check	1	MSp vs c	MSp vs c/Mse
Genotype * L	(g −1)(L −1)	MSg×l	MSg×l/Mse
Parent * L	(p −1)(L −1)	MSp×l	MSp×l/Mse
Lines* L	(l−1)(L −1)	MSl×l	MSl×l/Mse
Testers * L	(t−1)(L −1)	MSt×l	MSt×l/Mse
Line x Tester*L	(l-1)(t-1)(L-1)	MSlxt*L	MSlxt*L/Mse
Check * L	(c-1)(L-1)	MSc×l	MSc×l/Mse
Hybrid * L	(h-1)(L-1)	MSh×l	MSh×l/Mse
Hybrid vs check * L	(L-1)	MS(h vs c)×l	MS(h vs c)×l/Mse
Error	L(r −1)(g −1)	Mse	
Total	lrg −1	MST	

Source: Sharma *et al., (1999) and* Ceyhan *(2003).*

Key: DF = degree of freedom, L = number of location, r = number of replication, g = number of genotypes, b = block, p = number of parents, l = number of lines, t = number of testers, c = number of check, h = number of hybrid, hvsc = hybrid vs check, hvsp = hybrid vs parent, pvsc = parent vs check, MSL = mean square of location, MSr = mean square of replication, MSg = mean square of genotype, MSp = mean square of parent, MSl = mean square of line, MSt = mean square tester, MSlxt = mean square of line x tester interaction, MSc = mean square of check, MSh = mean square of hybrid, MS(hvsc) = mean square of hybrid vs check, MS(hvsp) = mean square of hybrid vs parent, MS(pvsc) = mean square of parent vs check, Mse = mean square of error, MST = mean square of total.

Model for combined analysis across locations:-

$$Yijkl = \mu + gi + sj + (g \times s)\, ij + r(s)\, jk + eijkl$$

Where, Yijkl is the observation, μ is the overall mean, gi is the effect of the ith genotype, sj is the effect of the jth site, (g × s) ij is the interaction effect of the ith genotype by the jth site, r(s) jk is the effect of the kth replication within the jth site and eijkl is the residual variance.

3.5.2 Combining Ability Analysis

The combining ability analysis was conducted to estimate general combining ability (GCA) effects of the parents and specific combining ability (SCA) effects of the hybrid combinations considering the genotypes as fixed effects. Significances of GCA and SCA effects of the parents and hybrids were determined by F-test using the standard errors of GCA and SCA effects. Genotypes were partitioned into the mean squares due to hybrids, inbred lines, testers and lines x testers effects. Analysis of variance model for line x tester of individual location was given below:-

$$Yijk = \mu + gi + gj + sij + rk + eijk$$

Where Yijk is the observed measurement for the ijth hybrid grown in the kth replication or site; μ is the population mean; gi and gj are the female and male effects respectively; sij the hybrid effect; and eijk the error term associated with the ijth hybrid evaluated in the kth replication.

Table 5: Skeleton of the analysis of line x tester for individual location at Mieso and Kobo in 2018/2019

SV	DF	Mean Square	F-Values
Rep	r-1	MSr	MSr/Mse
Genotypes (g)	g-1	MSg	MSg/Mse
Parents (p)	p-1	MSp	MSp/Mse
Parents vs hybrid	1	MSp vs h	MSp vs h/Mse
Hybrids(h)	h-1	MSh	MSh/Mse
Lines(l)	F-1	MSl	MSl/Mse
tester(t)	M-1	MSt	MSt/Mse
Line x tester	(l-1)(t-1)	MSl x t	MSl x t/Mse
Error	(r-1)(g-1)	Mse	
Total	(rg-1)	MST	

Source: Sharma (2006)

Key: DF = degree of freedom, number of replication, g = number of genotypes = number of parents, h = number of hybrid,l = number of lines, t = number of testers, lxt = number of line x tester interaction, pvsh = number of parent vs hybrids, MSr =mean square of replication, MSg = mean square of genotypes, MSp = mean square of parents, MSh = mean square of hybrids, MSl = mean square of lines, MSt = mean square of tester, MSc lxt = mean square of line x tester interaction, MSc pvsc = mean square of parent vs hybrid, Mse = mean square of error, MST = mean square of total.

The GCA effect of lines and testers, the SCA effect of lines x testers, and their interactions with the environments were determined by using the following model.

$$Yijk = \mu + gi + gj + sij + lk + rkl + (g \times l)\, ik + (g \times l)\, jk + (s \times l)\, ijk + eijk$$

Where Yijk = the performance of the hybrid made with ith female and jth males in the kth site, μ = the overall mean, gi = the effect of the ith line, gj = the effect of the jth males, sij = the interaction of the ith females with the jth males (effect of the ijth hybrid), lk = the effect of the kth location, rkl = replication effect in the kth location, (g x l)ik = the interaction of the gi and lk, (g x l)jk = the interaction of the gj and sk, (s x l)ijk = the interaction of sij and lk.

Table 6: Skeleton of the combining ability analysis of variance across location at Mieso and Kobo in 2018/2019

SV	DF	MS	F-Values
Location	L-1	MSL	
Rep	r-1	MSr	MSr/Mse
Parents	p-1	MSp	MSp/Mse
Hybrids	h-1	MSh	MSh/Mse
Lines	l-1	MSl	MSl/Mse
Testers	t-1	MSt	MSt/Mse
L x T	(l-1)(t-1)	MS(lxt)	MS(lxt)
Parents vs hybrid	1	MSp vs h	MSp vs h/Mse
Hybrids *L	(h-1)(L-1)	MSh*L	MSh*L/Mse
Lines * L	(l-1)(L-1)	MSl*L	MSl*L/Mse
Testers * L	(t-1)(L-1)	MSt*L	MSt*L/Mse
Lx T * L	(l-1)(t-1)	MSlxt*L	MSlxt*L/Mse
Error	(r-1)(g-1)	MSe	
Total	r(g-1)		

Source: Sharma (2006)

Key: DF = degree of freedom, r = number of replication, p = number of parents, h = number of hybrids, l = number of lines, t = number of testers, lxt = number of line x tester interaction, pvsc = number of parent vs crosses, MSr =mean square of replication, MSp = mean square of parents, MSh = mean square of hybrids, MSl = mean square of lines, MSt = mean square of tester, MSc lxt = mean square of line x tester interaction, MS pvsh = mean square of parent vs hybrid, Mse = mean square of error, MST = mean square of total.

Combining ability analysis was carried out by the method suggested by Kempthorne (1957) as follows:-

I. **General Combining Ability Effect *(GCA)*** - General combining ability (GCA) effect of lines and testers were defined as a deviation of line and tester-mean from mean of hybrids and calculated using the following equations:

a) GCA of Lines $GCAi = \frac{Xi..}{tr} - \frac{X...}{ltr}$

b) GCA of Testers $GCAj = \frac{X.j.}{lr} - \frac{X...}{ltr}$

Where GCAi = GCA effect for the ith lines with Σ GCAi = 0; GCAj = GCA effect for the jth testers with Σ GCAj = 0; Xi. = the total of ith line over all testers (t) and replications (r); X. j = the total of the jth testers over all lines (lt) and replication (r) and X. = the total of all the hybrids over all lines (lt), testers (t) and replications (r).

II. **Specific Combining Ability Effect *(SCA)*** - Specific combining ability (SCA) effect of hybrid combinations is the deviation of each hybrid mean from the mean of all hybrids adjusted for corresponding GCA effects of parents and was computed as:

$$SCAij = \frac{Xij}{r} - \frac{Xi.}{tr} - \frac{X.j}{lr} + \frac{X...}{ltr}$$

Where SCAij = SCA effect of the ijth hybrid with Σ Sij = 0 for each j; Xi j. = the total of ijth hybrid combination over all replications (r).

III. Standard errors for combining ability effects

The significance of GCA or SCA effects were tested by dividing the GCA effects of a particular line or males and SCA effects of a particular hybrid by its respective standard error.

Significance of GCA effects of lines was tested as, $t = \frac{gi}{SE}$ (gi)

Significance of GCA effects of testers was tested as, $t = \frac{gj}{SE}$ (gj)

Significance of SCA effects of hybrids was tested as, $t = \frac{gij}{SE}$ (Sij)

Therefore, the SE was computed using SAS software using the following formulae:

a) Standard errors for GCA for lines (gi) $= \sqrt{(mse/rt)}$

for testers (g*j*) $= \sqrt{(mse/rl)}$

b) Standard error for SCA for hybrids (Sij) $= \sqrt{(mse/r)}$

3.5.3 Estimation of Variance Components for Combining Abilities

The estimates of genetic variance components due to lines, testers and hybrids were obtained (Kempthorne, 1957) as follows:

$$\text{Variance of gcai} = \frac{MSl - MSlxt}{tr} \quad \ldots\ldots\ldots\ldots X$$

$$\text{Variance of gcaj} = \frac{MSt - MSlxt}{lr} \quad \ldots\ldots\ldots\ldots\ldots Y$$

$$\text{Average variance} = \frac{X + Y}{l + t + r}$$

$$\text{Variance of additive} = 4 \text{ x average variance}$$

$$\text{Variance of sca} = \frac{MSlxt - MSe}{r}$$

$$\text{Variance of dominance} = 4 \text{ x variance of sca}$$

Where, $\sigma^2gi = \sigma^2gcai$ = Variance due to general combining ability for females $\sigma^2gj = \sigma^2gcaj$ = Variance due to general combining ability for males $\sigma^2sij = \sigma^2scaij$ = Variance due to specific combining ability for hybrids r = Number of replications l = Number of lines, t = Number of testers, MSl = Mean square due to lines, MSt = Mean square due to testers, MSlxt = Mean square due to hybrids, MSe = Mean square due to error.

The predominance of additive *versus* non-additive gene actions was compared from the ratio of σ^2gca/σ^2sca. Proportional contribution of lines, testers and their interaction to the total variance:-

$$\text{Contribution of lines} = \frac{SSl}{SSh} * 100$$

$$Contribution\ of \text{ testers} = \frac{SSt}{SSh} * 100$$

$$Contribu \quad ion\ of \text{ lines } x \text{ testers} = \frac{SSlxt}{SSh} * 100$$

3.6 Estimation of heterosis

Heterosis in F1's was calculated as the difference of F1 hybrid performance from average heterosis, Standard heterosis and better parent as per formula given by Falconer (1996).

I. Mid parent heterosis (%) = $\frac{F1 - Mid\ parent}{Mid\ parent}$ x 100

II. Better parent heterosis (%) = $\frac{F1 - Better\ parent}{Better\ parent}$ x 100

III. Standard heterosis (%) = $\frac{F1 - Standard\ check}{Standard\ check}$ x 100

Where F1 is the estimated mean performance of the hybrid, MP, is the average of the estimated performance of the two inbred parents, and BP is the estimated mean values for the better performing inbred parent and SC is the mean value of standard check. The significance of the different types of heterosis was tested by using 't'test as suggested by Wynne *et al*., (1970). The standard error for testing the significance of heterosis was as follows:-

The standard error of the difference for heterosis over mid-parent (MP):-

$$\text{SE (m) for MP} = \pm\sqrt{(3Me/2r)}$$

The standard error of the difference for heterosis over better parent (BP) and standard check (SH)

$$\text{SE (m) for BP} = \pm\sqrt{(2Me/r)}$$

SE (d) for MP = SE (m) for MP x t at error degree of freedom

SE (d) for BP = SE (m) for BP x t at error degree of freedom

SE (d) for SC = SE (m) for SC x t at error degrees of freedom. Test of significance for heterosis was done by comparing (F1-MP) with SE (d) for mid parent, (F1 -BP) with SE (d) for better parent and (F1-SC) with SE (d) for standard heterosis. In this case, SE (m) is standard error of the mean, SE (d) is standard error of the difference, Me is error mean square and r is the number of replications.

3.7 Heterotic Grouping of Sorghum Inbred Lines

Heterotic grouping methods were used to assign female parents into different heterotic groups based on specific combining ability effects (SCA) for grain yield (Fan *et al*., 2009) and general combining ability of multiple traits (HGCAMT) method proposed by Badu-Apraku *et a*l. (2013).

4 RESULTS AND DISCUSSION

4.1 Analyses of Variance (ANOVA)

The mean squares due to the different sources of variations were estimated as per standard the procedure of analyses of alpha-lattice design for individual location and combined over the two locations. The mean squares due to genotypes exhibited significantly high ($P < 0.01$) for all the studied traits at both specific and combined over locations. Specifically, the mean squares due to genotypes revealed the existence of highly significant difference ($P < 0.01$) for days to 50% flowering, plant height (cm), panicle length (cm), panicle exertion (cm), panicle yield (g/plant), grain yield (kg/ha$^{)}$ and thousand seed weight (g) at both Mieso and Kobo (Appendix table 1). This implies the presence of sufficient variation to make selection among the tested genotypes.

The combined analysis of variance was done for all studied traits over locations and has showed significant variation for the majority of the traits measured (Table 6). The combined ANOVA revealed significantly high ($P < 0.01$) variation among tested genotypes for all studied traits, indicating the presence of considerable variation in the genetic materials and the variation resulted in all traits were due to genotypes rather than environmental effects. The mean squares due to hybrids were significantly high for days to flowering, plant height, panicle length, panicle exertion and thousand seed weight traits. Significant differences were also obtained for stay green and number of tillers traits which were driven due to the presence specific combining ability and heterosis. This indicates the possibility to identify superior hybrids for the concerned traits. Mean squares due to parents' *vs* hybrids were highly significant for all the traits except for number of tillers and panicle exertion. This provided evidence for further analysis of combining ability and heterosis.

The highly significant variation found due to hybrids *vs* check for days to flowering, plant height, days to maturity, stay green, panicle length and panicle width traits. This implies the possibility of estimation of standard heterosis between hybrids and check. The mean squares due to parents showed highly significant difference for days to flowering, plant height, stay green, panicle length, panicle width, panicle exertion, panicle yield, grain yield and thousand seed weight. This indicates the presence of further study for combining ability analysis in all highly significant traits while significant differences were also observed for days to maturity,

leaf area and numbers of tillers among parents. The mean squares due to inbred lines showed highly significant difference for days to flowering, plant height, stay green, panicle length, number of tillers, panicle exertion, panicle yield and thousand seed weight whereas highly significant difference was obtained in testers for plant height and leaf area. This clearly indicated the existence of genetic variation in inbred lines than testers for majority of the traits. The results from the analysis of variance due to parents *vs* check revealed highly significant variation for panicle length, panicle yield and grain yield while significant variation was obtained for days to maturity, number of tillers and leaf area.

The mean squares due to genotype x environmental interaction exhibited significantly high for days to flowering, plant height, days to maturity, stay green, panicle length, panicle width, leaf area, number of productive tiller, panicle exersion, panicle yield, grain yield and thousand seed weight. This implies the modification of genetic factors by environmental factors, and the role of genetic factors in determining the performance of genotypes in different environments. Genotype x environmental interaction is said to exist when genotype performance differs over environments. The performances of genotype vary greatly across environment because of the effect of environment on trait expression. Selection of superior genotypes in target environments is an important objective of plant breeding programs. In order to identify superior genotypes across multiple environments, plant breeders conduct trials across locations and years, especially during the final stages of cultivar development.

Table 7: Combined analysis of variance of sorghum genotypes for yield and yield related traits over location at Mieso and Kobo in 2018/2019

SV	DF	DTF	PHT	DTM	SG	PL	PW	LA	TL	PE	PY	GY	TSW
Location	1	1080.21**	14359.70**	1494.05**	63.14**	117.66**	308.34**	439598.44**	4864.38**	388.87**	183467.16**	858491.96**	7100.60**
Rep(L)	1	0.00	1955.70**	7.29	0.06	5.42	13.03**	16.35	233.35**	104.97**	9.24	5700.15**	0.86
Genotype	41	13.23**	7615.51**	13.10**	0.78**	27.08**	3.86**	5662.39**	36.13**	31.36**	2206.42**	5106.56**	60.41**
Hybrids	25	5.10**	4288.77**	7.41	0.64*	11.79**	1.62	2958.47	43.43*	19.85**	597.14	1264.76	41.95**
Parents	14	28.15**	10121.19**	8.88*	1.15**	19.44**	2.44**	4837.30*	42.53*	55.76**	884.64**	1678.98**	81.06**
Lines	12	8.12**	8724.51**	9.63	0.88**	19.27**	1.25	2606.25	63.09**	30.35**	778.78**	1390.63	76.62**
Testers	1	3.47	572.46**	0.47	0.24	2.28	0.34	18171.24**	29.93	0.16	58.80	318.85	13.37
Lines x Testers	12	2.22	162.71*	5.76	0.42	5.10	2.10*	2042.97	25.95	11.17**	460.36	1217.71	9.65
Parent Vs Hybrid	1	45.55**	95086.83**	198.48**	2.34*	468.66**	109.99**	96749.62**	7.05	4.42	71559.23**	167591.62**	792.48**
Parent Vs Check	1	44.63*	4268.95	4.00	2.40	216.60**	0.06	17539.75*	47.20*	52.46**	2496.15**	12511.98**	13.41
Hybrid Vs Check	1	21.37**	27004.72**	42.38**	4.23**	64.44**	12.85**	1243.09	65.23	2.56	1188.72	285.21	27.50
Genotype * L	41	5.51**	332.80**	15.74**	0.51	3.80	1.094*	3919.83	40.81**	7.47	762.70**	1708.55**	13.25**
Parent * L	14	13.41**	350.14**	28.74**	1.08**	4.25	1.11	2549.44	53.76**	11.42	289.02	617.07*	10.96
Hybrid * L	25	1.86	349.75**	4.90	0.31	3.59	0.83	3586.11	38.13*	5.48	723.61*	1020.53	11.74**
Lines* L	12	2.45	618.29**	6.71	0.32	5.57	1.38	3651.38	49.81*	3.73	1186.09**	1474.88	18.23**
Testers * L	1	7.00	48.74	7.00	0.24	1.16	0.01	3681.66	13.44	0.06	134.33	608.61	10.15
Lines *Testers * L	12	0.84	106.29	2.92	0.30	1.82	0.34	3512.88	27.43	7.86	310.23	600.51	5.39
Hybrid Vs Check * L	1	2.82	486.500	41.410**	0.017	0.275	2.488	7869.63	33.34	7.14	2142.88*	8760.63**	16.14
Hybrid Vs Parent * L	1	11.97	448.11	198.48**	1.51	0.68	9.65**	26771.48**	24.70	2.94	13909.47**	41045.72**	124.94**
Parent Vs Check * L	1	7.52	228.54	7.00	0.26	0.07	0.34	1307.80	51.25*	11.15	74.81	826.52	0.21
Error	72	2.62	70.47	4.67	0.35	2.99	0.65	2812.38	20.47	5.31	352.03	869.54	6.02
CV (%)		2.29	4.43	1.95	22.15	6.13	9.85	16.84	24.14	28.33	22.12	21.75	9.37
LSD (5%)		2.28	11.83	3.04	0.83	2.44	1.14	74.75	6.37	3.24	26.44	1.31	3.45
R-square		0.91	0.98	0.89	0.83	0.87	0.92	0.81	0.86	0.85	0.92	0.94	0.96

**, **- significant at 5% and 1% level respectively, DTF = days to flowering, PHT = plant height, DTM = days to maturity, SG = stay green, PL = panicle length, PW = panicle width, LA = leaf area, TL = number of productive tiller, PE = panicle exertion PY = panicle yield, GY = grain yield, TSW = thousand seed weight, L = location CV = coefficient of variation, LSD = least significant difference.*

4.2 Mean Performance of Sorghum Genotypes for Yield and Yield Related Traits

4.3 Mean Performance of Sorghum Genotypes for Studied Traits

The superior sorghum genotypes were identified based on mean performance for different traits as indicated in (Table 7). Interestingly, genotypes listed as number 17 (6.32 t/ha), 8 (5.92 t/ha), 1 (5.88 t/ha), 26 (5.78 t/ha) and 6 (5.57 t/ha) were high yielder whereas genotypes listed as number 34 (2.05 t/ha), 31 (2.13 t/ha), 32 (2.25 t/ha), 28 (2.34 t/ha), 33 (2, 36 t/ha) were low yielder as compared to the other genotypes. Generally, among the tested genotypes, twenty four genotypes gave higher than the average yield (4.29 t/ha). These included almost the hybrids other than lines and testers. The values of average yield performance of the genotypes ranged from 2.05 t/ha to 6.32 t/ha. In addition to yield performance, considering growth and morphological parameters contributing for the yield performance as a selection criterion in the development of drought tolerance genotypes were suggested (Rosenow *et al*., 1983; Henzell *et al*., 1992).

Days to flowering and maturity are among the most important attributes that need to be considered in selecting genotypes for drought affected areas. In this study, the mean number of days to flowering ranged from 68 days in the early flowered genotype (35) to 77 days in the late flowered genotypes (31). Similarly, mean number of days to maturity ranged from 108 to 114 for the same group of genotypes. Both early and late maturing genotypes had the same grain fill duration, However, variation was detected for grain yield and related yield components among these genotypes, indicating that, the variation in the other attributes might be associated with factors other than duration of grain fill.

The top yielder genotypes (17) required 69 days to flower and 108 days to mature which was close to the average for genotypes, 70 days for flowering and 111 days for maturity. This indicates that, the yielding potential is not necessarily associated with crop phenology provided that genes for high yield potential are incorporated in the genotypes. The global successes in improving sorghum yield by deploying high yielding early maturing hybrids also supports this idea. Meanwhile, delayed flowering for genotypes encountered severe drought condition was reported (Angus and Moncus, 1977), which would have considerable effect on the productivity of the crop (Blum *et al*., 1989). Similarly, the actual mean values showed variation among genotypes for plant height and leaf area and these appeared to be under strong genetic control, although environment could have marked effect.

Mean plant height ranged from 107.50 cm to 271 cm, and leaf area ranged from (220.36 cm^2 to 405.63 cm^2). Breeding for shorter plant height was one of the major goals of the sorghum breeding program for dry lowland areas where drought adversely affects the plants which had prolonged vegetative growth and to make commercial genotypes fit to mechanical harvesting. Drought resistance is a complex trait, expression of which depends on action and interaction of different morphological traits (earliness and reduced leaf area).

Among the various drought resistance related traits, leaf area is very relevant by narrowing the leaf length and leaf width when the drought becomes severe in order to limit water loss. Generally, genotypes that were best performing in terms of several traits, i.e. high yield, early flowering, early maturity, shorter plant height and narrow leaf at the same time are preferable than genotypes that vary with different traits for instance, high yielder but late maturity and *vice versa*.

Table 8: Top and bottom performing genotypes based on their mean performance for selected Traits at Mieso and Kobo in 2018/2019

Top 10 performing genotypes									
Genotypes	DTF	Genotypes	DTM	Genotypes	PTH	Genotypes	GY	Genotypes	LA
35	67.75^{m}	26	107.75^{j}	34	107.50^{t}	17	6.32^{a}	31	220.36^{l}
29	67.75^{m}	17	107.75^{j}	28	113.40^{ts}	8	5.92^{ba}	33	242.19^{lk}
42	68.00^{ml}	2	108.00^{ji}	29	119.70^{rs}	1	5.88^{ba}	34	258.48^{jlk}
39	68.00^{ml}	4	108.50^{jhi}	33	119.70^{rs}	26	5.78^{bac}	37	260.07^{jlik}
28	68.50^{mlk}	1	108.50^{jhi}	42	125.50^{rq}	6	5.57^{bac}	32	263.75^{jlihk}
26	68.75^{mljk}	16	108.75^{jhig}	27	131.30^{rq}	22	5.51^{bdac}	27	265.36^{jlihk}
17	69.00^{imljk}	35	109.00^{jhigf}	32	132.90^{q}	9	5.37^{ebdac}	36	266.59^{jlihkg}
16	69.00^{imljk}	22	109.00^{jhigf}	30	133.30^{q}	14	5.33^{ebdac}	30	268.89^{jlihkjf}
4	69.25^{imlhjk}	21	109.00^{jhigf}	39	133.60^{q}	20	5.25^{ebdacf}	28	279.45^{ejlihkg}
3	69.25^{imlhjk}	20	109.00^{jhigf}	41	137.10^{q}	24	5.14^{ebdacf}	24	289.11^{ejlidhkg}
Bottom 10 performing genotypes									
14	71.75^{fcebdg}	30	112.25^{ebdac}	11	237.90^{ef}	39	3.03^{kjmil}	15	343.22^{ebdacf}
37	72.00^{fcebd}	28	112.25^{ebdac}	12	243.50^{ef}	30	3.02^{kjmil}	26	345.14^{ebdac}
38	72.25^{cebd}	40	112.50^{bdac}	37	245.10^{ed}	36	3.00^{kjmil}	8	346.86^{ebdac}
32	72.25^{cebd}	41	112.75^{bac}	36	245.90^{ecd}	29	2.82^{kjml}	42	350.46^{ebdac}
18	72.25^{cebd}	42	113.00^{bac}	22	256.60^{bcd}	27	2.78^{kml}	16	351.73^{ebdac}
23	73.25^{cbd}	27	113.00^{bac}	24	257.70^{bc}	33	2.36^{ml}	1	353.84^{ebdac}
41	73.75^{bc}	33	113.50^{ba}	9	258.00^{b}	28	2.34^{ml}	13	355.22^{bdac}
27	73.75^{bc}	32	113.50^{ba}	25	259.10^{b}	32	2.25^{ml}	3	365.97^{bac}
40	74.00^{b}	23	113.50^{ba}	10	259.90^{ba}	31	2.13^{m}	5	3.78.56^{ba}
31	77.00^{a}	31	114.50^{a}	23	271.00^{a}	34	2.05^{m}	12	405.68^{a}
Mean	70.00		111.00		189.38		4.29		314.92
Maximum	77.00		114.50		271.00		6.32		405.68
Minimum	67.75		107.75		107.50		2.05		220.36
LSD (5%)	2.28		3.04		11.83		1.31		74.75
SD	1.62		2.16		8.39		0.93		53.03
R^2	0.91		0.89		0.98		0.94		0.81

4.3.1 Mean Performance of Parents, Hybrids and Check for Studied Traits

Hybrids gave the highest mean performance for grain yield trait in comparison to the parents and the check. This ensured the superiority of hybrids (39% to 80%) over open pollinated varieties for yield (Quinby, 1962). This also indicates the suitability of hybrids in moisture stress areas where other open pollinated varieties lacked the adaptive traits for diverse local environments. The mean grain yield for hybrids ranged from 3.98 t/ha to 6.32 t/ha. The highest yield was obtained from the hybrid cross of 4x14 (6.32 t/ha) followed by the hybrid combinations of 8x15 (5.92 t/ha), 1x15 (5.88 t/ha), 13x14 (5.78 t/ha) and 6x15 (5.57 t/ha). The mean value of hybrid is 5.01 t/ha, which is higher than the grand mean of the genotypes (4.29 t/ha), mean of lines (2.80 t/ha), mean of testers (3.84 t/ha), mean of check (4.47 t/ha). This implied that, the performances of the parents and the check was lower as compared to hybrids and heterosis breeding is effective to improve this trait.

The superiority of the hybrids over the check variety in grain yield indicates the potential positive economic advantage of hybrids in the diverse sorghum-growing environments. Hybrid (4 x14) stood first in grain yield and second in early maturity trait among all genotypes which are preferable in moisture stress areas. From the statistical point of view, the hybrids were significantly different from lines, testers and check at ($p<0.05$) level of significance for grain yield traits. There was statistically significant difference between hybrids and testers in terms of days to flowering and days to maturity, indicating earlier maturity of hybrids compared to testers and the significant difference was revealed between hybrids and check for days to maturity trait.

Table 9: Mean Comparison of genotypes, Parents, Hybrids and Check at Mieso and Kobo in 2018/2019)

Statistics	DTF	PHT	DTM	SG	PL	PW	LL	LW	LA	GY	TSW
Grand Mean	70.69	189.38	110.58	2.68	28.20	8.23	63.03	7.16	314.92	4.29	26.18
Max	77.00	271.00	114.5	3.5	33.45	10.1	70.08	8.50	405.68	6.32	34.33
Min	67.75	107.50	107.75	1.25	22.50	6.05	52.50	6.00	220.36	2.05	17.53
Mean of Hybrid	70.36	209.18	109.67	2.80	29.36	8.85	64.27	7.40	332.39	5.05	27.87
Max of Hybrid	73.02	269.58	112.86	3.58	32.65	9.86	68.60	8.50	405.68	6.32	34.26
Min of Hybrid	68.37	175.02	107.09	2.02	25.68	7.73	57.63	6.68	287.70	3.98	23.23
Mean of Line	71.08	160.42	111.87	2.54	25.65	6.95	59.87	6.61	275.45	2.80	22.13
Max of Line	77.00	245.90	114.50	3.50	29.50	7.60	66.00	7.33	333.62	3.94	27.53
Min of Line	67.75	107.50	109.00	1.25	22.50	6.05	52.50	6.00	220.36	2.05	17.53
Mean of Tester	73.88	151.60	112.63	2.62	27.13	8.65	63.95	7.38	325.15	3.84	30.99
Max of Tester	74.00	166.10	112.75	2.75	28.50	9.25	65.08	7.58	341.15	4.12	31.48
Min of Tester	73.75	137.10	112.50	2.50	25.75	8.05	62.83	7.17	309.14	3.55	30.50
Mean of Check	68.00	125.50	113.00	1.75	33.45	7.05	70.08	7.25	350.46	4.77	25.20
LSD (5%)	2.28	11.83	3.04	0.83	2.44	1.14	7.36	1.20	74.75	1.31	3.45
SD	1.62	8.39	2.16	0.59	1.73	0.81	5.22	0.85	53.03	9.32	2.45
CV (%)	2.29	4.43	1.95	22.15	6.13	9.85	8.28	11.93	16.84	21.75	9.37

4.4 Combining Ability Analyses

4.4.1 Combining Ability Analyses for Yield and Yield Related Traits

The GCA variance of parents and SCA variance of crosses for the different traits are the important basic criteria for selection and hybridization program. The significance of mean squares for line x testers provides a direct test of significance of dominance variance, σ^2D, while significance of σ^2A is provided by significance of lines and testers mean squares. The analysis of combining ability variance components was performed to determine precisely the importance of additive and dominance components in the inheritance of the traits under study. Combining ability analysis of variance over the two locations confirmed the presence of variation among the tested genotypes. The mean squares of general combining ability (GCA) and specific combining ability (SCA) estimates were analyzed for all the traits as indicated in (Table 9).

Significant lines and testers variance indicated substantial genetic variability for general combining ability among the lines and testers respectively for traits like days to flowering, plant height, stay green, panicle length, number of tillers, panicle exersion, panicle yield and thousand seed weight. But the highest contribution towards general combining ability for many of the traits was due to female parental lines. The significant mean squares due to parents also reflect the preponderance of additive gene variance which is important to improve the parents through selection breeding procedure. The mean squares due to lines x testers interaction revealed highly significant for panicle exertion and significant for plant height and panicle width, which indicated specific combining ability variances among the crosses. The non- additive gene variance was important to improve the concerned traits through heterosis breeding or hybridization breeding method.

The variation among the hybrids was further partitioned into genetic components attributable to general combining ability (GCA) and specific combining ability (SCA). Similarly, in earlier studies Xingming *et al*., (2001; Glover *et al*., (2005) and Kidanemariam Wagaw *et al*., (2018) recorded significant mean squares of GCA and SCA effects for yield and yield components in sorghum. The single degree of freedom of parents *vs* crosses indicated presence of average heterosis among the parents and hybrids for all traits except for number of tillers and panicle exersion.

The results clearly suggested considerable amount of average heterosis in the hybrids and this reflected the presence of adequate genetic variability in the genetic materials for the superiority of hybrids. Similar finding has been reported for average heterosis by comparing parent *vs* hybrid in single degree of freedom for fifty hybrids derived from ten female and five male sorghum lines (Kumar *et al.*, 2017). The variance due to environment x different source of variations like parents, lines, testers, hybrids and hybrid *vs* parent were found to be significant for the concerned traits of their respective interaction which indicates considerable amount of interaction between the different sources of variations and the environments.

Table 10: Combining ability analysis for yield and yield related traits in sorghum across locations at Mieso and Kobo in 2018/2019

SV	DF	DTF	PHT	DTM	SG	PL	PW	LA	TL	PE	PY	GY	TSW
Location	1	1080.21**	14359.70**	1494.05**	63.14**	117.66**	308.34**	439598.44**	4864.38**	388.87**	183467.16**	858491.93**	7100.60**
Rep(L)	1	0.00	1955.70**	7.29	0.06	5.42	13.03**	16.35	233.35**	104.97**	9.24	5700.15**	0.86
Parents	14	28.15**	10121.19**	8.88*	1.15**	19.44**	2.44**	4837.30*	42.53*	55.76**	884.64**	1678.97**	81.06**
Hybrids	25	5.10**	4288.77**	7.41	0.64*	11.79**	1.62	2958.47	43.43*	19.85**	597.14	1264.76	41.95**
Lines	12	8.12**	8724.51**	9.63	0.88**	19.27**	1.25	2606.25	63.09**	30.35**	778.78**	1390.63	76.62**
Testers	1	3.47	572.46**	0.47	0.24	2.28	0.34	18171.24**	29.93	0.16	58.80	318.85	13.37
Lines x Testers	12	2.22	162.71*	5.76	0.42	5.10	2.10*	2042.97	25.95	11.17**	460.36	1217.71	9.65
Parent Vs Hybrids	1	45.55**	95086.83**	198.48**	2.34*	468.66**	109.99**	96749.62**	7.05	4.42	71559.23**	167591.62**	792.48**
Parent * L	14	13.41**	350.14**	28.74**	1.08**	4.25	1.11	2549.44	53.76**	11.42	289.02	617.10*	10.96
Hybrid *L	25	1.86	349.75**	4.90	0.31	3.59	0.83	3586.11	38.13*	5.48	723.61*	1020.53	11.74**
Lines*L	12	2.45	618.29**	6.71	0.32	5.57	1.38	3651.38	49.81*	3.73	1186.09**	1474.88	18.23**
Testers *L	1	7.00	48.74	7.00	0.24	1.16	0.01	3681.66	13.44	0.06	134.33	608.61	10.15
Lines *Testers * L	12	0.84	106.29	2.92	0.30	1.82	0.34	3512.88	27.43	7.86	310.23	600.51	5.39
Hybrid v parent*L	1	11.97	448.11	198.48**	1.51	0.68	9.65**	26771.48**	24.70	2.94	13909.47**	41045.72**	124.94**
Error	72	2.62	70.47	4.67	0.35	2.99	0.65	2812.38	20.47	5.31	352.03	869.54	6.02
CV (%)		2.29	4.43	1.95	22.15	6.13	9.85	16.84	24.14	28.33	22.12	21.75	9.37
LSD (5%)		2.28	11.83	3.04	0.83	2.44	1.14	74.75	6.37	3.24	26.44	1314.4	3.45
R-square		0.91	0.98	0.89	0.83	0.87	0.92	0.81	0.86	0.85	0.92	0.94	0.96

**, **- significant at 5% and 1% level respectively, DTF=days to flowering, PHT=plant height, DTM=days to maturity, SG=stay green, PL=panicle length, PW=panicle width, LA=leaf area, TL=number of productive tiller, PE=panicle exersion PY=panicle yield, GY=grain yield, TSW=thousand seed weight, L=location, CV = coefficient of variation, LSD = least significant difference.*

4.4.2 Estimation of General Combining Ability (GCA) Effects of Parents

The primary criteria for selection of desirable parents are usually based on mean values and additive gene action (Nguyen *et al*., 1997). Girma *et al*., (2010) suggested that crossing two parents showing the highest general combining ability for a desirable trait may produce the best performing cross due to an increased frequency of favorable genes. Additive variance is associated with effective response to selection, which allows breeders to use small number of parental lines having the desired GCA for crossing (Valiolla, 2012). In this study, significant positive and negative GCA effects were observed for some traits (Table 10). This indicated the preponderance of additive gene effects for further improvements of significant traits through critical and intensive selection breeding method.

The GCA for the days to flowering was found to be significantly high for line 10 and significant difference was obtained in lines (3, 4, 5 and 13). This indicated the presence of additive genetic variance which controls the days to flowering trait. In areas where drought stress is a problem, negative GCA effects for days to flowering has positive effect through escaping terminal stress. Hence, the genotypes listed as number 3, 4 and 13 are suggested to be used for breeding for early maturity. The other rest lines and the two testers revealed non-significant for days to flowering of GCA analysis, which implied that either the non-additive gene controlled the trait or it is environmentally influenced. General combining ability of plant height varied significantly ($p<0.01$) for the parental lines. The GCA of all lines exhibited significantly high except for lines (5, 6 and 7) and the two testers were found non-significant for this trait. For the plant height, negative values of GCA are desirable under moisture stressed environments to hasten physiological maturity.

All parental lines showed significant negative GCA effects, except lines (5, 6 and 7) and are considered as good general combiners. For those with significant positive GCA effects of female parents will be selected when the biomass experimental research is needed unless the present study was conducted under moisture stressed areas, thus the focus on selecting short stature sorghum parents, which mature earlier and escape drought stresses and selection breeding method is effective to improve this trait. GCA analysis revealed non-significant difference among all the parental lines for days to maturity character except line 10 with maximum and significantly high GCA (2.44).

However, negative GCA values are desirable for days to maturity. Therefore, highest negative GCA effect (-1.55) was obtained in line 4 followed by line 2 (-1.18) to be considered, even if the values were found non-significant. GCA analysis due to stay green trait was found significantly high in line 2 and 7. This indicated, the additive gene is important for the selection of parental lines in moisture stressed areas. Highly significant of GCA was obtained for the parental lines (4, 10, 11, and 12) for panicle length, but positive GCA (2.29) analysis is desirable for panicle length. Hence, line 4 was identified as good general combiner for panicle length. This result implies the preponderance of additive gene action and the suggested breeding procedure would be population improvement to improve panicle length. The same results were also reported by Tadesse *et al*., (2008).

Neither additive nor non-additive effects were statistically significant for leaf area, panicle width and number of tillers in the analysis of variance, possibly because they were largely influenced by the environment. For leaf length, the GCA analysis of line 1 and line 11 were found to be significant, whereas the rest lines and testers showed non-significant effects. The highest negative GCA is desirable for leaf length. Therefore, the highest negative GCA was obtained in line 11(-5.81), which implies small leaf length that can limit the water loss during severe moisture stresses. The result of GCA analysis was significantly high in lines (3, 6, 9, and 10) and significant in lines (2. 7, 13, 14 and 15) for panicle exersion. This implied predominance of additive gene for the improvement of the trait. Excellent exsertion is one of important trait associated with drought tolerance in sorghum which, implies that, the higher exserted parental lines withstand moisture stress environments.

The results strongly agreed with the previous work of Kenga *et al*., (2004), Tadesse *et al*., (2008). All the parents were found to be non-significant for grain yield and panicle yield traits, which implied these traits, were governed either by non-additive gene or environmental effects. Thus, the breeding methodologies, which can be applied for the improvement of parental lines could be heterosis breeding since the environment x parental interaction was found non-significant. GCA analysis showed highly significant for thousand seed weight in parental line (6, 10, 12), while significance difference was obtained for parental line (5, 7, 9, 11), although positive GCA is preferable for thousand seed weight. Hence, lines (9, 10, 11, 12) were identified as good general combiner and this trait was governed by additive gene action. The same result was also reported by Tadesse *et al*. (2008).

Table 11: General combining ability (GCA) effect of parents for yield and yield related traits in sorghum over locations at Mieso and Kobo in 2018/2019

Traits	DTF	PH	DM	SG	PL	PW	LL	LW	LA	TL	PE	PY	GY	TSW
Lines														
1	0.51ns	-22.08**	0.07ns	-0.17ns	0.89ns	-0.07ns	4.06*	-0.15ns	10.64ns	-1.88ns	-1.33ns	0.83ns	562.5ns	0.44ns
2	-0.60ns	-27.48**	-1.18ns	0.57**	0.54ns	-0.52ns	0.76ns	-0.03ns	2.07ns	-3.25ns	-1.53*	-3.34ns	-165.0ns	-1.47ns
3	-1.23*	-30.93**	-0.80ns	0.32ns	-0.01ns	-0.75ns	1.10ns	0.30ns	26.35ns	-3.88ns	1.81**	-6.59ns	-216.5ns	-2.27ns
4	-1.23*	-28.83**	-1.55ns	-0.42*	2.29**	0.05ns	0.60ns	-0.53ns	-22.62ns	-2.88ns	-0.98ns	3.75ns	492.5ns	1.60ns
5	1.26*	-5.63ns	0.31ns	-0.17ns	0.91ns	0.09ns	1.39ns	0.21ns	16.54ns	2.36ns	-0.80ns	-11.49ns	-473.0ns	-3.09*
6	0.02ns	-12.38ns	0.81ns	-0.04ns	0.69ns	0.37ns	-0.47ns	0.21ns	5.85ns	2.49ns	4.24**	-17.49ns	277.5ns	-4.43**
7	-0.48ns	-16.33ns	-0.68ns	0.57**	1.41ns	-0.27ns	-1.73ns	-0.15ns	-17.99ns	0.99ns	-1.68*	-10.76ns	-14.5ns	-3.45*
8	0.02ns	-24.13**	0.31ns	0.07ns	0.49ns	-0.20ns	-2.14ns	0.09ns	-5.62ns	-1.63ns	-0.38ns	18.25ns	258.0ns	-1.29ns
9	-0.35ns	48.07**	-0.68ns	0.07ns	-0.16ns	0.47ns	-0.22ns	-0.03ns	-3.99ns	-2.75ns	2.46**	8.25ns	400.5ns	3.34*
10	2.02**	56.22**	2.44**	-0.29ns	-2.51**	0.64ns	-1.85ns	-0.32ns	-23.41ns	2.86ns	-2.40**	0.78ns	-681.0ns	4.01**
11	0.39ns	38.56**	0.81ns	-0.17ns	-2.63**	0.29ns	-5.81**	0.09ns	-25.43ns	4.86ns	-0.06ns	1.70ns	-480.5ns	3.34*
12	0.89ns	42.06**	0.94ns	-0.42ns	-2.35**	0.04ns	2.43ns	0.17ns	19.94ns	1.49ns	-0.88ns	10.30ns	-318.5ns	4.65**
13	-1.23*	-17.13**	-0.80ns	0.07ns	0.44ns	-0.15ns	1.89ns	0.13ns	17.68ns	1.24ns	1.56*	5.78ns	358.0ns	-1.35ns
SE (Lines)	0.53	8.04	0.87	0.19	0.80	0.39	1.88	0.31	20.52	2.39	0.65	11.69	412.527	1.45
Testers														
14	0.18ns	2.34ns	0.07ns	0.05ns	0.15ns	-0.06ns	-0.40ns	-0.25ns	-13.21ns	0.53ns	-0.10*	-0.75ns	55.34ns	-0.35ns
15	-0.18ns	2.34ns	0.07ns	-0.05ns	0.15ns	0.06ns	0.40ns	0.25ns	13.21ns	-0.53ns	0.10*	0.75ns	-55.34ns	0.35ns
SE(Testers)	0.25	0.77	0.25	0.04	0.11	0.01	0.51	0.05	5.94	0.35	0.02	1.13	76.49	0.31

**, ** - significant at 5% and 1% level respectively, DTF = days to flowering, PHT = plant height, DTM = days to maturity, SG = stay green PY = panicle yield, GY = grain yield, TSW = thousand seed weight, PL = panicle length, PW = panicle width, LL = leaf length, LW = leaf width, LA = leaf area, TL=number of productive tiller, PE = panicle exersion, SE = standard error.*

4.4.3 Estimation of Specific Combining Ability (SCA) Effects of Hybrids

The specific combining ability value of any cross is useful in predicting the performance of the better parents. The result of SCA effects of crosses across the two environments for the different traits is presented in (Table 11). The usefulness of a particular cross in the exploitation of heterosis is judged by specific combining ability effects. The result for SCA estimates detected both negative and positive SCA values for the lines crossed with the two testers with equal SCA values in magnitude and opposite in direction, but varied among the traits under study. This may be due to the two testers, which had equal combining ability in magnitude, but opposite in direction and the possible explanation is that both testers used in the hybrid may have the same gene controlling effect on the traits.

Similar result was reported in case of sorghum using 35 male line and two female lines as of the SCA effects was equal in magnitude but opposite in sign (Kidanemariam Wagaw *et al*., 2018) and in the case of maize using 16 female lines and 2 male lines (Ejigu *et al.*, 2017). Hybrids evaluated in this study revealed considerable variation in specific combining ability (SCA) effects for the traits studied. It was observed that some crosses involved good general combined parents which can produced hybrids, with poor specific combining ability for a given trait example yield. This indicated that, parents with high GCA effects might not always give hybrids with high SCA effects.

The possible explanation is that both testers used in the hybrid may have the same gene controlling effect to the trait(s) studied and hybrids were not able to take advantage of any additive gene action. Regarding days to flowering only two hybrid combinations were highly significant at ($p<0.01$), while four hybrids were significant at ($p<0.05$) probability level. For days to flowering, negative values of SCA is desirable. But, among the significant hybrids for SCA effects, only three (1 x 15, 8 x 14 and 10 x 15) hybrids showed significant negative *SCA* effects for earliness and the rest were positive combiner for this trait. Some female lines manifested significant negative GCA for this trait. Therefore, days to flowering was controlled by both additive and non-additive gene action and it is possible to look for both selection and heterosis breeding to improve the genetic materials for this trait. In conclusion, both additive and dominance variance are important under drought stress. Therefore, both selection and hybridization would be effective for improving drought tolerance under drought stress conditions. Out of the 26 hybrids, only two hybrids (11x14, 11x15) showed significant

SCA effect for plant height. For plant height, negative values of SCA are desirable. However, only one hybrid (11x15) showed significant negative *SCA* effects for dwarfness. As indicated in the Table 11 of the general combining ability, the combining ability effect was due to additive genetic effects. This implies that, GCA effects were more important than specific combining ability. Therefore, selection is the most effective breeding procedure to improve plant height. Girma *et al*., (2010) reported similar result for plant height. About eight hybrids revealed significance for days to maturity. However, negative SCA values are desirable for this trait. But only four hybrids showed significant negative SCA (1x15, 6x15, 10x15, 13x15) effects for earliness. SCA effects had a slightly higher influence than GCA as observed from both tables of GCA and SCA, and heterosis breeding is effective to improve days to maturity.

The estimates of SCA for stay green were found non-significant ($P \leq 0.05$) for all crosses. Hence, this trait was controlled by additive gene action, GCA effects had higher influence than SCA as observed from the table of GCA and selection is effective population improvement for stay green trait. In conclusion, additive variance is important under drought stress. Therefore selection would be effective for improving drought tolerance under drought stress conditions. SCA analysis of showed high significant in four hybrids, whereas it was significant in four hybrids for panicle length. But only four hybrids had positive desirable SCA for panicle length and these hybrids were identified as good specific combiners. SCA analysis revealed the panicle width was totally controlled by non-additive gene effects, which implied that, the breeding procedure would be heterosis breeding to improve this trait.

SCA analysis of some hybrids was found highly significant for thousand seed weight and panicle exersion. However, the present study revealed the preponderance of additive gene action rather than non-additive gene action, which implied the GCA, was more important as compared to SCA. Similar results were reported for thousand seed weight by Girma *et al*., (2010). None of the crosses had significant SCA effects for leaf area and number of tillers. The environmental effects could have played a major role on leaf area and numbers of tillers, as neither the additive nor the non-additive effects were significant. The SCA for grain yield was higher than that of GCA, because grain yield is a complex trait which results from the contribution of many grain yield components each adding varying levels of genetic effects (Umakanth *et al*., 2002).

This study revealed highest and positive significant *SCA* for yield in hybrid (4x14) and followed by some other cross combinations like 8x15 and 11x14 as presented in Table 11. It is evident that cross combinations, which expressed high SCA effects for grain yield, have invariable positive SCA effects for one or more yield related traits. Secondly to get best specific combination for yield, it would be important to give due attention to yield related traits. Grafius (1959) has already suggested that there may not be separate gene(s) for yield and yield related being end product of multiple gene interactions among various yield components.

Table 12: Specific Combining Ability (SCA) effects for line x tester interaction in sorghum across locations at Mieso and Kobo in 2018/2019

Line	Tester	DTF	PHT	DMT	SG	PL	PW	LL	LW	LA	TL	PE	PY	GY	TSW
1	14	0.69*	-1.09ns	1.18*	0.32ns	-1.24**	-0.79**	0.48ns	0.003ns	2.52ns	0.21ns	-1.20ns	-5.49ns	-331.34ns	-2.03**
1	15	-0.69*	1.096ns	-1.18*	-0.32ns	1.24**	0.79**	-0.48ns	-0.003ns	-2.52ns	-0.21ns	1.20ns	5.49ns	331.34ns	2.03**
2	14	0.31ns	-4.29ns	0.43ns	-0.17ns	1.01*	0.20ns	-0.38ns	0.544ns	21.86ns	-2.66ns	0.19ns	-8.67ns	40.15ns	-0.49ns
2	15	-0.31ns	4.29ns	-0.43ns	0.17ns	-1.01*	-0.20ns	0.38ns	-0.544ns	-21.86ns	2.66ns	-0.19ns	8.67ns	-40.15ns	0.49ns
3	14	-0.30ns	-5.84ns	-0.19ns	0.33ns	-0.05ns	0.58**	-0.55ns	0.212ns	6.09ns	-0.78ns	-2.70**	5.27ns	5.65ns	1.83*
3	15	0.30ns	5.84ns	0.19ns	-0.33ns	0.05ns	-0.58**	0.55ns	-0.212ns	-6.09ns	0.78ns	2.70**	-5.27ns	-5.65ns	-1.83*
4	14	-0.31ns	1.55ns	-0.44ns	-0.17ns	0.65ns	0.78**	-0.05ns	0.210ns	6.83ns	-0.28ns	0.54ns	15.97**	727.65**	1.21ns
4	15	0.31ns	-1.55ns	0.44ns	0.17ns	-0.65ns	-0.78**	0.05ns	-0.210ns	-6.83ns	0.28ns	-0.54ns	-15.97**	-727.65**	-1.21ns
5	14	0.44ns	-5.44ns	-0.06ns	0.08ns	0.23ns	-0.06ns	-2.00ns	-0.121ns	16.29ns	-1.28ns	0.92ns	-9.42ns	-428.84ns	-1.14ns
5	15	-0.44ns	5.44ns	0.06ns	-0.08ns	-0.23ns	0.06ns	2.00ns	0.121ns	-16.29ns	1.28ns	-0.92ns	9.42ns	428.84ns	1.141ns
6	14	0.44ns	-3.49ns	1.18*	-0.29ns	-0.14ns	-0.59**	0.53ns	-0.128ns	10.60ns	-0.66ns	-1.02ns	0.37ns	-310.34ns	0.17ns
6	15	-0.44ns	3.49ns	-1.18*	0.29ns	0.14ns	0.59**	-0.53ns	-0.128ns	-10.60ns	0.66ns	1.02ns	-0.37ns	310.34ns	-0.17ns
7	14	0.19ns	5.65ns	-0.06ns	0.07ns	-0.37ns	-0.34ns	0.11ns	-0.080ns	-2.74ns	-3.16ns	0.74ns	-5.84ns	163.65ns	0.19ns
7	15	-0.19ns	-5.65ns	0.06ns	-0.07ns	0.37ns	0.34ns	-0.11ns	0.080ns	2.74ns	3.16ns	-0.74ns	5.84ns	-163.65ns	-0.19ns
8	14	-1.06**	-2.04ns	-1.06ns	0.08ns	-1.59**	-0.41*	-1.21ns	-0.079ns	-6.77ns	1.96ns	0.64ns	-6.57ns	-675.84**	0.58ns
8	15	1.06**	2.04ns	1.06ns	-0.08ns	1.59**	0.41*	1.21ns	0.079ns	6.77ns	-1.96ns	-0.64ns	6.57ns	675.84**	-0.58ns
9	14	-0.18ns	-3.04ns	-0.06ns	-0.17ns	0.80ns	0.55**	4.11**	0.044ns	18.84ns	0.83ns	-0.40ns	3.67ns	15.65ns	0.72ns
9	15	0.18ns	3.04ns	0.06ns	0.17ns	-0.80ns	-0.55**	-4.11**	-0.044ns	-18.84ns	-0.83ns	0.40ns	-3.67ns	-15.65ns	-0.72ns
10	14	0.69*	3.20ns	1.30*	-0.29ns	0.90*	0.63**	-1.34ns	0.086ns	-4.37ns	0.21ns	-0.32ns	0.75ns	-163.84ns	0.92ns
10	15	-0.69*	-3.20ns	-1.30*	0.29ns	-0.90*	-0.63**	1.34ns	-0.086ns	4.37ns	-0.21ns	0.32ns	-0.75ns	163.84ns	-0.92ns
11	14	-0.43ns	7.55*	-1.06ns	0.07ns	0.22ns	-0.06ns	-0.55ns	-0.079ns	-4.73ns	2.21ns	1.32ns	10.07ns	527.65*	-0.20ns
11	15	0.43ns	-7.55*	1.06ns	-0.07ns	-0.22ns	0.06ns	0.55ns	0.079ns	4.73ns	-2.21ns	-1.32ns	-10.07ns	-527.65*	0.20ns
12	14	0.06ns	5.45ns	0.05ns	0.32ns	-0.59ns	-0.41*	-1.55ns	-0.663*	-40.01ns	3.08ns	0.24ns	-3.22ns	104.65ns	-1.44ns
12	15	-0.06ns	-5.45ns	-0.05ns	-0.32ns	0.59ns	0.41*	1.55ns	0.663*	40.01ns	-3.08ns	-0.24ns	3.22ns	-104.65ns	1.44ns
13	14	-0.55ns	1.85ns	-1.19*	-0.17ns	0.20ns	-0.06ns	2.40ns	-0.204ns	8.17ns	0.33ns	1.04ns	3.10ns	325.15ns	-0.32ns
13	15	0.55ns	-1.85ns	1.19*	-0.17ns	-0.20ns	0.06ns	-2.40ns	0.204ns	-8.17ns	-0.33ns	-1.04ns	-3.10ns	-325.15ns	0.32ns
SE(ij)		0.31	3.59	0.58	0.18	0.45	0.19	1.44	0.336	20.13	1.77	0.95	5.98	263.22	0.78

**, **- significant at 5% and 1% level respectively, DTF = days to flowering, PHT = plant height, DMT = days to maturity, SG = stay green, PL = panicle length, PW = panicle width, LL = leaf length, LW = leaf width, LA = leaf area, TL=number of productive tiller, PE = panicle exersion, PY = panicle yield, GY = grain yield, TSW = thousand seed weight, SE = standard error*

4.4.4 Estimation of Combining Ability Effects and Genetic Component of Variances

The combining ability analysis provides information about the gene action involved in the expression of different traits and thus helps in deciding the breeding procedure to be followed for the genetic improvement of traits. The present study indicated that, the magnitudes of specific combining ability (sca) variances were higher than the general combining ability (gca) variances for all the characters except for plant height trait. This indicates that, the provides information that greater amount of genetic variability was due to specific combining ability effects, which implies non-additive type of gene action being involved for these traits. The traits are desirable for heterosis breeding and can be exploited in hybrid production.

The variance of lines was higher than testers for all studied traits, except leaf width and leaf area for which testers were higher than lines. The total variance components of parents contributed by the lines for cross (hybrid) variances. That means of the total hybrid (line * tester interaction) variances were due to line's variation. So, selection for line parents for this hybrid production was successful and the next parental selection for hybrid sorghum grain production should be emphasized for parental variances which can contribute towards the hybrid production. The estimates of variance due to combining ability revealed that σ^2gca was found lower than σ^2sca for all the traits, except days to flowering, plant height, leaf length, leaf width and leaf area.

However, the ratio of σ^2gca / σ^2sca revealed the preponderance of dominance gene action for all traits except for plant height, where additive gene action was more with σ^2gca /σ^2sca ratio being more than unity. Generally, the ratio of σ^2gca/σ^2sca was less than unity for almost all the considered traits except plant height, indicating preponderance of non- additive gene action (dominance and epistasis). Similar results were reported for forage sorghum hybrids (Dehinwal *et al.*, 2017, Kidanemariam Wagaw *et al*., 2018). The magnitude of GCA/SCA variance ratio for plant height was specifically sizable, indicating the predominance of additive gene action. However, the specific effects were also highly significant for some lines, suggesting the involvement of non-additive effects in controlling this trait. Even though, for days to 50 % flowering, the preponderance of dominance gene effect was found higher than the additive gene effects and this indicates that hybrids are earlier than their parental effect.

Similar investigation was done for 7 lines and 8 testers of 28 forage hybrids in relation to days to 50 % flowering (Mohammed, 2009). So, for all traits that sca variances were found higher, there were preponderance of non-additive gene action and heterosis breeding will be effective. In contrast, for traits such like plant height gca variance is higher than sca variances, which indicates additive type of gene action being involved for this trait. This trait can be improved by simple selection methods in early generations. The degree of dominance (σ^2D/σ^2A) was found greater than unity for all the traits, except days to flowering, plant height, leaf length, leaf width and leaf area indicating the over dominance behavior of interacting alleles. Since the dominance gene action is involved for inheritance of grain yield, heterosis breeding would be most effective approach to improve the trait.

The significance of mean square for line x tester provides a direct test of significance of dominance variance, while significance of σ^2A is provided by significance of lines and testers mean squares (Nduwumuremyi *et al.*, 2013). The results revealed that for plant height, stay green score, and other few traits. The additive genetic effects were more pronounced than non-additive effects, and the general combining ability variance was higher than specific combining ability. This result suggesting that the inheritance of these traits was mainly controlled by additive genes and selection of parents should be more important in breeding procedure.

Table 13: Estimate of Variance components of combining ability and gene effects across location at Mieso and Kobo in 2018/2019

Variance components (σ^2)	DTF	PH	DM	SG	PL	PW	LL	LW	LA	PE	TSW	GY
Line Variance (σ^2l)	8.42	8142.56	9.53	0.86	18.09	1.22	50.08	0.46	2605.53	30.35	70.57	1408.81
Tester Variance (σ^2t)	2.01	537.66	0.06	0.16	2.88	0.07	14.87	6.63	17861.24	0.16	11.42	205.16
Line x Tester Variance (σ^2l∗ t)	2.23	155.42	6.37	0.42	4.89	1.05	22.41	0.60	2019.28	11.17	9.21	1235.70
Vgca ($\sigma^2 gca$)	0.09	118.32	0.03	0.01	0.19	0.001	0.39	0.01	44.46	0.26	0.91	0.21
Vsca ($\sigma^2 sca$)	-0.01	42.48	0.85	0.04	0.95	0.20	-2.43	-0.07	-396.55	2.93	1.60	183.08
Unity variance ($\sigma^2 gca/\sigma^2 sca$)	-7.06	2.78	0.04	-0.16	0.20	0.001	-0.16	-0.17	-0.11	0.09	0.56	0.01
Additive variance ($\sigma^2 A$)	0.36	473.29	0.13	0.02	0.75	0.001	1.56	0.05	177.85	1.03	3.62	0.86
Dominance variance ($\sigma^2 D$)	-0.05	169.90	3.39	0.14	3.80	0.80	-9.70	-0.26	-1586.19	5.86	6.38	732.32
Degree of dominance (σ^2D/σ^2A)	-0.14	0.35	26.33	6.13	5.01	745.37	-6.22	-5.74	-8.91	5.70	1.75	851.53
Proportional contribution to total variances												
Lines	77.03	95.43	58.75	68.47	73.12	51.97	67.91	28.77	42.63	73.37	89.39	52.80
Tester	1.53	2.52	0.02	1.08	0.97	0.25	1.68	34.27	24.35	0.03	1.20	0.64
Line x Tester	20.45	1.82	39.25	33.57	19.76	44.76	30.38	36.91	33.04	27.00	11.66	46.31

σ^2 = variance, $\sigma^2 l$ = lines variance, $\sigma^2 t$ = testers variance, $\sigma^2 l * t$ = line x tester variance, $\sigma^2 gca$ = general combining ability variance, $\sigma^2 sca$ = specific combining ability variance, $\sigma^2 gca/\sigma^2 sca$ = ratio of general combining ability variance to specific combining ability variance, $\sigma^2 A$ = additive variance, $\sigma^2 D$ = dominance variance, $\sigma^2 D/\sigma^2 A$ = ratio of dominance variance to additive variance.

The proportional contributions of lines (female), testers (male) and their interactions (crosses) to the total variance for different traits (Table 12) revealed that females lines contributed higher compared to male lines under drought stress conditions in all studied traits. The results showed that, the female parents play the most important role under drought stress conditions. Female parents should be used in further programs to improve drought stress tolerance and it also suggested that more attention should be given to the selection of female parents for the hybrid development of sorghum. Perhaps these results are due to expression of cytoplasmic genes. Studies have shown that proportional contributions of line, tester and line × tester change for different traits (Sarker *et al.,* 2002; Rashid *et al.,* 2007).

The highest contribution was recorded for plant height followed by thousand seed weight, days to flowering, panicle exersion, panicle length, stay green, leaf length, days to maturity, grain yield and panicle yield by female parents. Line x tester interaction showed the highest contribution to grain yield, panicle width and days to maturity. The higher contribution of female parents than the line x tester interaction (crosses). This implies the higher estimates of variances due to additive gene action among the female parents. In contrast, the contribution of interactions of line x tester was higher than testers for all traits, indicating that, the higher estimates of non-additive variances were revealed for the studied traits. In general, the proportional contribution of lines to the total variance was greater than both those of testers and line x testers for all the traits under study. This implies that, the sorghum hybrid breeding program should be focused on the selection of lines.

4.5 Magnitude of Heterosis for the Combined Analysis over Locations

The existence of heterosis demonstrates the presence of degree of genetic variation between parents and some degree of dominance. The heterosis over mid parent (Relative heterosis), over better parent (heterobeltiosis) and over standard check (standard heterosis/useful heterosis) were estimated for all the traits studied. Among the parents, testers were greater than inbred line in mean values whereas inbred lines showed the presence of genetic diversity than testers.

All of the hybrids manifested significant positive heterosis over mid parents for grain yield, while 25 and 18 hybrids recorded significant positive heterosis over the better parent and the standard check for grain yield respectively. Similar work was reported by Kumar., (2013). This result demonstrated the superiority of hybrids over their respective parents and the commercial hybrid variety under cultivation. Eleven and three hybrids showed significant negative heterosis over mid parents and better parents for days to flowering respectively. Since negative heterosis is desirable for days to flowering, those hybrids with negative heterosis were selected to enhance earliness and escape the erratic and terminal drought which affects the hybrid production under moisture stress areas.

Sixteen, seven and twenty hybrids manifested significant positive heterosis for thousand seed weight over mid parents, better parents and standard check respectively. This indicates that, the large seeds in weight were vigorous and good in germination as compared to those seeds with small in weight. As far as heterotic performance for stay green is concerned, seventeen, twenty two and twenty six hybrids exhibited significant and positive heterosis in desirable direction over mid parents, better parents and standard hybrid check variety respectively. This result implied that, hybrids exhibited superiority in terms tolerance or resistance, where drought adversely affects crop growth and production over their parents and standard check. Most of the hybrids exhibited significantly high heterosis over their parents and standard check for panicle exersion trait, which is associated with drought tolerance in sorghum.

Table 14: Mean, range and number of hybrids with positive effect for mid-parent, high parent and standard heterosis (%) at Mieso and Kobo in 2018/2019

	MPH (%)				BPH (%)				SH (%)			
Traits	Mean	Max	Min	#of Hybrids with Positive effects	Mean	Max	Min	#of Hybrids with Positive effects	Mean	Max	Min	#of Hybrids with Positive effects
DTF*	-2.91	1.07	-6.06	25	-0.61	3.69	-4.99	14	3.47	7.38	0.54	0
PHT*	34.74	50.95	22.48	0	51.83	77.70	32.66	0	66.37	114.80	39.46	0
DTM*	-2.29	1.68	-4.54	25	-1.69	3.07	-4.44	24	-2.95	-0.12	-5.23	26
GY	53.27	112.41	6.26	26	31.70	68.71	-0.23	25	5.81	30.71	-16.4	18
TSW	4.78	23.95	-7.48	16	-10.02	12.33	-26.21	7	10.60	35.95	-7.82	20
PL	11.43	26.04	-1.70	25	10.00	100.39	-7.05	21	-12.22	-2.39	-23.23	0
PW	13.79	36.88	1.58	26	2.87	19.88	-12.43	15	25.58	39.86	9.65	26
LL*	4.33	16.01	-5.14	20	8.08	29.90	-1.77	23	-8.29	-2.11	-17.77	26
LW*	5.93	17.24	-5.18	22	12.58	31.58	-3.47	23	2.13	17.24	-7.86	13
LA*	10.82	34.99	0.01	0	22.39	71.99	3.32	0	-5.16	15.76	-17.91	5
LN	3.04	66.23	-10.50	16	8.37	66.86	-9.56	22	5.13	75.47	-11.29	17
TL*	26.38	119.45	-43.09	4	78.80	210.89	-39.64	2	-28.37	24.34	-65.66	24
SG	10.05	51.50	-23.05	17	23.45	142.40	-19.20	22	60.13	104.57	15.43	26
PE	45.98	152.56	-28.85	23	-8.17	40.17	-53.67	11	-9.40	47.50	-41.14	6

** Those traits which are preferable for the negative effect*

4.5.1 Estimation of Magnitude of Heterosis over Locations

Heterosis is the key determinant for hybrid production especially for traits governed by non-additive gene action. Heterosis over the mid parents, better parents and standard check of the hybrids among 13 inbred lines and two testers were summarized in (Table 14). There were genetic variations for levels of heterosis among the parental genotypes and hybrids. The magnitudes of heterosis varied from cross to cross and trait to trait. For a specific trait, considerable high heterotic effects were observed in certain crosses and low in others, which revealed that, the nature of gene action varied with the genetic makeup of parents. The results indicated those both positive and negative heterosis were observed for studied traits.

A negative heterosis estimate for days to flowering is desirable which means the crosses flowered earlier than the parents. Eleven crosses were better than the mid-parents while only three crosses surpassed the better- parents for days to flowering with the maximum heterosis of -6.06% for the cross 5x15 and -4.99% for cross 1x15 respectively. Thus, it appeared that the earliest tester parent (15) has contributed for earliness, in comparison of mid-parent and better parent heterosis. In general, the lowest value of negative heterosis was preferable than higher value of positive heterosis for days to flowering. Similar findings were reported by Bhardwaj *et al*., (2010), Gadekar *et al*., (2013) and Mishra *et al*., (2013).

The use of early maturing sorghum varieties are encouraged to overcome the drastic effect of drought in semi-arid tropics regions where either seasonal rainfall is short or its distribution is erratic. These varieties may not be necessarily superior to long maturing cultivars in terms of yield, but give more stable yield under water stress environments by escaping the terminal drought. The majority of the hybrids exhibited negative significantly high and negative significant heterosis for days to maturity over mid-parents, better parents and standard check. Similar results were reported by Bantilan *et al*., (2004). For the lowland areas, negative heterosis is desirable for plant height in order to shorten days to flowering and physiological maturity as well as to get lodging free hybrids. As indicated in (table 14) all hybrids exhibited positive and significantly high heterosis over their parents and standard check for plant height. As a result, none of the hybrids are preferable for this trait in moisture stress areas. For both stay green and panicle exertion traits, the development of superior hybrids are very critical to withstand the stress environments were drought is the limiting factor for sorghum production. From the present study, both stay green and panicle exsertion found highly significant for all

the crosses over the parents and standard check. For stay green, percentage heterosis ranged from-23.05 to 51.50%,-19.20 to 142.40%and 15.43 to 104.57% over mi-parent, better parent and standard check respectively. From the obtained results, hybrids have more tolerance to abiotic stress and resistance to premature leaf and stalk death induced by post-flowering drought (Rosenow and Clark, 1981). For panicle exsertion trait, -28.85 to 152.56%, -53.67 to 40.17% and -41.14 to 47.50% percentage heterosis were obtained over mi-parent, better parent and standard check respectively and well exserted hybrids are more preferred for drought tolerant trait. Panicle exsertion is an important attribute that often determine the quality of the grains. Poor panicle exsertion is disadvantageous because the leaf sheath provides favorable conditions for fungi and insects to develop at the base of the panicle and can extend to the whole panicle as also reported by (Dogget, (1988).

The mid-parents heterosis for grain yield ranged from 6.26 to 112.41 (%) across locations with mean value of 53.27%. The better parent heterosis for grain yield ranged from -0.23 to 68.71% with the mean value of 31.70 %, whereas the magnitude of heterosis of the hybrids over the standard check hybrid ranged from -16.49 to 30.71% with the mean value of 5.81 % over the environments. This result implied the highest yield advantages obtained in hybrids over the mid-parents, better parents and commercial hybrid variety (ESH-4). The findings of the present investigation are consistent with the earlier reports of Jain and Patel., (2013).

Among the 26 hybrids, 15 potential hybrids get greater than 50 % heterosis over mid-parents and 5 hybrids showed greater than 50% heterosis over better parents whereas 15 hybrids displayed positive and significantly high heterosis over the standard check (ESH-4) in desirable direction for grain yield. Among the genotypes, the maximum grain yield was obtained by the hybrid cross of 4 x 14 (6.32 t/ha) which recorded 30.71% yield advantage over standard check and promising candidate hybrid was obtained to be released after making critical evaluation of yield stability across location over years. Thus, out of twenty six hybrids, as mentioned in (Table 14), twenty six, twenty five and eighteen hybrids exhibited positive and significantly high heterosis for grain yield over mid-parents, better parents and standard check respectively. From this result, promising hybrids were identified over environments and these can be exploited for heterosis breeding programme. Similar results were reported by Borikar *et al.,* (2000) and Kenga *et al.,* (2004).

The mid-parent values ranged between -6.06 to 1.07% and the better parent heterosis was ranged from -26.4 to 12.33 %, whereas the standard heterosis estimate was between -7.82 to 35.55% for thousand seed weight. Sixteen crosses exhibited positive heterosis over the mid-parent and seven crosses performed the better than better parents. All hybrids manifested highly significant over standard heterosis and out of this, twenty hybrids showed positive significant heterosis for thousand seed weight. Since the seed weight is strongly influenced by post flowering drought (Sayed and Gadallah, 1983). The large seed size and weight are important indication of vigor and drought tolerance. All of the 26 studied crosses manifested significantly high heterosis over mid-parent, better parent and standard check for panicle length. Twenty five crosses showed positive in desirable direction and the highest mid-parent heterosis for this trait was 26.04% for the cross 8X15.

All crosses expressed highly significant better parent heterosis for panicle length and out of all the hybrids, twenty one crosses showed positively highly significant in desirable direction. The highest percent of better parent heterosis was 100.09%, which was manifested by cross 2X15 and all crosses negative in their magnitude over standard check which displayed the mean of crosses were lower than the mean of the standard check for panicle length. But some crosses revealed significantly high and significant in this trait. The present results agreed with the results reported by Giriraj and Goud (1984 and Rafiq *et al.,* (2003). All the crosses manifested highly significant heterosis over the mi-parents, better parents and standard check with the range of 1.58 to 36.88%, -12.43 to 19.88% and 9.65 to 39.86% of the panicle width respectively.

All of the hybrids showed positive and significantly high heterosis over both standard and mid-parent heterosis which has direct relation with yield and contributed to yield in advance level. However, some hybrids showed negative and highly significant heterosis were observed for better parent heterosis for panicle width, which indicates the mean performance of some hybrids were lower than the particular better parents. Hemlata and Vithal (2006) reported superiority of hybrids over mid and better parents for grain yield as associated with manifestations of heterotic effects in yield components including panicle length and panicle width. For number of leaves per plant, almost all of the crosses exhibited positive and negative significantly high heterosis over mid-parent, better parent and standard heterosis with the range from -10.50 to 66.23%, -9.56 to 66.86% and -11.29 to 75.47% respectively.

Significantly high negative heterosis is desirable for number of leaves per plant, which is critical in moisture stress areas by limiting number of leaves per plant. Similar results were obtained by different authors (Liang *et al*., 1973, Harer and Bapat, 1982). For leaf length, leaf width and leaf area traits, all crosses exhibited non-significant heterosis over the mid parent, better parent and standard check. All the hybrids appeared positive in their mean over the above mentioned heterosis but significantly high negative heterosis is desirable for leaf length, leaf width and leaf area to reduce transpiration effects in moisture stress areas. All of the hybrids revealed non-significant heterosis was over mid-parent and better parent for number of productive tillers, while the highest negative significant standard heterosis expressed in the crosses 2x14, 3x14, 3x15, 8x15, and 9x15.

In sorghum, productive tillers contribute to overall grain yield when water supply is not limiting but profuse tillering is undesirable in dry lowland agro-ecologies, because would it reduce water use efficiency as also reported by Madhusudhara and Patil, (2013). The detailed analysis for heterosis regarding of mid-parents, better parents and standard heterosis were presented in (Table 14). In general, lower value negative heterosis was preferable than higher value of positive heterosis for days to flowering, plant height, days to maturity, leaf length, leaf width, leaf area and number of tillers. In another way, higher value of positive heterosis was preferable for the rest of the traits such as grain yield, panicle yield, thousand seed weight, panicle length, panicle width, stay green and panicle exertion traits.

Table 15: Mid-parent heterosis, Heterobeltiosis and Standard heterosis for yield and yield component trait of sorghum across location at Mieso and Kobo in 2018/2019

	DTF			PHT			DTM			SG			GY		
Hybrid	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)
1X14	-2.55ns	-2.39ns	5.87ns	27.37ns	44.25ns	50.92ns	-1.11ns	-0.88ns	-1.33ns	8.36**	16.00**	70.29**	54.32**	29.13**	11.59**
2X14	-1.05ns	2.92ns	3.68ns	28.99ns	58.96ns	43.63ns	-2.72*	-2.83ns	-3.26*	31.20**	31.20**	87.43**	55.52**	21.83**	5.28**
3X14	-2.18ns	2.33ns	1.96ns	22.48ns	46.22ns	39.46ns	-2.43ns	-1.77ns	-3.51*	43.20**	43.20**	104.57**	43.56**	20.97**	4.54**
4X14	-5.54**	-3.72*	0.88ns	22.67ns	37.76ns	46.33ns	-4.54**	-4.44*	-5.07**	-20.36**	-10.33**	25.14**	74.65**	51.26**	30.71**
5X14	-4.83**	-2.79ns	5.66ns	26.68ns	33.76ns	59.24ns	-3.51*	-2.65ns	-3.08*	26.59**	53.71**	53.71**	31.49**	-0.23**	-13.78**
6X14	-3.00ns	-1.83ns	4.31ns	31.67ns	48.12ns	56.85ns	-0.79ns	-0.35ns	-0.79ns	-9.33**	-4.80**	36.00**	55.02**	19.74**	3.48**
7X14	-3.38*	-1.87ns	3.54ns	41.27ns	68.65ns	60.85ns	-3.14*	-2.71ns	-3.14*	25.82**	38.40**	97.71**	60.86**	26.55**	9.36**
8X14	-4.45**	-2.61ns	2.04ns	35.34ns	72.23ns	47.53ns	-2.71*	-2.17ns	-3.68*	-0.33**	19.60**	70.86**	51.13**	13.17**	-2.20**
9X14	-0.95ns	3.62ns	3.24ns	32.40ns	40.79ns	104.14ns	-1.60ns	-0.02ns	-3.56*	51.47**	127.20**	62.29**	46.94**	36.36**	17.84**
10X14	1.07ns	3.57ns	7.38ns	30.86ns	42.08ns	114.80ns	1.68ns	3.07ns	-0.12ns	-7.60**	-7.60**	32.00**	20.66**	4.30**	-9.86**
11X14	-3.75*	-2.42ns	3.32ns	24.92ns	54.62ns	104.65ns	-2.75*	-2.43ns	-3.50*	10.40**	10.40**	57.71**	27.38**	24.63**	7.70**
12X14	-2.09ns	-0.90ns	5.29ns	30.14ns	56.23ns	106.76ns	-1.16ns	-0.94ns	-1.81ns	10.00**	10.00**	57.14**	33.26**	18.50**	2.41**
13X14	-3.70*	0.54ns	0.54ns	30.19ns	46.03ns	47.32ns	-4.06**	-3.30*	-5.23**	15.37**	21.78**	56.57**	60.80**	39.57**	20.61**
1X15	-4.99**	-4.99*	3.04ns	37.77ns	40.81ns	47.39ns	-4.16**	-4.05*	-4.27**	-17.91**	-14.18**	34.86**	89.43**	68.71**	25.71**
2X15	-2.31ns	1.43ns	2.18ns	47.69ns	63.12ns	44.36ns	-3.47*	-3.25*	-3.89*	31.43**	38.00**	97.14**	61.20**	33.58**	-0.47**
3X15	-2.57ns	1.74ns	1.37ns	41.10ns	51.35ns	40.90ns	-2.95*	-2.18ns	-3.91*	3.24**	8.40**	54.86**	47.54**	32.40**	-1.35**
4X15	-4.55**	-2.88ns	1.76ns	30.79ns	32.66ns	64.69ns	-3.48*	-3.26*	-3.90*	-14.43**	-10.55**	40.57**	43.20**	32.39**	-1.35**
5X15	-6.06**	-3.99*	4.13ns	44.29ns	38.35ns	57.91ns	-3.30*	-2.55ns	-2.76ns	8.89**	40.00**	40.00**	71.48**	37.21**	2.24**
6X15	-4.10*	-3.10ns	2.96ns	46.80ns	49.12ns	47.64ns	-3.22*	-2.90ns	-3.12*	11.27**	11.27**	74.86**	94.85**	58.99**	18.47**
7X15	-4.33*	-3.00ns	2.35ns	44.31ns	54.80ns	47.10ns	-3.47*	-3.15*	-3.36*	13.04**	16.67**	85.71**	62.56**	35.33**	0.84**
8X15	-1.67ns	0.06ns	4.84ns	50.95ns	71.73ns	105.94ns	-0.93ns	-0.26ns	-1.81ns	-11.04**	1.09**	58.86**	112.41**	67.50**	24.81**
9X15	-0.71ns	3.69ns	3.31ns	44.39ns	54.94ns	107.24ns	-1.40ns	0.29ns	-3.26*	51.50**	142.40**	73.14**	53.05**	52.50**	13.63**
10X15	-0.51ns	1.79ns	5.53ns	35.81ns	50.01ns	89.63ns	-0.13ns	1.35ns	-1.79ns	7.05**	12.40**	60.57**	38.61**	27.90**	-4.70**
11X15	-2.52ns	-1.33ns	4.47ns	24.53ns	73.58ns	94.12ns	-0.62ns	-0.18ns	-1.28ns	-4.76**	0.01**	42.86**	6.26**	1.01**	-16.49**
12X15	-2.59ns	-1.58ns	4.57ns	31.76ns	77.70ns	48.81ns	-1.57ns	-1.24ns	-2.12ns	-23.05**	-19.20**	15.43**	35.79**	29.20**	-3.73**
13X15	-2.26ns	1.87ns	1.87ns	37.98ns	39.79ns	47.32ns	-2.06ns	-1.17ns	-3.14*	21.20**	34.67**	73.14**	52.99**	41.79**	5.65**

Continued... Table 14

	TSW			TL			PL			LN			PW		
Hybrid	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)
1X14	-3.72ns	-18.17*	2.22**	18.84ns	27.03ns	-36.48ns	6.23**	1.75**	-13.30ns	2.43**	2.79**	10.40**	1.89**	-12.43**	14.89**
2X14	-0.06*	-19.31ns	0.79**	-43.09ns	-39.64ns	-65.66*	14.20**	8.49**	-7.56**	-3.99**	3.24**	-3.64**	1.58**	-9.41**	18.87**
3X14	1.51*	-14.58*	6.71**	-35.27ns	-24.48ns	-57.03*	4.74**	2.81**	-12.41ns	-7.85**	4.18**	-11.29**	1.77**	-10.05**	18.01**
4X14	11.11**	-2.92**	21.27**	0.52ns	7.45ns	-46.28ns	12.68**	10.87**	-2.39**	0.39**	4.09**	4.09**	24.03**	6.59**	39.86**
5X14	-4.06ns	-25.32ns	-6.71**	5.85ns	45.94ns	-16.97ns	12.08**	8.25**	-7.77**	0.08**	2.61**	4.89**	7.54**	-2.05**	28.51**
6X14	-5.59ns	-26.21ns	-7.82**	4.91ns	54.18ns	-12.28ns	17.73**	5.33**	-10.25*	5.14**	13.05**	5.51**	20.39**	-0.43**	30.64**
7X14	-4.59ns	-23.38ns	-4.29**	5.70ns	5.70ns	-39.86ns	15.27**	6.77**	-9.03*	-2.61**	0.62**	1.33**	6.37**	-8.86**	19.57**
8X14	8.39**	-14.64*	6.63**	58.04ns	87.67ns	-22.34ns	8.63**	-0.14**	-14.92ns	-2.21**	0.26**	2.49**	5.38**	-11.14**	16.60**
9X14	6.73**	0.03**	24.96**	10.77ns	12.50ns	-37.93ns	14.09**	5.58**	-10.04*	3.97**	17.54**	0.09**	15.82**	1.73**	33.48**
10X14	13.97**	3.65**	29.48**	60.57ns	70.30ns	-3.10ns	2.07**	-1.51**	-16.08ns	11.30**	17.22**	13.78**	16.07**	5.41**	38.30**
11X14	7.48**	-2.13**	22.26**	47.18ns	118.55ns	24.34ns	2.64**	-4.39**	-18.54ns	3.23**	4.68**	9.33**	7.31**	-3.14**	27.09**
12X14	8.96**	-2.64**	21.63**	74.54ns	87.76ns	6.83ns	3.38**	-7.05**	-20.81ns	-0.71**	0.34**	5.51**	2.41**	-8.11**	20.57**
13X14	-7.48ns	-17.15*	3.49**	32.11ns	52.12ns	-13.45ns	4.72**	2.95**	-9.21*	7.18**	18.85**	4.80**	6.75**	-7.68**	21.13**
1X15	16.92**	0.69**	21.87**	32.26ns	72.67ns	-46.41ns	21.04**	20.50**	-6.19**	-10.50**	-9.56**	-4.18**	23.95**	13.17**	29.22**
2X15	8.61**	-11.25**	7.42**	33.96ns	104.67ns	-36.48ns	11.25**	100.39**	-14.53ns	-1.43**	5.24**	-1.78**	10.98**	5.47**	20.43**
3X15	-6.46ns	-20.26ns	-3.49**	-12.52ns	50.67ns	-53.24*	10.60**	7.65**	-12.05ns	3.81**	16.49**	-0.80**	2.05**	-3.98**	9.65**
4X15	5.98**	-6.13**	13.61**	23.23ns	60.89ns	-50.07ns	11.78**	5.44**	-7.77**	0.56**	3.56**	3.56**	14.42**	4.47**	19.29**
5X15	9.81**	-13.54*	4.64**	42.21ns	200.22ns	-6.83ns	14.65**	13.32**	-10.37*	1.45**	3.30**	5.60**	19.36**	16.02**	32.48**
6X15	-2.63ns	-23.02ns	-6.83**	26.63ns	188.44ns	-10.48ns	24.06**	16.23**	-10.52*	-6.69**	-0.38**	-7.02**	36.88**	19.88**	36.88**
7X15	-1.17ns	-19.67ns	-2.78**	119.45ns	210.89ns	-3.52ns	23.64**	20.16**	-7.50**	-3.66**	-1.15**	-0.44**	23.55**	12.42**	28.37**
8X15	8.40**	-13.64*	4.52**	19.05ns	38.89ns	-56.90*	26.04**	21.51**	-6.46**	-9.65**	-8.00**	-5.96**	25.14**	11.93**	27.80**
9X15	5.81**	0.66**	21.83**	-0.32ns	38.44ns	-57.03*	12.48**	9.20**	-15.93ns	10.88**	24.43**	5.96**	16.01**	8.45**	23.83**
10X15	10.80**	2.23**	23.73**	81.53ns	177.33ns	-13.93ns	-1.70**	-3.09**	-23.23ns	7.62**	12.55**	9.24**	11.54**	8.07**	23.40**
11X15	12.69**	4.10**	25.99**	20.48ns	177.78ns	-13.79ns	4.59**	2.25**	-21.29ns	3.17**	3.91**	8.53**	19.87**	15.40**	31.77**
12X15	23.95**	12.33**	35.95**	17.71ns	83.11ns	-43.17ns	12.99**	6.41**	-18.09ns	66.23**	66.86**	75.47**	20.91**	15.65**	32.06**
13X15	-1.19ns	-10.26**	8.61**	41.51ns	139.78ns	-25.59ns	7.19**	0.37**	-11.48*	0.82**	10.99**	-2.13**	16.62**	7.20**	22.41**

Continued... Table 14

	LL			LW			LA			PE		
Hybrid	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)	MPH (%)	BPH (%)	SH (%)
1X14	8.41ns	8.66ns	-2.54ns	6.91ns	17.33ns	-2.90ns	16.34ns	25.93ns	-4.65ns	5.71**	-6.67**	-41.14**
2X14	3.11ns	4.23ns	-8.53ns	12.51ns	18.31ns	6.07ns	16.77ns	22.97ns	-1.94ns	-15.54**	-40.76*	-28.98**
3X14	-0.32ns	2.09ns	-8.38ns	6.38ns	6.90ns	5.79ns	9.34ns	12.67ns	0.27ns	-28.85**	-53.67ns	-26.02**
4X14	4.42ns	5.98ns	-7.75ns	0.89ns	7.58ns	-6.07ns	4.82ns	12.66ns	-13.56ns	57.23**	35.73**	-9.77**
5X14	10.08ns	20.91ns	-9.42ns	9.13ns	18.91ns	-0.28ns	20.48ns	44.75ns	-8.98ns	45.75**	14.73**	-3.52**
6X14	4.78ns	7.87ns	-8.68ns	11.11ns	17.60ns	4.14ns	18.19ns	28.36ns	-3.40ns	52.67**	6.51**	30.11**
7X14	5.54ns	13.05ns	-11.27ns	2.43ns	8.41ns	-4.00ns	8.97ns	24.03ns	-14.29ns	41.33**	25.27**	-21.70**
8X14	2.21ns	8.78ns	-13.58*	3.47ns	7.35ns	-1.24ns	8.01ns	18.60ns	-12.53ns	62.96**	40.17**	-6.02**
9X14	9.71ns	11.90ns	-3.52ns	-1.38ns	-0.27ns	-1.38ns	8.29ns	8.95ns	-5.06ns	2.41**	-33.68*	8.52**
10X14	-0.73ns	1.98ns	-13.30*	0.81ns	6.70ns	-5.52ns	0.32ns	8.32ns	-17.60ns	-15.63**	-35.68*	-40.80**
11X14	-5.14ns	-1.77ns	-17.77**	5.63ns	12.64ns	-1.66ns	1.09ns	10.62ns	-17.91ns	17.61**	-19.74**	6.25**
12X14	5.07ns	7.24ns	-7.68ns	-5.18ns	-3.47ns	-7.86ns	0.06ns	3.32ns	-14.44ns	1.34**	-27.58**	-18.52**
13X14	6.90ns	8.51ns	-2.44ns	-2.50ns	-1.93ns	-3.03ns	8.03ns	10.46ns	-2.05ns	43.84**	0.09**	23.41**
1X15	6.32ns	7.93ns	-2.71ns	9.72ns	24.17ns	2.76ns	15.86ns	32.41ns	0.25ns	152.56**	37.66**	-13.18**
2X15	3.86ns	6.88ns	-6.21ns	1.42ns	9.85ns	-1.52ns	5.80ns	17.48ns	-6.32ns	13.12**	-40.76*	-28.98**
3X15	1.50ns	2.21ns	-5.08ns	4.11ns	6.48ns	6.48ns	8.28ns	9.50ns	4.24ns	78.42**	-7.62**	47.50**
4X15	3.70ns	7.16ns	-6.72ns	-0.36ns	9.48ns	-4.41ns	3.96ns	17.93ns	-9.52ns	110.71**	14.36**	-23.98**
5X15	16.01ns	29.90ns	-2.68ns	17.13ns	31.58ns	10.34ns	34.99ns	71.99ns	8.14ns	68.35**	-10.14**	-24.43**
6X15	2.10ns	7.05ns	-9.38ns	10.71ns	20.72ns	6.90ns	12.67ns	29.20ns	-2.77ns	130.76**	20.74**	47.50**
7X15	4.56ns	14.15ns	-10.42ns	8.57ns	18.38ns	4.83ns	13.53ns	36.72ns	-5.52ns	85.67**	1.27**	-36.70**
8X15	5.54ns	14.46ns	-9.08ns	9.75ns	17.24ns	7.86ns	15.51ns	33.98ns	-1.18ns	116.88**	17.63**	-21.14**
9X15	-4.08ns	-0.38ns	-14.11*	1.95ns	3.68ns	4.83ns	0.01ns	5.87ns	-7.74ns	42.95**	-26.04*	21.02**
10X15	2.70ns	7.44ns	-8.66ns	3.71ns	13.08ns	0.14ns	7.43ns	22.46ns	-6.85ns	30.93**	-30.49*	-36.02**
11X15	-4.00ns	1.24ns	-15.24*	12.72ns	23.85ns	8.14ns	8.15ns	25.01ns	-7.23ns	9.63**	-42.83*	-24.32**
12X15	9.40ns	13.71ns	-2.11ns	17.24ns	22.83ns	17.24ns	28.51ns	39.78ns	15.76ns	30.77**	-31.31**	-22.73**
13X15	-1.23ns	-1.23ns	-8.28ns	7.22ns	9.66ns	9.66ns	5.81ns	8.20ns	0.77ns	53.83**	-19.54**	-0.80**

4.5.2 Heterotic Grouping of Elite Sorghum Inbred Lines

The selection of parents and breeding strategies for the successful hybrid production facilitated by heterotic grouping of parental lines and determination of combining abilities of them. Assigning germplasm into different heterotic groups and patterns is fundamental for exploitation of heterosis for hybrid development. Two heterotic grouping methods were used to assign parental lines into different groups based on SCA effects of grain yield (Pswarayi and Vivek, 2008) and heterotic grouping based on GCA of multiple traits (HGCAMT) method proposed by Oyekunle *et al.*, (2013). These were carried out and presented by dendrogram of cluster analysis. For the achievement of heterotic grouping based on GCA effects, ward methods of Euclidean distance was used for multiple traits.

As two testers (14 and 15) were used in this cross, the principle of SCA effects method is as follows: female parents showing negative SCA effects when crossed with 14 and exhibiting positive SCA effects with 15 were classified into heterotic Group A. female lines showing negative SCA effects with 15 and positive effects with 14 were assigned into heterotic Group B. similar result were reported by Akata *et al.*, (2017) for heterotic grouping of 19 male lines crossed with two female lines into 4 groups based on their SCA effects and similar results were reported by Kidanemariam *et al*.,(2018). Based on the SCA of heterotic grouping, 5 elite lines were classified under group A with negative SCA effects for hybrids derived from tester 14 and the rest 8 elite lines were classified under group B, which had positive SCA effects for cross of tester 15.

Table 16: Heterotic groups of Ethiopian sorghum elite parental lines based on SCA of grain yield trait

	14		15		Heterotic groupings	GCA of females
Females	Mean GY	SCA	Mean GY	SCA		
1	5.32	-331.34ns	5.88	331.34ns	A	562.50ns
2	4.97	40.15ns	4.78	-40.15ns	B	165.00ns
3	4.88	5.65ns	4.76	-5.65ns	B	-216.50ns
4	6.32	727.65**	4.75	-727.65**	B	492.50ns
5	4.19	-428.84ns	4.94	428.84ns	A	-473.00ns
6	5.06	-310.34ns	5.57	310.34ns	A	277.50ns
7	5.24	163.65ns	4.81	-163.65ns	B	-14.50ns
8	4.67	-675.84**	5.92	675.84**	A	258.00ns
9	5.51	15.65ns	5.37	-15.65ns	B	400.50ns
10	4.25	-163.84ns	4.47	163.84ns	A	-681.00ns
11	5.14	527.65*	3.98	-527.65*	B	-480.50ns
12	4.88	104.65ns	4.56	-104.65ns	B	-318.50ns
13	5.78	325.15ns	5.02	-325.15ns	B	358.00ns
Mean	5.09		4.99			

A= Lines had negative SCA effects with Tester 14

B= Lines had negative SCA effects with Tester 15

Grouping of inbred lines based on their GCA effects of multiple traits should give a better and practical heterotic group of the lines since GCA deals with the additive gene effects for each trait. Dendrogram based on HGCAMT method grouped sorghum inbred lines into three heterotic groups as indicated in (Fig. 1). In group I four inbred lines were grouped together and in group II five inbred lines were classified together whereas group III accommodated four inbred lines on the basis of days to flowering, plant height, days to maturity, stay green, grain yield, thousand seed weight, panicle length, panicle width and leaf areas traits. Inbred lines from the same heterotic group show similar character with respect to combining ability and heterosis when crossed with other inbred lines from genetically divergent groups. Heterotic grouping is used to identify suitable parents for crosses. Crosses between inbred lines from groups with differing genetic backgrounds exhibit high levels of heterosis than those among lines from the more genetically related groups Fato *et al*., (2012).

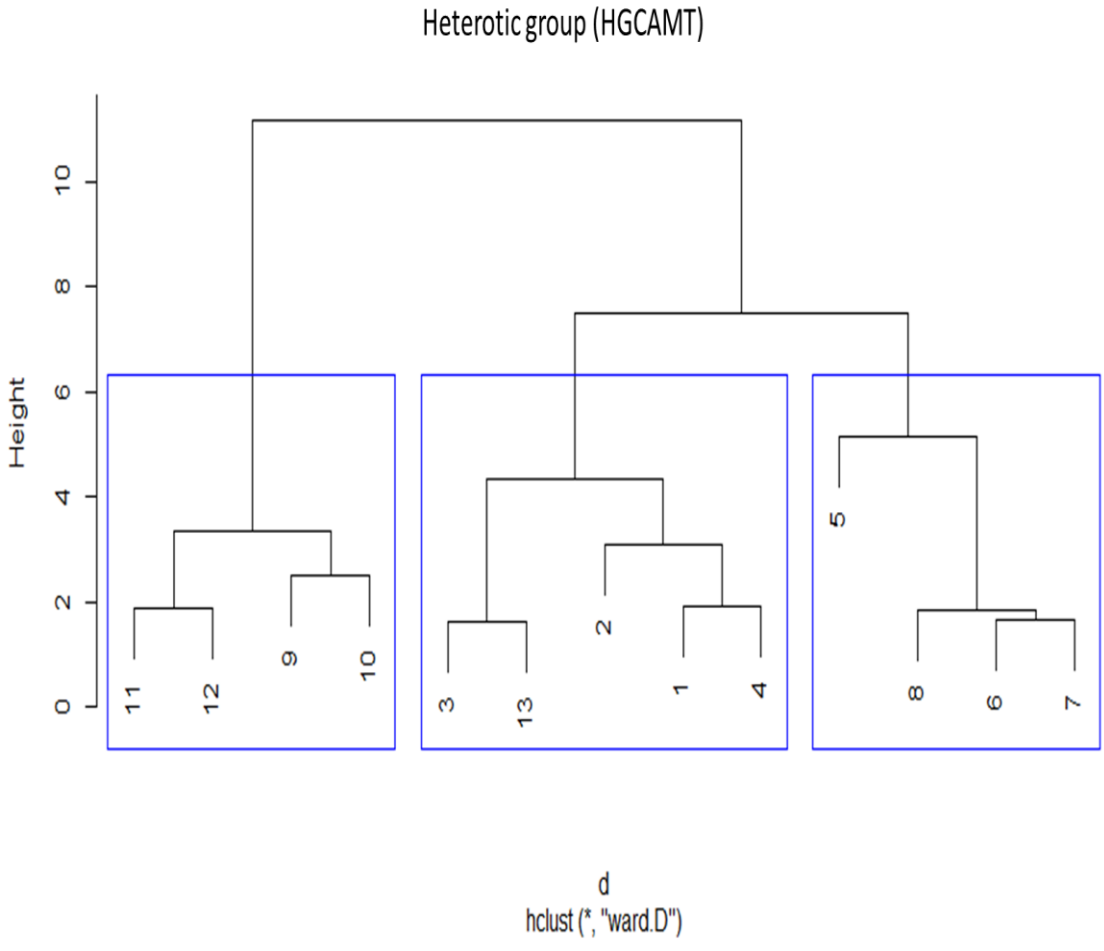

Figure 1: Heterotic grouping of sorghum elite female lines based on HGCAMT

5 SUMMARY AND CONCLUSIONS

Sorghum is the world's fifth most important cereal grain, after wheat, maize, rice and barley in terms of production, and is largely a subsistence food crop in Africa. It is widely grown for food, feed, fodder and fuel in the semi-arid tropics of Asia, Africa, the Americas and Australia. Drought is one of the most important factors that affect crop production worldwide and continues to be a challenge to plant breeders, despite many decades of research. This agricultural constraint may nevertheless be addressed by developing crops that are well adapted to drought prone environments. Understanding the different mechanisms underlying drought tolerance is vital for the breeding to alleviate adverse effects of drought. Combining ability and heterosis are the most powerful genetic term which used for the selection of suitable parents with high GCA and hybrids with SCA in order to boost productivity.

The present investigation entitled Combining Ability and Heterosis Estimation in line x tester Mating Design of Sorghum [*Sorghum bicolor (L) Moench*] was conducted at the Mieso and Kobo during the 2018/2019 of cropping season. The experiment consisted of 42 genotypes in which twenty six hybrids along with their fifteen parents and one standard check were included. The experiment was conducted in alpha lattice experimental design with two replications at each location. The mean squares due to different sources of variations were estimated over the environments and presented in pooled analysis of variance for combining ability. The results showed significantly high variability among all the genotypes for different traits at individual and over locations. The presence of genetic variation among genotypes implies selection could be effective to improve genotypes for different traits.

The mean squares due to lines, tester and line x tester exhibited significantly high and significant, which allow further assessment of combining ability analysis and heterosis estimation. The mean squares due to parent was significantly high for almost all of the traits, except days to maturity and leaf area, which were found significant, indicating the presence of genetic variation among the parents (GCA). The variances due to hybrids (SCA) were significantly high for all the traits except for days to maturity, panicle yield, grain yield, panicle width and leaf area. Potential and promising parents and hybrids were identified based on general and specific combining ability analysis for different traits.

The types of genes action involved in the expression of the traits were also identified to formulate and execute an efficient breeding program for achieving maximum genetic gain and improving the studied traits. The general combining ability effects of promising parents based on desirable direction and consistent performance over two environments were identified. For the days to flowering, inbred line 3, 4 and 13 were identified as best general combiners, whereas all inbred lines were identified as best general combiners, except inbred line 5, 6, 7 and the two testers for plant height. This implied the preponderance of additive gene action in the expression of plant height and the selection breeding strategy would be effective to improve the population for this trait.

Inbred lines (2, 4, 7) for stay green, inbred lines (4) for panicle length, inbred line (11) for leaf length, inbred line (2, 3, 6, 7, 9, 10, 13, 14 and 15) for panicle exersion, inbred line (9, 10, 11 and 12) for thousand seed weight were identified as best general combiners and the all above mentioned inbred lines for their respective traits were controlled by additive gene actions in which population improvement could be achieved through effective selection. Based on specific combining ability analysis hybrid cross (1x15,8x14 and 10x15) for days to flowering, (11x15) for plant height, (1x15, 6x15, 10x15 and 13x15) for days to maturity, (1x15, 2x14, 8x15 and 10x14) panicle length,(1x15, 3x14, 4x14, 6x15, 8x15, 9x14, 10x14 and 12x15) for panicle width, (9x15) for leaf length, (12x14) for leaf width, (3x15) for panicle exersion, (4x14) for panicle yield, (4x14, 8x15, 11x14) for grain yield, (1x15) for thousand seed weight were identified as best specific combiners. The dominant gene actions were involved in the expression of the traits and heterosis breeding strategy is effective to improve the traits.

The predictability ratio (GCA *vs*. SCA) over the environments were found to be less than unity for most of the traits (viz., days to 50 percent flowering, days to maturity, stay green, panicle length, panicle width, leaf length, leaf width, leaf area, panicle exersion, grain yield and thousand seed weight). This indicates, the importance of non-additive gene action in the inheritance of these traits and greater is predictability based on specific combining ability alone for improvement the of respective traits. The predictability ratio GCA *vs*. SCA was found to be more than unity over the environments for plant height, indicating importance of additive gene action for inheritance of this trait and greater is the predictability based on general combining ability alone for improvement of the respective trait.

The highest contribution for grain yield and its components was due to inbred lines, whereas the lowest contribution was due to testers for the studied traits. This study identified significant and valuable heterobeltiosis, average heterosis and economic heterosis for yield and yield components in sorghum that could be harnessed for improving productivity. The highest yield was obtained from hybrid cross 4x14 (6.32 t/ha) followed by hybrid combination 8x15 (5.92 t/ha), 1x15 (5.88 t/ha), 13x14 (5.78 t/ha) and 6x15 (5.57 t/ha) with the average value of 5.01 t/ha which had higher mean value than the grand mean of check and mean of parent. The Relative heterosis, heterobeltiosis and useful heterosis were estimated for all the studied traits. Eleven crosses were better than the mid-parents while three crosses surpassed the better- parents for days to flowering with the maximum heterosis of -6.06% for the cross 5x15 and -4.99% for the cross 1x15 respectively. The above hybrids matured earlier than their parents and are more important under water stress environments by escaping the terminal drought.

The mid-parents heterosis for grain yield ranged from 6.26 to 112.41 (%) across locations with mean value of 53.27%. The better parent heterosis for grain yield ranged from -0.23 to 68.71% with mean value of 31.70 %, whereas the magnitude of heterosis of the hybrids over the standard check hybrid ranged from -16.49 to 30.71% with mean value of 5.81 % over the environments. These results implied the highest yield advantages obtained in hybrids over the mid-parents, better parents and the commercial hybrid variety. Based on the SCA of heterotic grouping, 5 elite lines were classified under group A with negative SCA effects for hybrids derived from tester 14 and the rest 8 elite lines were classified under group B, which had positive SCA effects for cross of tester 15. Based on HGCAMT heterotic grouping method, sorghum inbred lines grouped into three heterotic grouping as indicated in (Fig. 1).

Generally there was the possibility of improving traits under the study through selection and heterosis breeding program. Based on mean yield performance, heterotic response, combining ability estimates and nature of gene action for grain yield and yield related traits, the most promising parents and hybrids were identified. Inbred line 4, 10, 11, 12, 13 and the hybrid crosses 4x14, 4x15, 8x14, 8x15, 11x14 and 11x15 were found to be the most promising and potential genetic materials which could be exploited after critical evaluation for their superiority and yield stability across the locations over years.

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7 APPENDICES

Appendix Table 1. Analysis of variance for yield & related characters of individual location (Mieso and Kobo in 2018/2019)

SV	DF	Site	DTF	PHT	DTM	SG	PL	PW	LA	Tiller	PE	PY	GY	TSW
Replication	1	MI	4.29	2656.68**	17.19	0.01	5.15	28.35**	24.88	21.00**	14.41**	34.20	1951.28*	0.38
	1	KB	4.29	120.96	0.11	0.19	1.05	0.05	46.74	198.10*	17.01*	385.71	3918.61	3.72
Blocks	10	MI	1.44	50.21	4.62	0.07	2.55	2.47**	600.34	0.97	0.72	27.83	574.55	16.49
	10	KB	3.56	81.04	8.78**	0.19	3.54	1.03*	2674.69	29.76	4.02	358.19	889.12	3.47
Genotypes	41	MI	6.40**	2824.32**	9.86*	1.15**	13.16**	1.55*	3486.39**	6.44**	18.15**	808.07**	1129.39**	25.78**
	41	KB	12.85**	5219.57**	19.57**	0.51	17.32**	3.08**	6771.79	61.21*	13.75**	2363.67**	5863.35**	46.54**
Parents	14	MI	12.01	2033.06**	17.33	1.28**	7.58	1.15	3329.19**	1.44	29.87**	370.53**	371.38	21.08*
	14	KB	19.38	4735.35**	13.80	0.52	13.03**	1.24*	2107.97	83.80	13.97	574.92	1188.52	36.29**
Hybrids	25	MI	2.54	1259.79**	6.25*	1.11**	4.39	0.77	2795.72**	7.46**	10.79**	508.44**	481.71	26.65**
	25	KB	4.46*	3129.2**	6.01	0.38	9.76**	0.96	4135.04	65.28	9.64**	810.17	1828.52	19.60**
Lines	12	MI	3.21	2470.00**	7.68	1.02**	6.40	1.23	3159.00**	5.74**	14.76**	598.19**	693.81	46.24**
	12	KB	7.22**	6122.85**	7.19	0.56	15.78**	0.95	4261.15	94.40*	12.72**	1328.01*	2221.19	36.61**
Testers	1	MI	1.00	94.07	3.45	0.06	2.18	0.04	135.91	0.10	6.79**	84.43	58.58	12.06
	1	KB	9.89*	502.88*	6.27	0.04	0.11	0.20	19234.27*	41.30	0.03	0.96	649.47	0.37
L x T	12	MI	2.02	78.25	5.11	1.24**	2.38	0.37	2662.71**	9.73**	6.84**	482.56**	300.06	8.15
	12	KB	1.14	190.96	4.55	0.24	4.24	1.05	2889.96	42.05	7.88**	0.87	1598.13	5.84**
Par0entsvs.	1	MI	13.06	482.24	2.58	0.1	74.14**	0.02	17521.85**	0.32	10.73	866.12	8214.85**	27.21
check	1	KB	20.02	3474.38	21.42	1.52	80.64**	1.52	37.8	97.52	13.26	152.38	7.78	30.51
Hybridsvs.	1	MI	6.13	9391.62**	0.03	0.78	14.26	1.88	12587.82**	6.06	2.21	49.08	1302.60	0.0039
Check	1	KB	26.66**	14419.60**	49.22**	2.44**	32.86*	8.59**	112.85	79.56	3.09	2721.08	4048.32	25.76
Parentvs.	1	MI	3.54	41911.95**	1.25	6.90**	247.36**	27.42**	13968.73**	39.54**	0.93	15071.77**	23905.64**	127.53**
hybrids	1	KB	56.46**	47485.88**	350.19**	0.1	220.60**	72.80**	101353.14**	9.41	0.10	66201.66**	176905.76**	628.29**
Error	31	MI	2.44	69.01	5.69	0.09	4.20	0.76	426.10	12.29	1.99	17.64	0.42	6.17
	31	KB	2.56	75.61	2.98	0.44	1.87	0.42	3970.86	35.37	3.84	497.81	1.38	2.93
CV (%)		MI	2.29	4.61	2.21	7.36	7.49	12.76	7.41	30.03	15.07	7.36	31.82	14.53
		KB	2.18	4.37	1.52	18.93	4.71	6.81	17.21	30.05	20.32	18.93	17.97	4.25

Appendix Table 2. Mean performance of genotypes for yield and in yield related traits in sorghum at Mieso and Kobo in 2018/2019)

Entry	DTF	PHT	DMT	PY	GY	SG	TSW	PL	PW	LN	LL	LW	LA	PE	PAS
1	70.00	185.90	108.50	107.80	5.88	2.25	30.70	31.35	9.65	11.34	68.25	7.50	353.84	7.95	1.75
2	69.25	183.70	108.00	106.80	4.78	3.50	27.25	28.75	8.20	11.00	65.83	7.08	325.93	6.35	2.50
3	69.25	181.80	109.00	89.60	4.76	2.75	24.13	29.25	7.60	10.75	66.33	7.75	365.97	12.60	3.13
4	69.25	176.50	108.50	89.25	4.75	2.50	28.63	30.85	8.20	11.42	65.33	6.92	316.25	6.55	2.25
5	71.00	206.70	110.00	99.40	4.94	2.50	26.28	29.90	9.10	11.50	68.08	8.00	378.56	6.35	2.50
6	69.75	198.00	109.25	83.60	5.57	3.00	23.63	30.05	9.90	10.92	63.67	7.75	340.97	13.35	2.50
7	69.50	184.90	109.00	96.55	4.81	3.25	24.58	31.00	9.00	11.25	62.83	7.58	330.47	5.65	2.25
8	71.25	184.80	111.00	126.30	5.92	2.75	26.35	31.30	9.15	10.75	63.75	7.83	346.86	7.05	2.25
9	70.00	258.00	109.00	106.05	5.37	3.00	30.85	28.25	8.85	12.25	60.34	7.58	322.88	10.95	2.75
10	71.50	259.90	110.75	101.50	4.47	2.75	31.33	25.80	8.95	12.75	64.17	7.25	326.68	6.00	3.00
11	71.00	237.90	111.50	93.10	3.98	2.50	31.78	26.35	9.30	12.25	59.42	7.83	325.01	6.70	2.75
12	71.00	243.50	110.50	115.00	4.56	2.00	34.33	27.45	9.40	19.92	68.67	8.50	405.68	6.95	2.25
13	69.50	187.90	110.00	104.15	5.02	3.00	27.20	29.45	8.85	11.00	64.17	8.00	355.22	8.60	2.50
14	71.75	188.40	111.00	95.30	5.33	3.00	25.93	29.15	7.95	12.50	68.42	7.00	332.45	5.35	2.75
15	70.25	179.80	109.00	87.95	4.97	3.25	25.55	31.05	8.50	11.17	64.25	7.67	343.22	6.55	2.00
16	69.00	174.80	108.75	98.65	4.89	3.50	27.08	29.45	8.65	10.58	64.42	7.67	351.73	7.00	2.50
17	69.00	184.30	107.75	119.70	6.32	2.25	30.33	32.45	9.65	11.17	64.42	6.83	303.49	7.45	2.50
18	72.25	200.50	110.00	79.05	4.20	2.75	23.28	30.65	8.85	11.25	63.25	7.25	319.53	8.00	2.50
19	71.00	195.70	111.75	82.85	5.06	2.50	23.25	30.05	8.60	11.25	63.92	7.50	335.74	11.10	2.25
20	70.25	200.90	109.00	83.35	5.25	3.50	24.25	30.55	8.20	11.34	62.25	6.92	298.54	6.95	2.00
21	69.50	185.40	109.00	111.65	4.68	3.00	26.80	28.40	8.20	11.42	60.50	7.17	306.88	8.15	2.75
22	70.00	256.60	109.00	111.90	5.51	2.75	31.58	30.15	9.85	11.83	67.75	7.17	334.13	9.95	2.50
23	73.25	271.00	113.50	101.50	4.25	2.25	32.45	27.90	10.10	12.92	60.67	6.92	291.49	5.15	2.88
24	70.50	257.70	109.50	111.75	5.14	2.75	30.65	27.10	9.05	12.17	57.50	7.17	289.11	9.15	2.25
25	71.50	259.10	110.75	107.05	4.88	2.75	30.73	26.55	8.45	11.92	64.75	6.67	299.21	7.25	2.50
26	68.75	196.30	107.75	108.85	5.78	2.75	25.83	30.15	8.60	11.50	68.17	7.09	345.14	10.50	2.00
27	73.75	125.50	113.00	65.80	2.78	3.00	22.03	26.10	6.65	12.17	63.17	6.00	265.36	5.55	3.25
28	68.50	113.40	112.25	39.80	2.33	2.50	19.35	25.65	7.25	10.50	61.50	6.50	279.45	10.55	4.00
29	67.75	119.70	111.00	49.45	2.82	2.50	21.50	27.45	7.10	9.58	66.00	7.25	333.62	14.05	4.00
30	71.25	133.30	112.25	55.80	3.02	3.00	23.53	29.45	6.65	11.25	61.00	6.33	268.89	5.85	3.75
31	77.00	149.40	114.50	42.75	2.13	1.75	17.53	26.55	7.60	11.50	52.50	6.08	220.36	7.40	3.75

Continued…

32	72.25	132.90	113.50	39.45	2.25	2.75	17.73	22.50	6.05	10.50	59.33	6.42	263.75	10.75	4.25
33	71.75	119.70	113.50	40.05	2.36	3.00	19.08	24.30	6.60	11.33	55.00	6.42	242.19	5.50	4.00
34	71.25	107.50	111.25	52.80	2.05	3.50	18.10	23.90	6.35	11.50	55.67	6.67	258.48	5.90	3.75
35	67.75	220.90	109.00	67.65	3.53	1.25	27.53	24.25	7.00	9.58	60.42	7.34	305.40	14.40	3.00
36	70.50	245.90	109.50	67.35	3.00	2.50	25.78	26.50	7.55	10.92	59.58	6.42	266.59	8.10	4.00
37	72.00	245.10	111.75	78.50	3.94	2.50	25.85	24.60	7.45	11.75	58.67	6.34	260.07	11.65	3.25
38	72.25	232.70	112.00	59.45	3.21	2.50	24.78	22.75	7.35	11.84	60.34	6.92	290.22	9.90	3.50
39	68.00	133.60	110.75	46.15	3.03	2.25	24.90	29.50	6.75	9.92	65.08	7.25	326.41	10.85	3.00
40	74.00	166.10	112.50	87.45	4.12	2.50	31.48	28.50	9.25	12.08	62.84	7.17	309.14	4.25	1.75
41	73.75	137.10	112.75	67.80	3.55	2.75	30.50	25.75	8.05	11.92	65.08	7.58	341.15	0.50	3.75
42	68.00	131.30	113.00	83.15	4.78	1.75	25.20	33.45	7.05	11.25	70.08	7.25	350.46	8.80	2.00
Mean	70.69	189.38	110.58	84.81	4.29	2.68	26.18	28.20	8.23	11.56	63.03	7.16	314.92	8.13	2.83
Min	67.75	107.5	107.75	39.45	2.05	1.25	17.53	22.5	6.05	9.58	52.5	6.00	220.36	0.50	1.75
Max	77	271	114.5	126.3	6.32	3.50	34.33	33.45	10.1	19.92	70.08	8.50	405.68	14.4	4.25
LSD (5%)	2.28	11.83	3.04	26.44	1.31	0.83	3.45	2.44	1.14	3.78	7.36	1.20	74.75	3.24	0.93
CV (%)	2.29	4.43	1.95	22.12	21.75	22.15	9.37	6.13	9.85	23.19	8.28	11.93	16.84	28.33	23.54

Appendix Table 3. Mean performance of parents of yield and yield related traits at Mieso and Kobo in 2018/2019)

Line	DTF	PHT	DTM	SG	PL	PW	LN	LL	LW	LA	TL	PE	PY	GY	TSW	PAS
1	73.75	131.30	113.00	3.00	26.10	6.65	12.17	63.17	6.00	265.36	7.25	5.55	65.80	2.78	22.03	3.25
2	68.50	113.40	112.25	2.50	25.65	7.25	10.50	61.50	6.50	279.45	9.25	10.55	39.80	2.34	19.35	4.00
3	67.75	119.70	111.00	2.50	27.45	7.10	9.58	66.00	7.25	333.62	11.00	14.05	49.45	2.82	21.50	4.00
4	71.25	133.30	112.25	3.00	29.45	6.65	11.25	61.00	6.33	268.89	7.25	5.85	55.80	3.02	23.53	3.75
5	77.00	149.40	114.50	1.75	26.55	7.60	11.50	52.50	6.08	220.36	14.50	7.40	42.75	2.13	17.53	3.75
6	72.25	132.90	113.50	2.75	22.50	6.05	10.50	59.33	6.42	263.75	16.00	10.75	39.45	2.25	17.73	4.25
7	71.75	119.70	113.50	3.00	24.30	6.60	11.33	55.00	6.42	242.19	8.25	5.50	40.05	2.36	19.08	4.00
8	71.25	107.50	111.25	3.50	23.90	6.35	11.50	55.67	6.67	258.48	6.00	5.90	52.80	2.05	18.10	3.75
9	67.75	220.90	109.00	1.25	24.25	7.00	9.58	60.42	7.33	305.40	8.00	14.40	67.65	3.53	27.53	3.00
10	70.50	245.90	109.50	2.50	26.50	7.55	10.92	59.58	6.42	266.59	9.25	8.10	67.35	3.00	25.78	4.00
11	72.00	245.10	111.75	2.50	24.60	7.45	11.75	58.67	6.33	260.07	16.25	11.65	78.50	3.94	25.85	3.25
12	72.25	232.70	112.00	2.50	22.75	7.35	11.83	60.33	6.92	290.22	9.50	9.90	59.45	3.21	24.78	3.50
13	68.00	133.60	110.75	2.25	29.50	6.75	9.92	65.08	7.25	326.41	10.75	10.85	46.15	3.03	24.90	3.00
Mean	71.08	160.42	111.87	2.54	25.65	6.95	10.95	59.87	6.61	275.45	10.25	9.27	54.23	2.80	22.13	3.65
Tester																
14	74.00	166.10	112.50	2.50	28.50	9.25	12.08	62.83	7.17	309.14	8.25	4.25	87.45	4.12	31.48	1.75
15	73.75	137.10	112.75	2.75	25.75	8.05	11.92	65.08	7.58	341.15	4.50	0.50	67.80	3.55	30.50	3.75
Mean	73.88	151.60	112.63	2.63	27.13	8.65	12.00	63.96	7.38	325.14	6.38	2.38	77.63	3.84	30.99	2.75

Appendix Table 4. Mean performance of hybrids and check for yield and its components in sorghum at Mieso and Kobo in 2018/2019)

Cross	DTF	PHT	SG	DTM	PY	GY	PAS	TL	TSW	PL	PW	LN	LL	LW	LA	PE
1	70.07	184.89	2.36	108.18	108.91	5.99	1.64	7.77	30.71	31.38	9.11	10.78	68.18	7.45	351.35	7.64
2	69.48	184.98	3.45	108.60	107.95	4.75	2.53	9.21	27.07	28.59	8.49	11.05	65.73	7.14	328.31	6.25
3	68.93	181.17	2.71	108.58	87.31	4.71	3.19	6.78	24.32	29.42	7.73	11.16	66.52	7.72	365.31	12.98
4	69.20	176.83	2.46	108.59	88.68	4.70	2.30	7.24	28.63	30.85	8.41	11.65	65.37	6.93	317.11	6.69
5	70.81	206.69	2.45	109.88	97.86	4.88	2.57	13.51	26.37	29.98	9.34	11.88	68.20	8.00	378.99	6.65
6	70.01	198.18	3.06	109.48	85.63	5.65	2.42	12.98	23.48	29.93	9.65	10.46	63.51	7.75	340.76	12.98
7	69.60	185.29	3.25	109.20	97.17	4.81	2.25	13.99	24.50	30.94	9.05	11.20	62.78	7.60	331.12	5.57
8	71.29	184.61	2.78	110.96	126.76	5.95	2.22	6.25	26.34	31.29	9.01	10.58	63.72	7.82	346.32	6.94
9	70.25	258.46	3.03	109.32	107.86	5.42	2.70	6.23	30.70	28.12	8.73	11.92	60.19	7.60	323.32	10.65
10	71.76	260.08	2.81	110.98	103.53	4.55	2.92	12.48	31.18	25.68	8.70	12.29	64.01	7.26	326.46	5.63
11	71.04	237.98	2.50	111.55	93.34	3.98	2.74	12.50	31.75	26.33	9.29	12.21	59.40	7.84	325.12	6.66
12	71.11	243.62	2.02	110.61	115.84	4.59	2.22	8.24	34.26	27.40	9.31	19.74	68.60	8.50	405.68	6.80
13	69.27	186.76	3.03	109.45	102.89	5.04	2.49	10.79	27.37	29.61	8.63	11.01	64.28	7.95	353.16	8.73
14	71.99	189.40	2.98	111.50	96.67	5.32	2.75	9.21	25.76	29.00	8.10	12.42	68.30	7.04	334.18	5.18
15	70.50	180.26	3.28	109.32	89.76	5.02	1.95	4.98	25.40	30.92	8.38	10.84	64.10	7.69	343.65	6.25
16	69.33	175.02	3.58	109.03	101.27	4.99	2.39	6.23	26.89	29.30	8.32	9.98	64.21	7.67	351.41	6.51
17	68.60	183.64	2.19	107.27	116.81	6.32	2.59	7.79	30.56	32.65	9.86	11.71	64.65	6.81	302.94	7.94
18	71.85	199.84	2.69	109.52	76.16	4.11	2.59	12.04	23.51	30.85	9.06	11.80	63.48	7.23	318.98	8.49
19	70.93	196.85	2.38	112.11	81.63	4.94	2.38	12.72	23.23	30.02	9.21	11.87	64.00	7.55	338.55	11.45
20	70.41	201.87	3.46	109.45	84.13	5.22	2.02	8.72	24.12	30.43	8.43	11.40	62.18	6.96	300.38	6.89
21	69.39	185.15	2.99	108.84	110.92	4.66	2.77	11.26	26.87	28.46	8.22	11.53	60.56	7.16	306.55	8.27
22	70.20	256.20	2.84	108.98	113.77	5.62	2.39	9.00	31.49	30.09	9.41	11.26	67.61	7.15	332.73	9.55
23	73.02	269.58	2.31	112.86	100.45	4.30	2.84	14.05	32.63	28.07	9.75	12.80	60.76	6.85	288.78	5.21
24	70.26	256.83	2.76	109.04	110.27	5.14	2.26	18.03	30.81	27.25	8.96	12.30	57.63	7.13	287.70	9.35

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25	71.60	259.49	2.75	110.95	107.67	4.88	2.50	15.49	30.65	26.49	8.50	11.87	64.70	6.68	299.86	7.17
26	68.37	195.09	2.74	107.09	106.40	5.75	2.04	12.55	26.08	30.37	8.54	11.79	68.37	7.03	343.29	10.86
Mean	70.36	209.18	2.80	109.67	100.76	5.05	2.45	10.39	27.87	29.36	8.85	11.83	64.27	7.41	332.39	7.97
Max	73.02	269.58	3.58	112.86	126.76	6.32	3.19	18.03	34.26	32.65	9.86	19.74	68.60	8.50	405.68	12.98
Min	68.37	175.02	2.02	107.09	76.16	3.98	1.64	4.98	23.23	25.68	7.73	9.98	57.63	6.68	287.70	5.18
Check	68	125.50	1.75	113.00	83.15	4.77	2.00	14.50	25.20	33.45	7.05	11.25	70.08	7.25	350.46	8.80

Appendix Table 5: List of parents and hybrids with their symbolical representation

Lines (code)	Name of parents and hybrids	Lines (code)	Name of parents and hybrids
1	TX-623	3x15	P-9505XICRA-14
2	P-9501	4x14	P-9534XMelkam
3	P-9505	4x15	P-9534XICRS-14
4	P-9534	5x14	P-851015XMelkam
5	P-851015	5x15	P-85101XICRS-14
6	P-850341	6x14	P-850341XMelkam
7	B5	6x15	P-850341XICRS-14
8	B6	7x14	B5XMelkam
9	MARC1	7x15	B5XICRS-14
10	MARC2	8x14	B6XMelkam
11	MARC3	8x15	B6XICRS-14
12	MARC6	9x14	MARC1XMelkam
13	P9511	9x15	MARC1XICRS-14
14	Melkam	10x14	MARC2XMelkam
15	ICRS-14	10x15	MARC2XICRS-14
16	ESH-4	11x14	MARC3XMelkam
1x14	TX-623XMelkam	11x15	MARC3XICRS-14
1x15	TX-623XICRS-14	12x14	MARC6XMelkam
2x14	P-9501XMelkam	12x15	MARC6XICRS-14
2x15	P-9501XICRS-14	13x14	P9511XMelkam
3x14	P-9505XMelkam	13x15	P9511XICRS-14

Appendix Table 17 Appendix Monthly Meteorological data of the testing sites during the experimental season

Site		Mieso						Kobo					
Month		June	Jul	Aug	Sep	Oct	Nov	June	Jul	Aug	Sep	Oct	Nov
RF (mm)		63	141.2	150.3	44.6	43.1	4.1	15	163	186	47	22	22
Temp (^{0}c)	Min	16.3	15.8	15.5	10.6	11.4	10.4	15.9	16.1	15.6	15.4	13.8	12.4
	Max	35.5	33	33	33.5	34	33	34.3	31.2	29.8	30.5	30	28.7

Source: World Online Weather (2018)