GENOTYPE X ENVIRONMENT INTERACTION AND YIELD STABILITY OF EARLY MATURING SORGHUM [*Sorghum bicolor (*L.) Moench] GENOTYPES IN DRY LOWLAND AREAS OF ETHIOPIA

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Genotype x Environment Interaction and Yield Stability of Early Maturing Sorghum [*Sorghum bicolor* (L.) Moench] Genotypes in Dry Lowland Areas of Ethiopia

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DEDICATION

I dedicate this thesis manuscript to my father Ato Semahegn Yitayeh and My mother W/ro Emiye Ayalew, who were committed to grow me up in the process of education..

STATEMENT OF THE AUTHOR

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LIST OF ABBREVIATIONS AND ACRONYMS

AMMI	Additive Main Effects and Multiplicative Interaction
ANOVA	Analysis of Variance
ASV	AMMI Stability Value
CV	Coefficient of Variation
DAP	Diammonium Phosphate
DF	Degrees of Freedom
EIAR	Ethiopian Institute of Agricultural Research
ESIP	Ethiopian Sorghum Improvement Program
G x E	Genotype x Environment
GGE	Genotype and Genotype by Environment
IBPGR	Institute for Biodiversity of Plant Genetic Resources
ICRISAT	Institute of Crop Research Institute for the Semi Arid Tropics
IDRC	International Development Research Centre
IPCA	Interaction Principal Component Axis
JLR	Joint Genotypear Regression
LMM	Linear Mixed Model
MARC	Melkassa Agricultural Research Center
m.a.s.l.	Meter above sea level
MET	Multi-environment Trials
MS	Mean Square
PCA	Principal Component Analysis
PGRC/E	Plant Genetic Resources Centre/Ethiopia
RCBD	Randomized Complete Block Design
REML	Residual Maximum Likelihood
SV	Source of Variation

BIOGRAPHICAL SKETCH

The author was born on June 14, 1989 in Bure, West Gojjam of Ethiopia. He attended elementary and junior Secondary school at Bure Ras Bit Woded Mengesha Atikem School from 1997 to 2004. He pursued high school and preparatory School at Bure Shikudad from 2005 to 2008. After the completion of his high school education, he joined the then Hawassa University in 2009 and graduated with a Bachelor of Science degree (B.Sc.) in Horticulture on July, 2011. Soon after graduation, he was employed by Burea of Agriculture as Horticulture expert in Womberma woreda Agricultural office from October 2011 to April 2014 and from May 2014 to September 2016 as assistance researcher I in Ethiopian Institute of Agricultural Research. In the year 2016, he joined the School of Graduate Studies at Jimma University to pursue his graduate study in Plant Breeding.

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TABLE OF CONTENTS

CONTENTS **PAGES**

LIST OF TABLES

Tables Pages

LIST OF FIGURES

LIST OF TABLES IN APPENDICES

Tables **Pages**

LIST OF FIGURES IN APPENDICES

ABSTRACT

The yield performance of crop varieties is highly affected by genotype x environment interaction, which is the major concern to plant breeders while developing improved varieties. In Ethiopia, high yielding, early maturing and stable varieties that wisthstand drought in the dry lowland areas are limited. In view of this, the yield performance of 60 early maturing advanced sorghum genotypes were tested at five locations with the objectives of estimating the magnitude of GxE for grain yield and other traits and to identify high yielder and stable genotypes across locations. The experiment was conducted using Randomized Complete Block Design with Row Column arrangement and three replications. Grain yield, phenological and other traits were recorded. The Residual Maximum Likelihood combined analysis of variance across locations showed very highly significant ($P \leq 0.0001$) difference for grain yield among locations and significant ($P \leq 0.05$) among genotypes and highly significant ($P \leq 0.0001$) among interactions for most of the traits studied. Significant variation for locations and genotype indicates variation in the performance of genotypes for grain yield, phonological and other traits in different environments. On the other hand, significant GxE interaction showed inconsistency in the performance of sorghum genotypes across locations. Based on Eberhart and Russell'stability analysis, genotypes 05MW6026, 14MWLSDT7207, 14MWLSDT7332, 12MW6444, 12MW6302 and 14MWLSDT7042 were the most stable and high yielders. The AMMI stability value showed that genotypes 14MWLSDT7207, 05MW6026 and 14MWLSDT7234 were the high yielders and stable, while the GGE stability value showed that genotypes 14MWLSDT7207, 05MW6026, 14MWLSDT7209 and 12MW6440 were the best yielders and stable ones. Results of ASV parameter also showed six most widely stable and high yielder genotypes i.e., 13MWF6#6037, 05MW6026, 14MWLSDT7207, 14MWLSDT7234,14MWLSDT7042 and 12MW6440. Genotypes 05MW6026 and 14MWLSDT7207, were selected with four stability parameters as a high yielder and stable, and therefore, are the promising ones. Generally, this study showed the importance of testing early maturing sorghum genotypes for their yield and stability across diverse dry lowland areas of Ethiopia.

Keywords: Early maturing, Sorghum, AMMI, GGE, Stability, Joint regression

1. INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) *Moench*] is a C4 tropical crop (Smith and Frederiksen, 2000). It is a monocot crop, which belongs to the family *Gramnieae* (Harlan and De Wet, 1972). Sorghum is naturally self-pollinated short day plant with the degree of spontaneous cross pollination, in some cases, reaching up to 30%, depending on panicle types. It has 2n = 2x = 20 chromosomes and it has relatively small size of 730 Mbp (Paterson *et al*., 2009). The genus sorghum is very diverse and all cultivated sorghums belong to Sorghum bicolor species, which is divided, based on morphology, into five races: bicolor, caudatum, guinea, durra, and kafir (Harlan and De Wet, 1972). Sorghum is an indigenous crop to Ethiopia where it is grown in a wider area of adaptation ranging from hot, dry lowland, intermediate to the highland environments.

The world sorghum production is estimated to be 62.3 million tons from 42 million hectares of land (USDA, 2017). In Africa, sorghum production is 29.14 million tons from 26.03 hectares of land (USDA, 2017). In Ethiopia, it ranks third in area coverage, after maize and teff (CSA, 2017). In Ethiopia, sorghum is contributing 16.4% of the total annual cereal grain production (CSA, 2017). In Ethiopia, the area covered with sorghum is 1.9 million ha, and its total production is 4.8 million tons of grain (CSA, 2017). It is the dominant crop in the dry lowlands, which accounts for 66% of the total cultivated areas of the country and the national average productivity of sorghum in Ethiopia is 2.5 tons/ha (CSA, 2017). However, research has shown that there is a potential to increase sorghum productivity from 3 to 6 tones/ha using improved varieties and production practices (Asfaw *et al*., 2005).

In the arid and semi-arid tropics of Africa and Asia, sorghum is primarily grown as a food grain crop while in the developed world the majority of the grain produced is used for animal feed (Rakshit *et al*., 2014). Sorghum grain is preferred next to tef, a small cereal grain crop, used as injera (Fantaye and Hintsa, 2017). Although there is variability in the grain quality depending on the end use product, larger seed size, white and light red types of sorghum grains are predominantly preferred for the preparation of injera. The grain is also used for the preparation of local beverages. In addition, the stover is equally valued as the grain, which is used for animal feed, fuel wood and construction purposes (Taye *et al*., 2016).

In Ethiopia, the current rate of yield increment in sorghum is not adequate. Although a number of biotic (diseases, insects, striga etc.) and abiotic factors (drought, poor soil fertility, soil salinity etc.) contributed to the lower grain yield increment, drought is considered as one of the major abiotic factors impeding sorghum productivity in Ethiopia. Drought is occurring due to delay in onset, dry spell after sowing, drought during critical crop stage (flowering and grain filling stage) and too early cessation of rain. This limitation is reduced by developing sorghum genotypes which are more adapted to moisture stress areas (Fantaye and Hintsa, 2017). Over eighty percent of sorghum in Ethiopia is produced under high to moderate drought stress condition (Fantaye and Hintsa, 2017). In Ethiopia, drought occurred in any stage of sorghum development with the high frequency of terminal stress in dry lowland areas. Genetic improvement is considered as an integral part of overcoming the challenges of drought in the dry lowlands of the country. A major challenges of sorghum production in the dry lowland parts of the country is lack of early maturing improved varieties that can escape drought or tolerant to stresses, such as drought and lack of stable varieties across environments (Fantaye and Hintsa, 2017). Development of an early maturing and/or varieties that can withstand terminal stress through introgression of stay-green trait are the two major strategies being implanted in the sorghum breeding in Ethiopia.

In countries such as Ethiopia, where environmental differences are very diverse and unpredictable (Dugan and Labuschahne, 2002) and led to significant G x E interaction even within a small geographic area, making genotype improvement and recommendation is more problematic. Under such conditions, testing of genotypic performance at various locations delivers valuable information to determine their adaptation and stability (Crossa, 1990). As a result, it is not only average genotype performance that is important in selection of superior genotypes, but also, the magnitude of the interactions (Gauch and Zobel, 1997). As a result, several methods of measuring and describing genotypic response across environments have been developed and utilized (Luthra et al, 1974).

Various studies have been conducted to analyze the effect of GxE interaction in sorghum varieties. Asfaw (2007) studied yield stability in sorghum and tested 14 hybrids and one open pollinated variety and he recommended four genotypes for the drought stressed sorghum growing areas of Ethiopia. Abiy and Firew (2016) studied genotype x environment interaction and stability of early maturing sorghum genotypes in Ethiopia and identified three genotypes suitable for lowland areas of Ethiopia. Kinde *et al.* (2016) evaluated sorghum varieties and environments for yield performance and stability and recommended two varieties for moisture stress area of West Hararghe. Sintayehu and Kassahun (2017) studied genotype-by-environment interaction and yield stability in sorghum genotypes and identified three genotypes for the North Shewa sorghum growing areas. Similarly, Fantaye and Hintsa (2017) studied 12 sorghum hybrids in the moisture stress conditions of Abergelle District, Northern Ethiopia and identified three hybrid genotypes for moisture stressed areas of Abergelle. These authors reported the existence of high interaction of genotypes with environments. However, the previous authors conducted their trials with previously released and very limited genotypes.

Yield stability is one of the impediments facing plant breeders in developing widely adapted varieties with superior yield (Asfaw, 2007). Several research institutions have been working and able to identify sorghum varieties for yield that resist or tolerate harsh environmental conditions and produce consistently better grain yield. In line with this, the national and regional sorghum improvement programs have released a number of stable and early maturing sorghum genotypes for the moisture stress lowland areas of Ethiopia (EIAR, 2014). Information on nature and extent of genotype by environment interaction of sorghum genotypes is important to identify superior and stable variety in drought areas of Ethiopia. However, there is no information on genotype by environment interaction of early maturing sorghum genotypes developed by the natonal program. Therefore, this study was conducted with the following objectives

General Objectives

- To assess the performance of early maturing sorghum genotypes for yield and stability across locations.

Specific Objectives

- To estimate the magnitude of GxE interactions and performance of early maturing sorghum genotypes for yield and yield related traits.
- To identify high yielder and stable genotypes across locations

2. LITERATURE REVIEW

2.1. Sorghum Research in Ethiopia

The Ethiopian Sorghum Research was commenced in 1957 by Haramaya University, the then College of Agriculture with the subsequent initiation of Ethiopian Sorghum Improvement Program (ESIP) with the fund from International Development Research Centre (IDRC), and Canada (Firew Mekbib, 2005). Sorghum breeding activities were conducted in the diverse ecological parts of the country by support of different national and international organizations (Firew Mekbib, 2005). The collection, evaluation, characterisation and conservation were one of the primary sorghum activities. Closer to 8000 indigenous collections were done (PGRC/E, 1986).

Currently different types of crossing programs with designed product concept were undertaken by the national sorghum improvement program to solve sorghum production problems related to production and productivity. Research has also been conducted to develop technologies in the areas of variety development, management and cropping system, protection, food science, socio economics and research extension with the major products in the variety development (EIAR, 2014). On the past five decades more than 50 improved sorghum varieties with different desirable features were released for the four major agro-ecologies of Ethiopia (dry lowlands, humid lowlands, intermediate and highland elevation areas) (MARC unpublished document).

2.2. Genotype by Environment Interaction

Living organisms are identified neither by their genes nor by their environment; they are the result of the interaction of genes and environment (Suzuki *et al*., 1981). A genotype x environment interaction is a change in the relative performance of two or more genotypes tested in two or more environments. Interactions may involve change in rank order for genotypes between environments and change in the absolute and relative magnitude of the genetic, environmental and phenotypic variances between environments (Bowman, 1972). In general, genotype by environment interactions happen when two or more genotypes perform differently in several environments, and are selected as differential genotypic sensitivities to environments (Sarah and Maria, 2011) and GXEs are also considered as a challenge to crop improvement in a target region (Kang, 1998).

The genotype by environment interaction and yield stability have been challenges to the breeders and biometricians for many years. A significant genotype by environment interaction is used to diminish the genotype means across environments for choosing and advancing high yielder genotypes to the next stage of selection (Pham and Kang, 1988, Asfaw, 2007). A non-significant genotype by environment interaction simplified the selection because the 'best' genotype in one environment would also be the 'best' genotype for all target environments (Basford and Cooper, 1998, Asfaw, 2007).

The phenotype of an individual is determined by the effects of its genotypes, the environment, and the interaction between the genotype of the individual and the environment (Yan and Tinker; 2005, Abiy and Firew, 2016). The genotype by environment interaction results in non-stable performances between the genotypes across environments. Thus, significant GXE results from the changes in the degree of differences between genotypes in diverse environments or changes in the relative ranking of the performance of the genotypes (Falconer, 1952) and (Fernandez, 1991). According to Baker (1990) and Cornelius *et al.* (1996) GXEs have been categorized in to crossover and non-crossover interactions.

The change in the response of genotypes to different environments is called a crossover interaction when genotype ranks change from one environment to another. A main characteristic of crossover interaction is intersecting genotypes in a graphical illustration. If the genotypes do not intersect, there is no crossover interaction (Kang, 1998). Non-crossover (quantitative) interactions indicate changes in extent of genotype performance, but rank order of genotypes across different environments remains constant.

Genotype x environment interaction is one of the main challenge in the selection of broad adaptation and stable genotypes in most breeding programs. Numerous studies have shown that both environmental and genetic factors are the cause for the interaction, but in some studies the large difference of genotypes or environments has been the real cause of the interaction (Hagos and Fetien, 2011; Mahnaz *et al.*, 2013; Sewagegne *et al.,* 2013).

Domitruk *et al* (2001) showed that the analysis of variance technique is a valuable tool for estimating the presence and magnitude of GXE. In multi-environment trial, the combined analysis of variance is vital for estimating variance components related to different sources of variation, including genotypes, environment and GXE. In multi-environment trial, environment describes 80 % or greater of the total yield variation (Yan and Hunt, 2002; Abiy and Firew, 2016). The environmental factors that are causal to the variances in mean grain yield across various environments and years may include soil types, sowing dates, temperature and amount of rainfall during the crop cycle (Dagnachew *et al.,* 2014; Abiy and Firew, 2016).

Different authors have evaluated their experiment on various crops and as they have stated in a multi environment trial for yield, the total variation of the contribution of environmental sum square takes the largest share Abiy and Firew (2016); Kinde *et al*. (2016); Asfaw (2007, 2008), and Vangge *et al*. (2014) on sorghum genotypes;Hagos and Fetien (2011) on sesame; Sewagegne *et al.* (2013) on rice; Muez *et al*. (2014) on malt barely; Akcuraet *et al*. (2006) on durum wheat; Shrestha *et al.* (2012) on maize; Dagnachew *et al.* (2014) on triticale.

The effects of genotype and environment on sorghum grain were investigated using 15 sorghum genotypes, which were tested during three years (2003–2005) at three different locations (Melkasa, Kobo, and Mieso) to evaluate the effect of GXE on sorghum yield performance in the drought stressed parts of Ethiopia (Asfaw, 2007). This study showed that the effect of environments and genotypes were different and the performance of genotypes in various environments was different. The contribution of genotypes, environments and GXE were 5.9 %, 73.8 % and 20.3 % of the total sum of squares, respectively. The magnitude of the GXE sum of squares was 3.41 times larger than the genotypes, indicating, that there were significant differences in genotype response across environments.

Different authors such as Kinde *et al*. (2016) studied on the effect of genotype and environment on sorghum yield to improve the yield potential and stability of sorghum genotypse. Genotype and environment effect were investigated using 5 sorghum varieties were grown during 2013 at three different locations (Mechara, Mieso and Hawi Gudina) to test the effect of GxE on sorghum yield performance. The contribution of genotype, environment and GxE were 4.53%, 86.89% and 2.28% of the total sum of squares, respectively. The environment where the genotype tested was very diverse, while the genotypes were not diverse due to small total of square of variety. The magnitude of the GxE sum of squares was 2 times smaller than that of genotypes. Genotype and environment effect were evaluated using 25 sorghum genotypes were grown during 2014 at four different locations (Erer, Kobo, Mieso and Shewa Robit) to test the effect of GxE on sorghum yield performance (Abiy and Firew, 2016). The contribution of genotypes, environments and GxE were 6.86 %, 74.19 % and 18.98 % of the total sum of squares. This study showed that the effect of environments and genotypes were different and the performance of genotypes in various environments was different. The magnitude of GXE sum of squares was 2.78 times larger than that of genotypes.

The strategies for crop development for drought resistance include identification and selection of traits that contribute to the well performance of the crop under drought conditions. This allows selective addition of the traits that contribute to drought resistance or tolerance for a specific target environment (Blum, 1983; Rosenow *et al.,* 1983). Taye *et al.* (2008) reported that grain yield is a function of linear additive effects of various yield components, it has always been important to pay close attention to these traits. The relative contribution of the traits may differ also depending upon the environment and crop management conditions where the crop is grown.

In terms of yield, Ludlow and Muchow (1990) reported that late flowering varieties tend to yield higher than early flowering ones. Early flowering varieties mostly produce fewer assimilating organs (i.e., leaf area) which results in less production of assimilates but good to escape late season drought stress (Assar *et al*., 2009). Bakheit (1990) studied 22 sorghum genotypes for drought stress and omitting one irrigation during stages of before flowering period, kernel filling period, and physiological maturity period and reported that moisture stress was reduced grain yield, plant height and panicle weight during flowering stage while 1000 seed weight was during grain filling period.

Drought stress during grain development also shortens the grain filling period, which reduces the final grain size and if the stress is extreme the grain will be small, and shrunken which finally reduce yield (Younesi and Moradi, 2009). Water deficient during grain development frequently interrupts development and results in small grain size (Cruz-Aguado *et al*., 2000). The reduction in grain size is due primarily to a shortening of the grain filling period rather than an inhibition of grain growth rate (Vieira *et al*., 1992).

2.3. Causes of Genotype X Environment Interaction

Genotype x environment interaction is one of the main challenges in the selection of wide adaptation in most breeding programs. The phenotype effect of an individual is determined by the combined effect of the environment, the genotype and the interaction. Several studies have revealed that both environmental and genetic factors are the cause for the interaction, but in some studies have shown that the large difference of genotypes or environments has been the real cause of the interaction (Asfaw, 2007; Hagos and Fetien, 2011; Mahnaz *et al*., 2013; Sewagegne *et al*.2013; Abiy and Firew, 2016; Kinde, 2016).

Environmental effect is the greatest (Asfaw, 2007; Hagos and Fetien, 2011; Mahnaz *et al*., 2013; Sewagegne *et al*., 2013; Abiy and Firew, 2016; Kinde, 2016) but it is challenging to selection. In Ethiopia, the relationship between selection environments and target production environment had been a major problem because many of the selected activities performed by the conventional approach are in on-stations which are good production environments (Temesgen *et al*., 2015). Many statistical approaches consider all of the phenotypic variation (i.e., means across environments), which may be misleading. Genotype by environment interaction is not merely a problem, it is also an opportunity" (Simmonds, 1991). The varietal stability could be challenged not only due to the change in the test environment but also due to change in growing season per environment (Dagnachew *et al*., 2014). Specific adaptations can make the difference between a good variety and a superior variety. Some environmental variations are predictable (soil type, soil fertility, plant density) and others also may be unpredictable (rainfall, temperature, humidity *etc*.,) (Allard and Bradshaw, 1964).

2.4. Concept of Stability

Stability refers to the adaptation or suitability of genotypes to diverse sets of environments and used to select stable genotypes (MOORTHY *et al*., 2012). The term stability is used to characterize a genotype, which shows a relatively consistent yield, independent of change in environmental conditions. Due to this idea, genotypes with a minimal variance for yield across different environments are considered to be stable (Sabaghnia *et al.,* 2006; Abiy and Firew., 2016). Yield stability affected by genotype X environments interaction. The cause of differences between genotypes in their yield stability is the wide occurrence of GXE.

A variety or genotype is considered to be more adaptive or stable if it has a high mean yield but a low degree of fluctuation in yielding ability when grown over diverse environments. Two basic phenotypic stability concepts are distinguished as the biological or static concept, and the agronomic or dynamic concept. The biological concept of stability refers to the constant performance of a genotype over a wide range of environments. According to Becker and Leon (1988), in biological stability, a genotype possesses unchanged performance regardless of variation of the environments, thus, implying that its variance among environments is zero. On the other hand, dynamic stability, also termed as agronomical concept of stability, implies that a stable genotype should always give high yield expected at the level of productivity of the respective environments, which means that a variety with GXE as small as possible (Becker, 1981, cited by Abiy and Firew, 2016).

Becker and Leon (1988) stated that all stability procedures based on quantifying GXE effects belong to the dynamic stability concept. This includes the procedures for partitioning the GXE of Wricke's (1962) ecovalence and Shukla's (1972) stability of variance, procedures using the regression approach such as proposed by Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Perkins and Jinks (1968), as well as non-parametric stability statistics.

Lin *et al.* (1986) identified three concepts of stability: type one concept a stable genotype possesses an unchanged performance regardless of any variation of the environmental conditions. Parameters used for this type of stability are coefficient of variability used by Francis and Kannenburg (1978) for each genotype as a stability parameter and the genotypic variances across environments. Becker and Leon (1988) called this stability a biological concept of stability. Type two stability concepts select a stable genotype, if a genotype has no deviations from the general response to environments and thus permits a predictable response to environments. A regression coefficient by Finlay and Wilkinson (1963) and Shukla (1972) stability variance can be used to measure this type of stability. Becker and Leon (1988) called this stability agronomic concept of stability. Type three stability concept refers to a genotype that has a small mean deviation. Therefore a genotype is considered to be stable if the residual mean square from the regression model on the environmental index is small. Breeding for broad adaptability requires a different interpretation and approach to the stability analysis procedure than breeding for specific adaptability. According to Becker and Leon (1988) this is part of the agronomic stability concept. Methods to describe this type of stability are the methods of Eberhart and Russell (1966) and Perkins and Jinks (1968).

2.5. Methods of Statistical Analysis of G x E Interaction

The statistical analysis of G x E interaction is important in the analysis of experiments in plant breeding and crop production (Kang, 1996, Zerihun T., 2011). Different statistical methods have been used for the estimation and partitioning of G x E interactions. The most common methods are the conventional analysis of variance, stability analysis, multivariate methods and qualitative methods (Freeman, 1990; Zerihun, 2011).

2.5.1. Conventional analysis of variance

In an experiment the yield of genotypes (G) is measured in environments (E) and each with replicates (R), the classic model for analyzing the total yield variation contained in GXE observations is the analysis of variance (Fisher R.A, 1925; Alberts, 2004). The residual mean square within environment measures the error in estimating the genotype. After removing the replicate effect when combining the data, the GXE observations are partitioned into two sources: (a) additive main effect for genotypes and environments and (b) non-additive effects due to GXE interaction. The analysis of variance of the combined data expresses the observed (Yij) mean yield of the ith genotype at the jth environment as;

$$Yij = \mu + Gi + Ej + (GXE)ij + eijk$$

Where, μ is the general mean; Gi, Ej and GXEij represent the effect of the genotype, environment, and G x E interaction, respectively; and eij is the average of the random errors associated with the kth plot that receives the ith genotype in the jth environment.

The non-additivity interaction (GXEij) implies that the expected value of the ith genotype in the jth environment (Yij) depends not only on the levels of G and E separately but also on the particular combination of levels of G and E (Crossa, 1990, Zerihun, 2011). The major problem in ANOVA is that the error variances over environments should be homogenous to test for genotypic differences.

2.5.2. Spatial and linear mixed model

In evaluation of sorghum trials in Mali, (Leiser *et al*., 2012, Sarker and Singh, 2015) concluded that spatial models add further value to experiment over the classical complete block design model. Plant breeders evaluate much larger number of genotypes, e.g. 70 genotypes of sorghum in trials in Mali evaluated by Leiser *et al*. (2012). In such situations, a row–column design with most suitably identified spatial model would be expected to result in even further higher efficiency, heritability and genetic gain over the conventional complete block designs.

There is a need to identify sources of variation to fit an appropriate model to data set. This is due to spatial analysis taking into account variations that result from plot or row and column location in field experiment data. Spatial variation modeling is particularly important at the early stages of selection when there are many varieties grown in few locations with few replicates. When modeling spatial variation, the error variation is broken up. Local trends are modeled using a covariance structure while global and extraneous variation is modeled using design factors and functions of the co-ordinates of the plots. The model for spatial analysis is the same as the linear mixed model and is proposed by Gilmour et al. (1997).

$$y = X\tau + Zu + e$$

Where y is the observed outcomes, τ is the fixed effects (over all mean and genotype effects) and u is the random effects (replication, row and column effects). X is the design matrix associated with the fixed effects, Z is the design matrix associated with the random effects and e is the residual.

The linear mixed model is an expansion of the classical linear model and so its basic properties may be applied to the analysis of mixed models. The difference of the mixed model, compared to the linear model presented is that the mixed model assumes that some effects are random variable such as replicate, row and column etc., termed as random effects. In the linear model only the residual terms are considered as random.

The mixed model is essential in the analysis of plant genotype selection data. Growing areas for crops differ greatly in location and season; therefore it is important to consider that not all genotypes prosper to the same level in different environments (GXE). The advantage of the linear mixed model approach is that it can handle unbalanced data, and can easily be extended to include complex covariance structures between trials and genotypes. Genotype effects made be considered as fixed or random, but GXE interactions are always regarded as random. Regarding genotype effects as random allows for more reliable predictions of the genotypes performance and addresses issues of selection bias. The linear mixed model and spatial model (Gilmour *et al*. 1997) are similar.

Multi-environment trial; a trial carried out at a series of different locations, perhaps one or over several years. Multi-environment trials are the typical experimental design for comparing multiple test new genotypes of a crop against existing genotype or standard for beneficial properties such as increased yield and drought tolerant. This is done to make recommendations on which varieties are to be identified and selected for a consistent performance of optimum yield in a diverse range of environments. Thus genotype by environment interaction is a crucial factor in selection programs and hence why MET's are the common design adopted when making variety recommendations.

There are several stages of testing and selection in the breeding of a new variety for improved yield. Selections are based on analysis of yield data, with minimal possible error to ensure accuracy in future grain yield predictions for new varieties. Multi-environment trial analysis is consisted of two stages; initially the mean yield for genotypes are estimated for the individual locations, followed by a combined overall analysis of genotype performance across all trials (Cullis et al, 1998). Both cases can be analyzed by linear mixed models, usually fitted using residual maximum likelihood (REML) estimation. The advanced Multi-environment trial analysis methods involve spatial modeling of the MET data. These models include genotype (G) and environment (E) effects as well as GXE. The effects G and GXE are regarded as random and assumed independent with constant variance. This constant variance assumption indicates that all environments have the same genetic variance which is unlikely to be true (Cullis. *et al*., 2006). A general mixed model for MET analysis is defined as:

$$y = X\tau + Z_g u_g + Z_p u_p + e$$

Where, Y is the combined individual plot yields across trials, τ is the fixed effects including an overall mean for each of the sites as well as other trial-specic fixed effects, with corresponding design matrix X, u_g are the variety effects in each environment with associated design matrix Z_g, u_p is the extraneous trend effects in each environment (for example, rows and columns) with corresponding design matrix Zp, e is the residual errors across all trials

2.5.3. Estimation of stability parameters

Stability analysis provides a summary of response of genotypes to environmental changes. To identify stable genotypes, the G x E interaction must be divided into stability statistics that are assigned to each genotype evaluated across environments. Stability indices have allowed researchers to identify widely adapted genotypes for use in breeding (Yayeh and Bosland, 2000).

2.5.3.1. Regression coefficient (bi) and deviation mean square (S^2di)

Joint regression analysis or joint linear regression is the main type of stability analysis and it is the regression of the genotypes means on environmental index (Freeman, 1973). Joint regression analysis provides testing whether the genotypes linear responses to changes in environments. Joint regression analysis was first proposed by Yates and Cochran (1938) and then widely used and reviewed by various authors (Alberts, 2004).

Eberhart and Russell (1966) method involves the use of joint linear regression where the yield of each genotype is regressed on the environmental mean yield. In this model the SS due to environments and GXE are partitioned into environments (genotypear), GXE (linear) and deviations from regression (pooled deviation over all the genotypes). The genotype regressions term was tested for significance using an F-ratio by taking the deviations from regressions mean square as the error term. The deviations from regressions mean square were tested for significance using the error term for overall GXE in the ANOVA.

Simple linear regression provides a model for genotypic stability and is the most widely used statistical technique in plant breeding (Ramagosa and Fox, 1993). This model is also called the Finlay and Wilkinson (1963) approach. During regression analysis the G x E interaction is partitioned into two: i) a component due to linear regression (bi) of the ith genotype on the environment mean and ii) a deviation (dij):

$$(GE)ij = biEj + S^2di \quad \text{and thus,}$$

$$Yij = \mu + Gi + Ej + (biEj + S^2di) + eij$$

Different authors used different bi values to define genotype stability. Finlay and Wilkinson (1963) defined a genotype with bi = 0 as stable (static concept) and Eberhart and Russell (1966) defined a genotype with bi = 1 as stable (dynamic concept). Becker and Leon (1988) suggested that ecovalence rather be used, since it combines bi and S^2di as a stability parameter. Many scientists consider bi as a response parameter and S^2di as a stability parameter.

Many Authors such as Abiy (2016) on sorghum, Parmar D.J et al (2016) on rice ; P. O. Kurt Polat (2016) on bread wheat; Dagnachew Lule (2014) on Triticale, conducted their trial experiment on yield stability and identified four, five, three, three stable and high yielder genotypes using Eberhart and Russel joint regression model, respectively.

2.5.3.2. Ecovalence (Wi)

Wricke (1964) defined the concept of ecovalence as the contribution of each genotype to the G x E interaction sum of squares. The ecovalence (Wi) or stability of the i^{th} genotype is its interaction with the environments squared and summed across environments. For this reason, genotypes with a low Wi value have smaller deviations from the mean across environments and are thus more stable. It is express as:

$$W_i = \sum_j \left(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..}\right)^2$$

Where, Yij is the mean performance of genotype i in the jth environment and $\overline{Y}i.$ and $\overline{Y}.j$ are the genotype and environment mean deviations respectively, and Y is the overall mean.

According to Becker and Leon (1988), ecovalence measures the contribution of a genotype to the G x E interaction; a genotype with zero ecovalence is regarded as stable. Genotypes with, an average, small residues are preferred because they show variability that is more predictable. The ecovalence, however, strongly depends on the environments included in the test and may lead to different ranking orders of genotypes.

2.5.4. Multivariate analysis methods

According to Crossa (1990), multivariate analysis has three main purposes: a) to eliminate noise from the data pattern (i.e., to distinguish systematic from non-systematic variation); b) to summarize the data; and c) to reveal a structure in the data. In contrast with classic statistical methods, the function of multivariate analysis is to elucidate the internal structure of the data from which hypotheses can be generated and later tested by statistical methods (Gauch, 1982a; Gauch, 1982b).

2.5.4.1. Additive main effects and multiplicative interaction (AMMI)

AMMI model has been used for statistical analysis of yield trials, and the best as compared to other statistical analysis such as ANOVA, principal component analysis and linear regression analysis (Gauch and Zobel, 1988, Zerihun T., 2011) because it combines the analysis of variance for the genotype and environment main effects with principal components analysis of the G x E interaction and several graphically represented interactions for principal component axis (IPCA) (Crossa *et al.*, 1990). AMMI is also used for predicting genotypic yields in specific environments (Annicchiarico, 1997) and summarizing the pattern and relationship of genotypes, environment and their interaction (Gauch and Zobel, 1988).

2.5.4.2. GGE Biplot Model

GGE biplot provides breeders with a complete and visual estimation of all features of the data by forming a biplot that simultaneously represents both mean performance and stability, optimized environments for specific genotypes and identifies mega-environments. GGE analysis partitions G + GE into principal components through singular value decomposition of environmentally centered yield data (Yan, 2001).

Different authors have been conducted multi-environment trials or GXE on different crops using GGE biplot such as Abay and Bjornstad (2009); Dehghani et al. (2006); Tesfaye et al. (2008) and Gasura et al. (2015) in their finding reported the existence of a good testing environment for selecting widely adaptable and high yielding cultivar.

3. MATERIALS AND METHODS

3.1 Description of the Study Area

The field experiment was conducted during the 2017 main cropping season at five locations (Sheraro, Kobo, Mieso, Shaorobit and Erer), representing the dry lowland areas of Ethiopia located in the altitude range of 1297 - 1513 m.a.s.l, where sorghum is widely grown. The detailed agro-ecological features of the locations are presented in Table 1.

Table 1: Agro-ecological features of the experimental locations.

Location	Longitude	Latitude	Altitude in m.a.s.l	Soil type	Rainfall in mm	Minimum T^o	Maximum T^o
Mieso	39°21´E	8°30´N	1470	vertisol	571.9	16.0	31.5
Erer	42° 15’E	9° 10’	1297	vertisol	510.0	15.5	31.1
Shoarobit	39° 93’E	10° 35’ N	1500	vertisol	713.0	17.7	32.6
Kobo	39°38’ E	12°09’N	1513	vertisol	677.8	14.8	32.1
Sheraro	38°9’ E	14°6’ N	1179	vertisol	615.0	20.4	33.7

Source: National Metrology data of 2017 main cropping season, m.a.s.l = meters above sea level, T^o = Temperature.

3.2. Genetic Materials

Planting materials used for the experiment comprised of fifty nine early maturing advanced sorghum genotypes, which were advanced from pedigree breeding at Melkassa Agricultural Research Center and one sorghum variety melkam (released from Melkassa Agricultural Research Center for low moisture stress areas of the Ethiopian lowlands in 2009) as a standard check. Originally, the parental genotypes were developed from germplasm collection and characterization and were crossed for grain yield and early maturity at Melkassa Agricultural Research Center, then genotypes were evaluated, and advanced to F6 stage through pedigree selection at Erer, Mieso, Shorobit, Kobo and Sheraro by the Ethiopian national sorghum breeding program. The selected genotypes were advanced to preliminary yield trial (the F7 stage) and tested for one year across five locations, then the best and superior genotypes with early type were selected and advanced to early maturing sorghum national variety trial in five locations, where represent the dry low land areas of Ethiopia (MARC unpublished Sorghum field book and manual).

Table 2: Description of sorghum genotypes tested at five locations during 2017 main cropping season

Entry#.	Genotype	Pedigree	Seed source	Status
1	Melkam	WSV 387	2016MS Breeder Seed Inc.	Standard check
2	14MWLSDT7060	Macia/76T1#23	2017MW Seed increase#2	Advanced genotype
3	12MW6251	WSV 387/76T1#23	2017MW Seed increase#3	Advanced genotype
4	14MWLSDT7410	ICSR24010/B-35	2017MW Seed increase#4	Advanced genotype
5	12MW6302	WSV 387/76T1#23	2017MW Seed increase#5	Advanced genotype
6	14MWLSDT7322	SDSL2690-2/76T1#23	2017MW Seed increase#6	Advanced genotype
7	14MWLSDT7395	MR812/76T1#23	2017MW Seed increase#7	Advanced genotype
8	14MWLSDT7400	WSV387/76T1#23	2017MW Seed increase#8	Advanced genotype
9	14MWLSDT7310	Teshale/B-35	2017MW Seed increase#9	Advanced genotype
10	13MWF6#6077	ICSR 24010/Brihan	2017MW Seed increase#10	Advanced genotype
11	14MWLSDT7325	SDSL2690-2/76T1#23	2017MW Seed increase#11	Advanced genotype
12	2005MI5069	M36121/P9402	2017MW Seed increase#12	Advanced genotype
13	14MWLSDT7196	WSV387/76T1#23	2017MW Seed increase#13	Advanced genotype
14	14MWLSDT7311	Teshale/B-35	2017MW Seed increase#14	Advanced genotype
15	14MWLSDT7157	WSV387/E-36-1	2017MW Seed increase#15	Advanced genotype
16	14MWLSDT7193	WSV387/E-36-1	2017MW Seed increase#16	Advanced genotype
17	14MWLSDT7332	SDSL2690-2/76T1#23	2017MW Seed increase#17	Advanced genotype
18	14MWLSDT7115	ICSR24010/B_35	2017MW Seed increase#18	Advanced genotype
19	14MWLSDT7176	WSV387/E-36-1	2017MW Seed increase#19	Advanced genotype

20	14MWLSDT7209	WSV387/76T1#23	2017MW Seed increase#20	Advanced genotype
21	12MW6440	LocalBulk(White)/SRN-39/76T1#23	2017MW Seed increase#21	Advanced genotype
22	14MWLSDT7201	WSV387/76T1#23	2017MW Seed increase#22	Advanced genotype
23	12MW6146	WSV 387/E-36-1	2017MW Seed increase#23	Advanced genotype
24	14MWLSDT7364	2005MI5060/B-35	2017MW Seed increase#24	Advanced genotype
25	Pipline 2	(Teshale/E-36-1)BC3F3	2017MW Seed increase#25	Advanced genotype
26	14MWLSDT7413	WSV387/E-36-1	2017MW Seed increase#26	Advanced genotype
27	13MWF6#6037	2001 MS 7007/SRN-39	2017MW Seed increase#27	Advanced genotype
28	14MWLSDT7207	WSV387/76T1#23	2017MW Seed increase#28	Advanced genotype
29	14MWLSDT7040	WSV387/76T1#23	2017MW Seed increase#29	Advanced genotype
30	14MWLSDT7036	WSV387/76T1#23	2017MW Seed increase#30	Advanced genotype
31	14MWLSDT7324	SDSL2690-2/76T1#23	2017MW Seed increase#31	Advanced genotype
32	12MW6243	WSV 387/76T1#23	2017MW Seed increase#32	Advanced genotype
33	12MW6420	LocalBulk(White)/SRN-39/E36-1	2017MW Seed increase#33	Advanced genotype
34	14MWLSDT7238	Macia/E-36-1	2017MW Seed increase#34	Advanced genotype
35	12MW6444	LocalBulk(White)/SRN-39/76T1#23	2017MW Seed increase#35	Advanced genotype
36	14MWLSDT7402	WSV387/76T1#23	2017MW Seed increase#36	Advanced genotype
37	14MWLSDT7234	Macia/E-36-1	2017MW Seed increase#37	Advanced genotype
38	12MW6471	IESV92084/E36-1	2017MW Seed increase#38	Advanced genotype
39	14MWLSDT7042	WSV387/76T1#23	2017MW Seed increase#39	Advanced genotype
40	14MWLSDT7033	WSV387/76T1#23	2017MW Seed increase#40	Advanced genotype

41	14MWLSDT7241	Macia/E-36-1	2017MW Seed increase#41	Advanced genotype
42	14MWLSDT7191	WSV387/E-36-1	2017MW Seed increase#42	Advanced genotype
43	2005MI5093	PGRCE22880/P9403	2017MW Seed increase#43	Advanced genotype
44	2401	(S35/B35)/S35	2017MW Seed increase#44	Advanced genotype
45	2004MW6197	SDSL-2690-2/SAR-39	2017MW Seed increase#45	Advanced genotype
46	2005MI5064	WSV387/P9403	2017MW Seed increase#46	Advanced genotype
47	2523	(ICSV111/B35)/ICSV111	2017MW Seed increase#47	Advanced genotype
48	04MW 6043	WSV387/Dabar	2017MW Seed increase#48	Advanced genotype
49	2005MI5057	WSV387/P9401	2017MW Seed increase#49	Advanced genotype
50	04MW 6079	SDSL2690-2/Dabar	2017MW Seed increase#50	Advanced genotype
51	14MWLSDT7202	WSV387/76T123	2017MW Seed increase#51	Advanced genotype
52	14MWLSDT7291	Macia/76T123	2017MW Seed increase#52	Advanced genotype
53	2001MS7036	PGRCE222878/ICSV708	2017MW Seed increase#53	Advanced genotype
54	90MW5319	85LPYT-224/(148/Framida)	2017MW Seed increase#57	Advanced genotype
55	99MW4047	((148/E-35-1)-4/CS3541derive5-4-2-1)/P9401	2017MW Seed increase#55	Advanced genotype
56	05MW6026	M36121/P9401	2017MW Seed increase#56	Advanced genotype
57	14MWLSDT7421	Macia/76T123	2017MW Seed increase#58	Advanced genotype
58	2003MW6053	ICSV112BF/SRN-39	2017MW Seed increase#59	Advanced genotype
59	2294	(S35/B35)/S35	2017MW Seed increase#60	Advanced genotype
60	2003MW6038	ICSV111/SRN-39	2017MW Seed increase#61	Advanced genotype

3.3. Experimental Design

The trial was conducted using RCBD with row column arrangement and three replications. The experimental plot consisted of 2 rows, each 5m in length with 0.75m between row spacing and 0.15m between plants. The total area of each plot had a size of 7.5m^2.

3.4. Trial Management

As per the recommendation for sorghum prduction in the lowland areas of Ethiopia, Di-ammonium phosphate (DAP) and urea were applied at the rate of 100 kg/ha and 50 kg/ha, respectively. Di-ammonium phosphate was applied by incorporating into the soil during planting of the seeds and Urea was applied as side dressing at knee height stage (35 days) after planting of the seed. Thinning was done after three weeks of planting to maintain the space between plants and to balance the plant density. Other crop management practices were applied following the recommended practices.

3.5. Data Collection and Sampling Techniques

Data were collected from the two rows for plot based data and five randomly sampled plants for Plant based data following the descriptors for sorghum (IBPGR/ICRISAT, 1993). The details of the data collection were as follow:

Days to emergency: the number of days from planting to when 50% of plants started emergency.

Days to flowering: the number of days from emergence to when 50% of plants started flowering.

Days to maturity: the number of days from planting to the date when 95% of the plants matured physiologically.

Plant height (cm): Plant height was measured from five randomly sampled main plants from the two rows at 75 % physiological maturity. The average height from the five plants was then recorded for the plot.

Panicle length (cm): the average length of five randomly selected plants from the base of the panicle to the tip was measured.

Panicle width: the average width of individual panicle as measured panicle width measurement in the widest diameter of the panicle on five randomly selected plants per plot at maturity.

Panicle weight (g): the total weight of panicles per plot after harvest was measured.

Number of panicle: the total number of panicles per plot during harvest was counted.

Panicle yield (g): the yield was obtained by threshing the total number of panicles per plot during harvest.

Grain filling rate (kg/ha/day): it is the ratio of grain yield (kg/ha) to grain filling period and calculated as follows:

$$\text{Grain filling rate (kg/ha/days)} = \frac{\text{Grain yield (kg/ha)}}{\text{Grain filling period (days)}}$$

Thousand seed weight (TSW): Weight of 1000 seeds in gram that was measured from each plot after the moisture level adjusted to 10%.

Drought score: tolerance to moisture deficit and scored as 1-5, 1= more tolerant, 2= mild drought tolerant, 3= moderate tolerant, 4= severe drought and 5= extreme drought.

Staygreen: level of greenness scored 1-5 after maturity, 1 indicates completely green normal size leaves (no leaf death), 2 = 25% of the leaves died, 3 =26 to 50% of the leaves died, 4 =51 to 75% are dead, 5 =76 to 100% of the leaves and stem are dead (complete plant death).

Panicle exersion: Score (1=well exserted more than 10cm between ligule of flag leaf to head base, 2=2-10cm exsertion, 3=less than 2cm but ligule below the head base, 4=peduncle recurved but head is below the ligule and clearly exposed splitting the leaf sheath, 5=head covered by leaf sheath).

3.6. Data Analysis

R software using spatial analysis and mixed model (Culllis *et al.* 1998, Gilmour *et al.* 1997) were used to analyze all the collected data from individual location and combined data over locations.

3.6.1. Analysis of data for each location and combined over location

Using the raw data collected on fifteen characters of sixty genotypes, which were grown at five locations, analysis of data using spatial and linear mixed and model of RCBD with row column arrangement was computed. Before pooling the data over locations, Bartlett's test of homogeneity of variance was adopted for most of the traits to determine the validity of the overall mixed analysis of the data of combined locations. This analysis revealed the homogeneity of error variance. Therefore, overall mixed analysis was done to determine the effects of the genotypes, locations and their first order interactions using mixed model. Genotypes were assumed to be fixed and environment effects random. Least significance difference was used to determine the significance of differences among the genotype means for each character. The model for spatial analysis is the same as the linear mixed model and is proposed by Gilmour et al. (1997).

$$y = X\tau + Zu + e$$

Where y is the observed outcomes, τ is the fixed effects (over all mean and genotype) and u is the random effects (replication, row and column effects). X is the design matrix associated with the fixed effects, Z is the design matrix associated with the random effects and e is the residual.

3.7. Stability Analysis

The following four analysis of the stability models were performed for grain yield (kg/ha) using R software.

3.7.1. Eberhart and Russell's joint regression model

Eberhart and Russell (1966) method involves the use of joint linear regression where the yield of each genotype is regressed on the environmental index. The behavior of the genotype was determined by the model: $Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$ using R Software.

Where: Y_{ij} = the mean performance of the i^th^ genotype in the j^th^ environment, μ_i = the grand mean of the i^th^ genotype over all the environments, β_i = the regression coefficient which measures the response of the i^th^ genotype on environmental index, I_j = the environmental index obtained by the difference between the mean of each environment and the grand mean and δ_{ij} = the deviation from regression of i^th^variety in the j^th^ environment.

The pooled deviations mean square was tested against the pooled error mean square by the F-test to evaluate the significance of the differences among the deviations of genotypes being evaluated from their expected performances. Therefore, to test the validity of the hypothesis that whether there is significant difference among the 60 genotypes with respect to their mean grain yields or not and whether there is significant difference among the regression coefficient or not, genotypes mean square and regression mean square were tested against the pooled deviation using the F-test.

3.7.2. The additive main effects and multiplicative interaction (AMMI) method

Additive main effects and multiplicative interaction (AMMI) model was performed for the mean data of grain yield (ton/ha) from each location using R software. The AMMI model equation is given as:

$$Y_{ij} = \mu + \alpha_i + ß_j + \sum_{n=0}^{N} \lambda_n \gamma_{in} \delta_{jn} + \theta_{ij} + \varepsilon_{ij}$$

Where:Y_{ij} = the mean yield of genotype i in environment j, μ = the grand mean, α_i = the deviation of the genotype mean from the grand mean, β_j= the deviation of the environment mean from the grand mean, λ_n= the singular value for the IPCA n, N = the number of PCA axis retained in the model, γ_{in} = the PCA score of a genotype for PCA axis n,δ_{jn} = the environmental PCA score for PCA axis n, θ_{ij} = the AMMI residual and E_{ij}= the residuals.

The degrees of freedom (DF) for the IPCA axis were calculated based on the following method (Zobel *et al.,* 1988). DF = G + E – 1 – 2n; Where: G = the number of genotypes, E = the number of environments and n = the n^{th} axis of IPCA.

3.7.3. GGE Biplot Method

Genotype by environment interaction analysis was done by GGE biplot, which uses singular value decomposition (SVD) to decompose GGE into two or more principal components. Each principal component consisted of a set of genotype scores multiplied by a set of environment scores, to generate a two-dimensional biplot (Ding *et al*., 2007). In GGE biplots genotype plus genotype × environment (G + GE) interaction was studied together and to achieve this G + GE effect is separated out from the observed mean from Equation (1) (by omitting random error and block effect) and eventually model becomes as ij j i ij Y μ β =α +αβ (2) The GGE (G + GE) effect was partitioned into multiplicative terms using SVD. The model based on singular value decomposition (SVD) of first two principal components (Ding *et al*., 2007) is:

$$Yij - \mu - \beta j = \lambda i\xi i1\eta 1j + \lambda 2\xi i2\eta 2i + \xi ij$$

Where λ1 and λ2 are the singular values of the first and second largest principal components, PC1 and PC2, respectively; ξ1 and ξ2 are the eigenvectors of genotype I for PC1 and PC2, respectively, and η1 and η2 are the eigenvectors of environment j for PC1 and PC2, respectively.

3.7.4. AMMI's stability value (ASV)

In order to compute and rank genotypes according to their yield stability, the additive main effect and multiplicative interaction effect stability value (ASV) was proposed by Purchase (1997). It was calculated using Microsoft excel (2007) by employing the following formula:

$ASV = \frac{\sqrt{[IPCA1\ sumofsquares(IPCA1\ score)]^2}}{IPCA2\ sumofsquare} + (IPCA2\ score)^2$, Where: ASV = AMMI's stability value, IPCA1= interaction principal component analysis one, and IPCA 2= interaction principal component analysis II.

4. RESULTS AND DISCUSSION

4.1. Data analysis of variance

4.1.1 Single Location data analysis

The heat map/plot map revealed the spatial trends within a field, which is a source of error that could potentially bias the estimation of genotype effects (Figure 1). Figure 1 showed areas of high, average and low yield and that neighboring plots tend to be more similar than plots a greater distance apart. In other words, plots located close to each other are more likely to have similar yields than distance apart (Gilmour *et al*., 1997). This correlation between plots can be used to adjust for trend reducing error. Spatial models [ar1 (row), id (col), id (row)] are used to adjust spatial variability within a field to each location (Gleeson and Cullis, 1987; Gilmour *et al*., 1997). These models were fitted to the dataset, while the model ar1 (column) was not fitted to dataset that is not significantly different in the column direction due to this reason it was rejected.

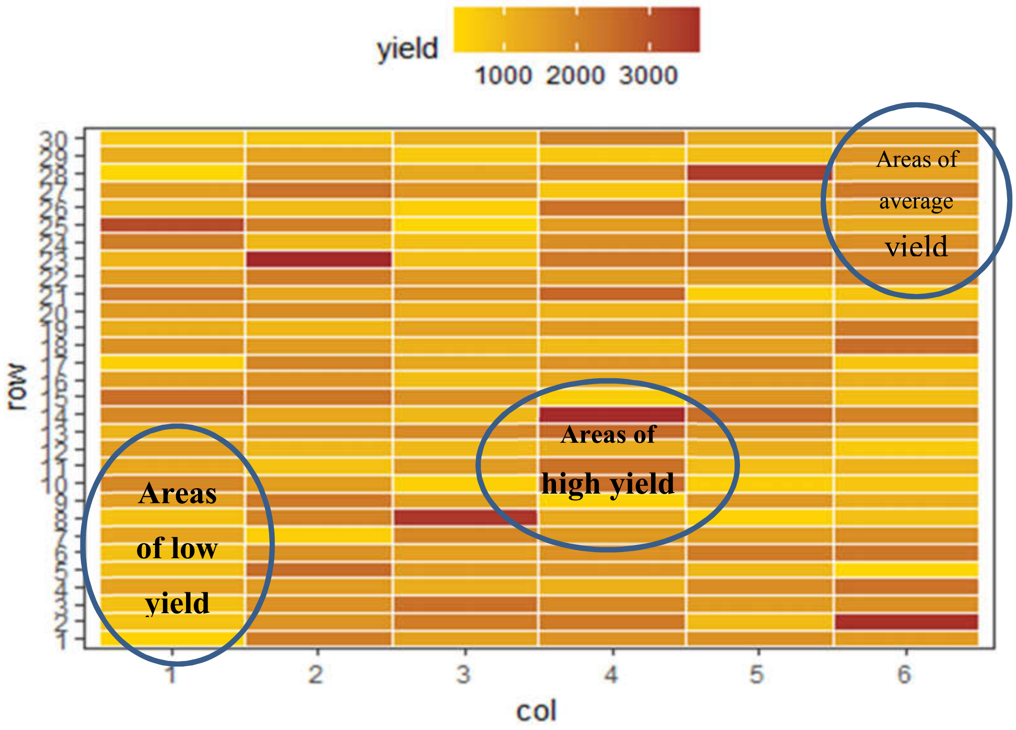


Figure 1: Heat map of spatial trend within a field of sixty early maturing sorghum genotypes on plot grain yield performance tested at Erer during 2017 cropping season.

The separate REML analysis of the six characters (days of flowering, days of maturity, plant height, grain filling period, grain filling rate, grain yield, plant height, panicle weight and thousand seed weight) for sixty early maturing sorghum genotypes is presented in Table 3. The result of spatial analysis which is the variance component for grain yield at each site revealed highly significant difference between genotypes (Table 3). This showed that at each location there were genetic diversity among genotypes for grain yield.

Genotypes were significantly different for days to flowering at each location (Table 3). This shows the observed numbers of days that genotypes spent to flower were statistically different at all locations. Genotypes were significant for days to maturity at Sheraro, Shaorobit, and Mieso (Table 3). This finding is in contrast to Abiy and Firew (2016) who indicated that genotypes were not significantly different for days to maturity at Shaorobit and Mieso, indicating the number of days that genotypes took to mature were similar. However, genotypes were not-significantly different for days to maturity at Erer and Kobo; show no genotypic effect for days to maturity.

Genotypes were significantly different at Shaorobit, Erer, Kobo and Mieso but non-significant for grain filling period at Sheraro. This showed that genotypes took different period to fill their grain at all locations except at Sheraro. Genotypes were significantly different for plant height, grain filling rate and 1000 seed weight at all locations. This indicates the performance of genotypes for plant height and grain filling rate are different in all locations.

Table 3: Variance component estimation by REML and spatial model of early maturing sorghum genotypes for grain yield, phenological and other major traits tested at Erer, Kobo, Mieso, Sheraro and Shewa Robit during 2017 main cropping season.

Site	Variance Component	Traits							
		DF	DTF	DTM	GFP	GFR	GY	PHT	TSW
SR	Genotype	59	14***	0.81**	9.92***	501.9***	520310*	1117***	10.4***
	Replicate	2	0.56ns	0.15ns	1.16ns	14.7ns	0.0042*	0.0001ns	0.001ns
	Error	118	5.87	1.18	6.39	96.34	41394.7	37.3	2.8
ER	Genotype	59	10.4***	0.55ns	15.4**	476***	449593*	411***	9.1***
	Replicate	2	0.001ns	2.14ns	2.68ns	5.62ns	0.00127*	0.002ns	0.1ns
	Error	118	10.5	18.9	26.8	77.89	12562.1	31.2	3.1
MS	Genotype	59	5.8**	2.16*	3*	114.5***	130520*	482***	13.39***
	Replicate	2	1.19ns	1.75ns	0.0001ns	0.11ns	0.0015*	0.001ns	0.006ns
	Error	118	9.32	9.41	7.14	14.41	14606.5	21.7	2.12
KB	Genotype	59	18.1***	2.13ns	15.8**	209***	688377*	732***	13.09***
	Replicate	2	0.43ns	0.001ns	0.84ns	1.01ns	941.948ns	0.001ns	0.04ns
	Error	118	12.8	12.1	20.1	32.64	55189.6	51	2.83
SH	Genotype	59	12.35***	6.52***	6.33ns	317.4***	244754*	735***	11.54***
	Replicate	2	0.0003ns	0.0001ns	0.001ns	0.000012ns	0.0006*	0.55ns	0.0023ns
	Error	118	1.78	6.83	35.4	179.9	57574.5	68	2.1

Where REML = Residual Maximum Likelihood, DF = Degree of Freedom, DTF = Days to flowering, DTM = Days to maturity, GY = Grain yield, PHT = Plant height, GFP = Grain filling period, GFR = Grain filling rate, TSW = 1000 seed weight, SR = Shaorobit, ER = Erer, MS = Mieso, KB = Kobo, SH = Sheraro, *** = vary highly significant (P≤ 0.0001), ** = highly significant (P≤ 0.001), * = significant (P≤0.05) and ^{ns} = insignificant (P>0.05).

4.1.2. Combined analysis of data

The combined variance component estimation by REML of the six characters (days of flowering, days of maturity, plant height, grain filling period, grain filling rate, grain yield, plant height, panicle weight and thousand seed weight) for sixty early maturing sorghum genotypes is presented in Table 4.

The result showed that there were highly significant ($P \leq 0.0001$) differences among locations, and differences among the genotypes were significant ($P \leq 0.05$) for grain yield. This indicates that the high diversity of the growing conditions in the five locations and the small variability in the genotypes for grain yield performance. Significant effect of location on yield of sorghum varieties was reported by Asfaw (2007); Maposa *et al*. (2010); Almeida *et al*. (2014); Abiy and Firew (2016); Lyle *et al*.(2016). Furthermore, the GxE was also very highly significant ($p \leq 0.0001$), showing inconsistencies in the performance of sorghum genotypes across locations which shows difference in the response of sorghum genotypes at different environments. This outcome is in agreement with the findings of Kenga *et al.* (2003); Asfaw (2007); Almeida *et al*. (2014); Abiy and Firew (2016);.

The result of the combined variance components showed that the total variation in yield was attributed to location (86.4 %), genotype (1.9 %) and GxE (10.9 %) effects (Table 4). The largest proportion of the variance showed on grain yield performance was due to locations than other variances. Therefore, high percentage of the location component of variation is an indication that environment is the major factor that affect grain yield performance of sorghum genotypes in the dry lowlands areas of Ethiopia. Similar results of large location effects were also reported by Akcuraet *et al*. (2006); Asfaw (2007, 2008); Hagos and Fetien (2011); Shrestha *et al.* (2012); Sewagegne *et al.* (2013); Muez *et al*. (2014); Dagnachew *et al.* (2014); Vangge *et al*. (2014); Abiy and Firew (2016); Kinde *et al*. (2016);. The variance component due to GxE was 5.74 times higher than that of the genotypes. The highest magnitude of the interaction as compared to the genotype component revealed that the grain yield performance of sorghum genotypes across locations was different (Asfaw, 2007; Abiy and Firew, 2016), indicating inconsistencies in the performances of sorghum genotypes across environments. A significant GxE may be either a non-cross-over or cross-over type (Baker, 1990; Cornelius *et* *al.,* 1996). In the current study, the interaction was of cross-over type as the ranking of genotypes for grain yield changed at every location.

Significant differences among genotypes were found for days of flowering (P≤ 0.0001), grain filling period (P≤0.0001), grain filling rate (P≤0.05), plant height (P≤0.0001), date of maturity(P<0.05) and 1000 seed weight (P≤ 0.0001). These indicates the presence of the effect of genetic differences for these traits. Differences among locations were non-significant (P>0.05) for these traits except grain yield, indicating the absence of variation among locations for these traits which are independent of location effect in contrast to Asfaw (2007); Abiy and Firew (2016); Kinde (2016) who indicated that the large presence of variation among locations had high effect for these traits. Genotype by environment were significant for days of flowering (P≤ 0.001), grain filling period (P≤ 0.001), days to maturity (P≤ 0.001), grain filling rate (P≤ 0.0001), plant height (P≤ 0.0001) and 1000 seed weight (P≤ 0.0001) (Table 4). The highest magnitude of the interaction revealed inconsistencies of the performance of sorghum genotypes for these traits across locations were different.

Table 4: Variance component estimation by REML of early maturing sorghum genotypes for grain yield, phenological and other major traits tested at five locations during 2017 main cropping season.

Traits	Estimate				Error (DF = 590)
	Genotype (DF = 59)	Replicate/Site (DF = 10)	Site (DF = 4)	Genotype:Site (DF = 236)	
GY	61140*	76.11ns	2743000***	346000***	25870
DTF	10.48***	0.08ns	23.15ns	1.49**	8.41
DTM	0.55*	0.54ns	53.95ns	1.8**	9.95
GFP	6.61***	0.46ns	73.55ns	3.31**	19.62
GFR	65.51*	2.07ns	2098.39ns	256.85***	82.54
PHT	491.94***	0.01ns	1138.56ns	203.7***	41.91
GY	61140*	76.11ns	2743000***	346000***	25870
TSW	4.25***	0.02ns	7.03ns	7.24***	2.61

Where REML = Restricted Maximum Likelihood, DTF = Days to flowering, DTM = Days to maturity, GY = Grain yield, PHT = Plant height, GFP = Grain filling period, GFR = Grain filling rate, TSW = 1000 seed weight, *** = vary highly significant (P≤ 0.0001), ** = highly significant (P≤ 0.001), * = significant (P≤0.05) and ^{ns} = insignificant (P>0.05).

4.2. General and relative performance of the genotype

Means for grain yield, phenolgical and other major traits of sixty early maturing advanced sorghum genotypes at Erer, Kobo, Mieso, Sheraro and Shewa Robit is presented in Table 5. Shaorobit and Sheraro were the highest yielding environments with mean values of 5174.0 kg/ha and 3706.7 kg/ha, respectively, indicating that the two environments are suitable for sorghum production, whereas Mieso, Erer and Kobo were the poorest yielding environments with mean grain yields of 1099.0 kg/ha, 1508.5 kg/ha and 2832.1 kg/ha, respectively (Table 5), revealing that these environments were not favorable for sorghum production. Therefore, Mieso and Erer were found to be the lowest yielding environment as compared to other environments. This is mainly attributed to the high drought observed during the study period (2017).

Flowering days of genotypes at Erer (70.1days) and Sheraro (69.9 days) were statistically similar. At these two locations the required mean flowering days of genotypes were early than mean days of flowering at Mieso (77.7 days), Shaorobit (72.3 days) and Kobo (80.7 days). Compared to the overall locations flowering date of genotypes was late at Kobo (80.7 days). This finding is similar to Abiy (2016) pointed out the flowering date of genotypes at Kobo was late. Compared to the overall locations maturity date, it was only at Kobo and Mieso, had above the mean of the five locations maturity date (109.9 days). At Sheraro and Erer, the mean maturity days were lower than the grand mean (Table 5). The mean maturity days of locations were different except Mieso and Shaorobit. At Sheraro (100.6 days), the required mean of maturity days of genotypes were early than mean days of maturity of genotypes at Erer (104.9 days), Mieso (112.1 days), Shaorobit (112.4 days) and Kobo (119.62 days). Compared to the overall locations maturity date, it was only at Kobo, Mieso and Shaorobit, had above the mean of the five locations maturity date (109.9 days. At Sheraro and Erer, the mean maturity days were lower than the grand mean (Table 5).

Average grain filling periods of genotypes at Erer (34.8 days) and Mieso (34.5 days) were similar. At these two locations, grain filling period of genotypes was short as compared to the other locations, except at Sheraro (31.1 days). At Sheraro, the average period of genotypes to fill their grain was 31.1 days, this makes the grain filling period of genotypes at Sheraro faster than Erer, Mieso, Shorobit and Kobo. This variation might be due to the differences in the amount of rain fall and temperature, (Table 5).

The average grain filling rates of genotypes were 45.8 kg/day/ha at Errer, 53.6 kg/day/ha at Kobo, 32.1 kg/day/ha at Mieso, 121.5 kg/day/ha at Sheraro and 130.8 at Shaorobit (Table 5). The variation among means of grain filling rate of genotypes in each location was diverse. The grand mean grain filling rate of locations was 76.5 kg/day/ha, Shewarobit and Sheraro were the two locations that had faster grain filling rate than the rest three locations. At Shewarobit, genotypes filled their grains at a faster rate than the genotypes in the other locations. At Mieso, grain filling rate was the poorest of all the locations.

The mean plant height of all the genotypes at the tested locations was 185.5 cm. Average height of genotypes at Errer (149.8 cm), Kobo (189.0 cm), Mieso (151.9 cm), Sheraro (216.5 cm) and Shewa Robit (220.1 cm) were different. The highest mean plant height of the genotypes was observed at Shaorobit, it is higher than the rest locations (Table 5). The lowest mean were observed at Erer and Mieso. This shows that drought is highly affected the performance of genotypes with plant height.

The mean 1000 seed weight of all the genotypes at the tested locations was 30.1 g. Average 1000 seed weight of genotypes at Kobo (31.6 g), Mieso (33.3 g), Sheraro (29.3 g) and Shewarobit (30 g) were statistically similar. The lowest 1000 seed weight was observed at Erer (26.2 g), shows drought is highly affected the performance of genotypes with seed weight.

Table 5: Means for grain yield, phenolgical and other major traits of sixty early maturing sorghum genotypes at Erer, Kobo, Mieso, Sheraro and Shewarobit during 2017 main cropping season.

Location	Traits						
	DTF	GFP	DTM	GFR	GY	PHT	TSW
Erer	70.1^{d}	34.8^{c}	104.9^{c}	45.8b	1508.5^{d}	149.8^{c}	26.2^{b}
Kobo	80.7^{a}	52.9^{a}	119.6a	53.6^{b}	2832.1^{c}	189.0^{b}	31.6^{a}
Mieso	77.7^{b}	34.5^{c}	112.1^{b}	32.1^{c}	1099.0^{e}	151.9^{c}	33.3^{a}
Sheraro	69.9^{d}	31.1^{d}	100.6^{d}	121.5^{a}	3706.7^{b}	216.5^{a}	29.3^{a}
Shaorobit	72.3^{c}	40.1^{b}	112.4^{b}	130.8^{a}	5174.0^{a}	220.1^{a}	30^{a}
Mean	74.1	38.68	109.9	76.5	2863.9	185.5	30.1
LSD(0.05)	1.9	2.5	1.2	11	238.74	13.5	2.6
CV (%)	3.8	11.3	2.8	11.7	5.6	3.5	5.4

Where DTF = Date of flowering, DTM = Date of maturing, GFP = Grain filling period, GFR = Grain filling rate, GY = Grain Yield, PHT = Plant height, TSW = 1000 seed weight, LSD = Least significance difference and CV = coefficient of variation.

Genotype by environment interaction for mean grain yield of sixty early maturing sorghum genotypes is presented in Table 6. In table 6 existence of cross-over GXE interaction is evident in which case a significant change in rank occurs from one environment to another. In the present investigation, the interaction is of cross-over type as the ranking of genotypes changed at every environment. Table 6 indicates relative performance of each genotype at each environment. Now we can see that, similarity and difference of overall performance of the genotypes considering the interaction of genotype by environment. For example, 14MWLSDT7238 has high performance in overall mean; is ranked 3rd in Erer, 30th in Kobo, 1st in Mieso, 12th in Sheraro and 1st in Shoarobit. Visibly one can detect that from the table, the mean yield of genotypes shows interactions across the test locations with the possible existence of crossover interaction (Table 6). In general, ranking of genotypes changed from one environment to another, indicates that, a remarkable GXE and require further investigation to understand the patterns of interactions.

Table 6: Genotype by environment interaction for mean grain yield of 60 early maturing sorghum genotypes.

Genotype code	Genotype Name	ER	KB	MS	SH	SR	Genotype mean
1	Melkam	1358	2851	1048	3661	4857	2755
2	14MWLSDT7060	1341	3193	1189	4300	5506	3105.8
3	12MW6251	1475	3398	1331	4763	6238	3441
4	14MWLSDT7410	1309	2746	983	3433	4527	2599.6
5	12MW6302	1622	2684	1080	3489	5145	2804
6	14MWLSDT7322	2184	2655	1289	3741	6413	3256.4
7	14MWLSDT7395	1024	3088	1019	3928	4546	2721
8	14MWLSDT7400	1145	2854	965	3549	4359	2574.4
9	14MWLSDT7310	1828	2519	1089	3288	5297	2804.2
10	13MWF6#6077	589	2742	697	3030	2816	1974.8
11	14MWLSDT7325	1926	2252	1013	2835	4991	2603.4
12	2005MI5069	1486	3018	1170	4047	5495	3043.2
13	14MWLSDT7196	1657	2896	1185	3909	5654	3060.2
14	14MWLSDT7311	1957	2442	1107	3212	5446	2832.8
15	14MWLSDT7157	1691	2799	1157	3745	5539	2986.2
16	14MWLSDT7193	1557	2856	1129	3778	5337	2931.4
17	14MWLSDT7332	1388	2965	1109	3893	5158	2902.6
18	14MWLSDT7115	2018	2282	1062	2941	5268	2714.2
19	14MWLSDT7176	1240	3342	1214	4527	5568	3178.2
20	14MWLSDT7209	2113	2146	1040	2736	5219	2650.8
21	12MW6440	1773	2613	1108	3435	5356	2857
22	14MWLSDT7201	1814	3099	1335	4381	6434	3412.6
23	12MW6146	1101	2897	966	3606	4342	2582.4
24	14MWLSDT7364	1460	3122	1205	4229	5644	3132
25	Pipline 2	1587	3235	1304	4514	6173	3362.6
26	14MWLSDT7413	1938	2537	1140	3381	5592	2917.6
27	13MWF6#6037	1115	3401	1190	4570	5392	3133.6
28	14MWLSDT7207	1435	2896	1097	3787	5129	2868.8
29	14MWLSDT7040	1478	3029	1172	4064	5500	3048.6
30	14MWLSDT7036	1426	2803	1053	3605	4918	2761
31	14MWLSDT7324	1693	2691	1111	3540	5325	2872
32	12MW6243	1269	2621	913	3176	4183	2432.4
33	12MW6420	835	3153	972	3947	4230	2627.4
34	14MWLSDT7238	2135	2857	1357	4098	6706	3430.6
35	12MW6444	1800	2700	1157	3616	5596	2973.8
36	14MWLSDT7402	1340	2720	984	3401	4549	2598.8

37	14MWLSDT7234	1436	3283	1266	4522	5913	3284
38	12MW6471	1994	2079	964	2543	4801	2476.2
39	14MWLSDT7042	1600	2868	1150	3824	5461	2980.6
40	14MWLSDT7033	1500	2980	1160	3983	5453	3015.2
41	14MWLSDT7241	1617	2924	1182	3940	5616	3055.8
42	14MWLSDT7191	1360	2399	853	2802	3947	2272.2
43	2005MI5093	1689	2721	1122	3594	5377	2900.6
44	2401	1515	2957	1156	3948	5444	3004
45	2004MW6197	1194	3146	1111	4130	5065	2929.2
46	2005MI5064	2084	2528	1194	3445	5921	3034.4
47	2523	733	2774	768	3172	3224	2134.2
48	04MW 6043	2356	2158	1141	2891	5815	2872.2
49	2005MI5057	1592	2922	1171	3924	5555	3032.8
50	04MW 6079	964	3351	1109	4393	4935	2950.4
51	14MWLSDT7202	1426	2868	1082	3730	5051	2831.4
52	14MWLSDT7291	1710	2749	1143	3660	5484	2949.2
53	2001MS7036	1273	2840	1010	3593	4634	2670
54	90MW5319	1273	3205	1167	4285	5370	3060
55	99MW4047	1414	2897	1089	3777	5080	2851.4
56	05MW6026	1244	3009	1071	3897	4906	2825.4
57	14MWLSDT7421	1430	2941	1115	3869	5207	2912.4
58	2003MW6053	988	2862	906	3478	4003	2447.4
59	2294	1685	2746	1131	3640	5418	2924
60	2003MW6038	1325	2620	935	3204	4313	2479.4
	Environment Mean	1509	2832	1099	3707	5174	2864.2
	LSD (0.05)	181.72	378.18	193.59	123.45	330.68	504.87
	CV (0.05)	7.45	8.26	10.89	2.06	3.95	5.6

Where ER = Erer, KB = Kobo, MS = Mieso, SH Sheraro, SR = Shoarobit.

The mean for grain yield, phenological and other major traits of the top fifteen early maturing genotypes for combined location is presented in Table 7. The mean grain yield over all the locations and genotypes was 2863.9 kg/ha; with genotype mean grain yield ranging from 2024.6 kg/ha to 3533.1 kg/ha, indicating wide difference in yield potential across locations (Table 7). The lowest yielding genotype is 14MWLSDT7191 (2024.6 kg/ha) and is mainly attributed to the high moisture stress occurred, during the study period, which is similar to the finding of Menezes *et al.* (2015); Tardin *et al.* (2013). All the top fifteen genotypes were statistically similar to each other. However, they were significantly different with all the genotypes at this bottom (Table 7).The grain yield performance of the standard check was statistically different to the first six top high yielder genotypes but not with the grand mean (2863.9 kg/ha) across locations (Table 7), indicating the grain yield performance of the standard check was not among the first six top yielder genotypes in similar to Abiy and Firew (2016).

Genotypes with mean grain yield, phenological and other major traits found in the top fifteen genotypes that vary in rank are better than the rest genotypes, which is high yielder, early flowering and maturing, short grain filling period, high grain filling rate, tall in plant height and high thousand seed weight traits are more preferable and vice versa (Table 7). From the top fifteen genotypes 13MWF6#6037, Pipline 2, 14MWLSDT7176 and 90MW5319 were early in days to flowering than other genotypes thus making it more adaptable in the moisture stress conditions of the locations while the remaining eleven genotypes and the check were late flowering.

Earlness indicates the response of genotypes that escape from moisture stress condition. The earlness traits (days to flowering, grain filling period and days to physiological maturity) enables them to flower, grain fill and mature early. That is why days to flowering and maturity are of the most important attributes that need to be considered in selecting genotypes for drought affected areas. In this study, number of days to flowering ranged from 64.6 to 79.8 days. The five bottom genotypes (14MWLSDT7325, 2001MS7036, 2523, 14MWLSDT7115 and 14MWLSDT7191) were statistically significant different with the check. However, the three genotypes (14MWLSDT7325, 14MWLSDT7191 and 14MWLSDT7115) were late flowering and low yielding in contrast with Ludlow and Muchow (1990) reported late flowering varieties tend to offer yield higher than early flowering ones. Early flowering genotypes consists of adapting the crop cycle to water availability and evaporative demand, usually by reducing its duration, thereby reducing the total demand for water and withstand terminal stress (Tardieu, 2013). Flowering time is the most critical factor to optimize adaptation, hence grain yield, in environments differing in water availability and distribution during the growing season (Richards, 2006).

Mean days to maturity ranged from 107.5 to 113.6 with a mean value of 109.9 days (Table 7). The top genotypes were statistically similar with the check and the all bottom genotypes except genotype 14MWLSDT7191. Genotype 14MWLSDT7191 was late maturing and low yielding in contrast with Ludlow and Muchow (1990) pointed out that late maturing varieties tend to yield higher than early maturing ones.

Mean grain filling period ranged from 34.9 to 47.8 days with a mean value of 38.7 days (Table 7). The top three genotypes (14MWLSDT7176, 04MW 6043 and 90MW5319) were significantly different from the check and these genotypes spent long time to fill their grain, indicating high yielder due to the amount of solar energy available for grain filling increase. Similarly, the bottom three genotypes were statistically significant from the check while the remaining genotypes were statistically similar from the check.

Mean grain filling rate ranged from 54.1 to 101.4 kg/day/ha with a mean value of 76.8 kg/day/ha (Table 7). The top genotypes were statistically similar to the check. Most of the top genotypes were statistically significant different from the bottom genotypes. This indicates high yielder genotypes had the faster grain filling rate and vice verca. However, the four bottom genotypes were statistically significant different from the check.

Plant height is a complex trait, it is being affected by environmental conditions and management practices. (Butler et al. 2005 and Al-Temimi et al. 2013) reports indicated that plant height is directly linked to the productive potential of plant in terms of grain yield since it represents a good storage organ for photosynthetic metabolites. Therefore, significant reduction in plant height was noticed due to water stress; however, tolerant cultivars attained more plant height.

Plant height plays a major role in the acceptance of varieties by users (farmers) in the study areas, with preference being given to tall plants, which can serve a dual purpose as food and feed. In plant height, there were a significant difference and statistical different between genotypes and check. Mean plant height ranged from 125 cm to 238.2 cm with average of 185.5 cm (Table 7). Most of the top fifteen genotypes were statistically significant different from the check, indicating the wide difference in plant height across locations. In addition, most of the bottom genotypes were stsistically significant different from the check in similar to Sintayehu (2017) reported that top of the genotypes were statistically significant different from the standard check. The check is small in stature as compared to most of the top and bottom genotypes.

Mean thousand seed weight ranged from 21.4 g to 34 g with average of 30.1 g (Table 7). All the top genotypes except 12MW6302 were statistically similar with the check. Most of the bottom genotypes were statistically similar with the check. Genotype 14MWLSDT7176 was the highest 1000 seed weight as compared to the other top genotypes except four genotypes (Pipline 2, 14MWLSDT7201, 12MW6251, 14MWLSDT7042 and 2005MI5057). Genotypes that had the maximum 1000 seed weight indicated post flowering drought tolerance. Hence, traits associated with post-flowering drought tolerance include improved longer grain filling period, stay-green and seed weight (Borrell *et al.*, 2000b; Burke *et al.*, 2010; Van Oosterom *et al.*, 1996). Drought stress during seed development shortens the seed filling period (Younesi and Moradi, 2009) which results earlier maturation of the seeds (Meckel et al., 1984).

Table 7: Means for grain yield, phenological and other major traits of the top 15 and the bottom 15 early maturing advanced sorghum genotypes tested across locations during 2017 main cropping season.

Genotype Name	GY	DTF	GFP	DTM	GFR	PHT	TSW
14MWLSDT7238	3533.1	75.7	37.1	110	98.4	193.1	28.3
14MWLSDT7234	3528.5	74.9	36.8	108.9	101.4	184.6	31
14MWLSDT7196	3494.6	73.7	38.2	109.1	90.9	176.7	30
13MWF6#6037	3465.1	71.9	38.8	107.9	88.7	165.9	29.2
Pipline 2	3462.7	71.9	38.8	107.9	96.9	204.9	30.5
14MWLSDT7176	3453.1	70.6	42.3	110.1	84.7	187.9	34
14MWLSDT7201	3343.6	74.3	37	108.5	93.8	190	31.7
12MW6251	3284.6	75.1	38.1	110.4	90.2	194.7	30.5
04MW 6043	3256.9	74.6	44.2	111.3	81	200.4	27.8
14MWLSDT7332	3249.2	76.2	36.9	110.3	90.4	180	29.2
14MWLSDT7042	3200.9	74.3	38.4	109.9	85	194.2	33.8
2005MI5057	3190.6	74.4	38.5	110.1	87	192.4	33.9
14MWLSDT7241	3174.8	76.4	36.3	109.9	89	197.7	29.6
90MW5319	3169.9	65.4	45.1	107.7	71.6	168.5	30.2
12MW6302	3099.9	76.4	35.3	108.9	89	146.8	26.2
2004MW6197	2594.4	74.7	37.7	109.6	70.6	176.5	32.2
99MW4047	2589.2	73.1	38.9	109.2	66.9	146.8	30

14MWLSDT7310	2579.1	76.2	38.5	111.9	69.4	218.4	27.5
14MWLSDT7402	2540.4	74.5	38.5	110.2	69.3	238.2	31.9
14MWLSDT7410	2435	76.6	36.5	110.3	69.3	192.2	27.3
14MWLSDT7325	2408.7	79.1	34.9	111.1	70.1	212	30.2
2003MW6038	2397	73	39.3	109.5	64	191.2	32.1
2001MS7036	2382.1	69.7	36.9	109.9	75.5	194.8	33.1
12MW6243	2380.7	75.3	36.5	109	65.8	125	25.9
2523	2380	67.1	44.3	108.6	54.1	160.2	30
2003MW6053	2368.3	70.8	41.3	109.3	58.4	171	30
14MWLSDT7115	2354.5	78.2	35.9	111.3	72.3	204.7	28
14MWLSDT7395	2343.4	69	44.9	111.1	54.6	160.3	29.1
13MWF6#6077	2086.8	76.7	35.9	109.9	60.6	129.5	21.4
14MWLSDT7191	2024.6	79.8	36.5	113.5	57.5	174.3	30.3
Check	2885.1	75.1	36.9	109.1	80.7	159.3	30.9
Maximum	3533.1	79.8	47.8	113.6	101.4	238.2	34
Minimum	2024.6	64.6	34.9	107.5	54.1	125	21.4
Mean	2863.9	74.1	38.7	109.9	76.8	185.5	30.1
LSD at 5%	504.9	2.6	3.9	2.8	21	18.4	3.5
CV (%)	5.6	3.8	11.3	2.8	11.7	3.5	5.4

Where DTF = Date of flowering, DTM = Date of maturing, GFP = Grain filling period, GFR = Grain filling rate, PHT = Plant height, GY = Grain yield and TSW = 1000 seed weight.

4.3. Stability analysis

4.3.1. Eberhart and Russel's Regression Model

The analysis of Variance by Eberhart and Russel's joint regression model of early maturing advanced sorghum genotypes on mean grain yield (kg/ha) tested at five locations is presented in Table 8. The result of Eberhart and Russell's ANOVA showed highly significant ($P \leq 0.001$) difference among the genotypes for grain yield, indicating differences in the performance of genotypes, which may attribute to the genetic make up of the materials. The GXE (linear) interaction was not significant ($P>0.05$). Thus, the GXE interaction was non-linear type and showed the non-existence of genetic differences among genotypes for their response to various locations, which is in agreement with earlier findings of Kenga *et al.* (2003), Wedajo (2014), and Fekadu *et al.* (2009), Abiy (2016). Pooled deviations were very highly significant against pooled error.

Pooled deviation (non-linear) in the joint regression analysis was very highly significant ($p \leq 0.0001$) difference (Table 8). The significance of the mean squares due to pooled deviations from regressions revealed the performance of some genotypes were not stable across various locations. This finding is similar to Abiy (2016). In addition, only 21 % of the GXE sum of squares accounted by regression sum of square, and the remaining 79 % was accounted for the SS of the regression deviation. This indicated that the largest proportion of the interaction component of variation was explained by the deviation from regression. Hence, according to Khan *et al.* (1988) and Ashraf *et al.* (2001), such differences in stability were due to deviation from linear regression only. This means the variation in the yield performance of genotypes are entirely unpredictable in nature.

Table 8: Genotype x Environment Interaction analysis of variance by Eberhart and Russel's Model of early maturing sorghum genotypes on mean grain yield (kg/ha) tested at five sites.

Sources of variation	Df	Sum Squares	Mean Squares
Total	299	782604108	2617405
Genotypes	59	38961387	660362**
Env + (Gen x Env)	240	743642721	3098511ns
Env (linear)	1	659944480	659944480ns
Gen xEnv (linear)	59	17443148	295647ns
Pooled deviation	180	66255093	368084***
Pooled error	600	5086911	8478

*** = very highly significant ($P \leq 0.0001$), ** = highly significant ($P \leq 0.001$), * = significant ($P \leq 0.05$) and ^{ns} = non-significant ($P > 0.05$).

The stability parameters of Eberhart and Russell's (1966) model for the yield of early maturing sorghum genotypes tested at five locations is presented in table 9. According to this model the genotype's performance is described in terms of three parameters, mean yield, regression coefficient and the deviation from the regression. Thus, a stable genotype is one with high mean yield, bi=1, and S^2_{di} is small value.

The bi estimate of genotypes 14MWLSDT7410 (0.85), 12MW6420 (0.86), 12MW6444 (0.87), 14MWLSDT7332 (0.83), 04MW 6043 (0.84), Melkam (0.98), 12MW6302 (0.89), 14MWLSDT7400 (0.91), 14MWLSDT7325 (0.88), 14MWLSDT7115 (0.94), 12MW6146 (0.91), 12MW6243 (0.89), 12MW6444 (0.87), 14MWLSDT7042 (0.97) and 2005MI5064 (0.95), 2003MW6053 (0.94), 05MW6026, 14MWLSDT7207 are relatively near to unity. The average yield performance of genotype 14MWLSDT7410, 12MW6420, 14MWLSDT7325, 12MW6146, 14MWLSDT7400, 12MW6243, and 2003MW6053 were below average (Table 9). Therefore, considering their above average mean grain yield, bi value closest to unity and the S2di value is small, genotype Melkam, 05MW6026, 14MWLSDT7207, 2005MI5064, 12MW6302, 14MWLSDT7332, 12MW6444, 14MWLSDT7209 and 14MWLSDT7042 were stable genotypes based on Eberhart and Russell's model. However, the check (Melkam) and 14MWLSDT7209 genotypes were low yielder as compared to these selected stable genotypes. Thus, genotypes 05MW6026, 14MWLSDT7207, 12MW6444, 12MW6302, 14MWLSDT7332 and 14MWLSDT7042 were the most stable and high yielder genotypes. In contrary, the S^2di value of genotype 14MWLSDT7060, 12MW6251, 14MWLSDT7310, 14MWLSDT7157,14MWLSDT7193,12MW6440, 14MWLSDT7201, 14MWLSDT7364, Pipline2, 14MWLSDT7040, 14MWLSDT7036, 14MWLSDT7324, 14MWLSDT7234, 14MWLSDT7238, 14MWLSDT7291, 14MWLSDT7402, 14MWLSDT7033, 14MWLSDT7241, 14MWLSDT7191, 2003MW6038, 2005MI5093, and 2004MW6197 had significantly deviation from regression (Table 9).

Wachira et al. (2002) grouped genotypes adaptability to specific environments based on their estimate of bi as adaptable to high and low yielding environments. The bi values above one define genotypes with higher sensitivity to environmental change (below average stability) and are suitable to high yielding environments, whereas bi below one delivers a measurement of more resistance to environmental change (above average stability), and are adaptable to low yielding environments. Based on this idea the present study shows (Table 9), genotype 14MWLSDT7060, 12MW6251, 14MWLSDT7322, 14MWLSDT7196, 14MWLSDT7193, 14MWLSDT7176, 12MW6440, and 14MWLSDT7201, 14MWLSDT7364, Pipline 2, 14MWLSDT7413,13MWF6#6037, 14MWLSDT7040, 14MWLSDT7238, 14MWLSDT7234, 14MWLSDT7033, 14MWLSDT7241, 14MWLSDT7291, 90MW5319 had bi value of greater than one and above mean yield performance in similar to Abiy and Firew (2016) reported that eight sorghum genotypes had bi value of greater than one. Therefore, these genotypes were highly contributed to the GXE and were suitable for conducive environments. In contrary, genotype 2003MW6038, 14MWLSDT7410, 13MWF6#6077, 14MWLSDT7324, 14MWLSDT7325, 12MW6243, 14MWLSDT7402, 12MW6471, 14MWLSDT7191, 2523, 04MW6043, and 2003MW6053 had b_ivalue less than one and these genotypes were contributed less to the GXE. Hence, these genotypes are suitable for harsh environments (Table 9).

Table 9: Eberhart and Russell’s (1966) stability parameters of early maturing sorghum genotypes tested at five locations.

Entry#	Genotype Name	b_i	S^2d_i	GY	Rank
1	Melkam	0.975	240745	2885.09	28
2	14MWLSDT7060	1.1904	76071.9985*	3013.5	22
3	12MW6251	1.3746	52648.5568**	3284.55	8
4	14MWLSDT7410	0.8537	202975	2434.99	50
5	12MW6302	0.8854	249180	3099.92	15
6	14MWLSDT7322	1.2583	1036075	2937.86	26
7	14MWLSDT7395	1.0267	429131	2343.43	58
8	14MWLSDT7400	0.9089	640670	2690.96	40
9	14MWLSDT7310	1.0765	174810.832*	2579.09	48
10	13MWF6#6077	0.5125	404144	2086.77	59
11	14MWLSDT7325	0.8765	513248	2408.68	51
12	2005MI5069	1.0592	604144	2617.49	45
13	14MWLSDT7196	1.0095	860163	3494.64	3
14	14MWLSDT7311	1.1796	432721	2652.33	21
15	14MWLSDT7157	0.9478	161901.518*	3028.49	44
16	14MWLSDT7193	1.1664	211478.473*	2882.85	30
17	14MWLSDT7332	0.8319	145175	3249.17	10
18	14MWLSDT7115	0.9398	1438882	2354.53	57
19	14MWLSDT7176	1.1377	813739	3453.1	6
20	14MWLSDT7209	0.8449	360775	2884.52	29
21	12MW6440	1.0625	112372.72*	2868.93	31
22	14MWLSDT7201	1.2498	262459.621*	3343.65	7
23	12MW6146	0.9069	364183	2670.21	43
24	14MWLSDT7364	1.1225	81966.2491*	3034.68	20
25	Pipline 2	1.1647	127102.647*	3462.67	5
26	14MWLSDT7413	1.176	461902	2950.72	24
27	13MWF6#6037	1.0772	709836	3465.1	4

28	14MWLSDT7207	0.812	179922	3050.93	19
29	14MWLSDT7040	1.1211	48725.9222*	3080.19	16
30	14MWLSDT7036	1.0547	28800.1309**	2685.27	41
31	14MWLSDT7324	0.9601	109177.745*	2847.04	32
32	12MW6243	0.89	212369	2380.68	54
33	12MW6420	0.8594	317889	2673.53	42
34	14MWLSDT7238	1.2476	130011.226*	3533.08	1
35	12MW6444	0.8681	536943	3052.16	18
36	14MWLSDT7402	0.869	19555.8851*	2540.45	49
37	14MWLSDT7234	1.0279	32651.5533*	3528.52	2
38	12MW6471	0.6455	1641709	2818.12	35
39	14MWLSDT7042	0.9733	190083	3200.93	11
40	14MWLSDT7033	1.12	186283.566*	3067.98	17
41	14MWLSDT7241	1.0565	23459.6288**	3174.82	13
42	14MWLSDT7191	0.8137	49118.5803*	2024.65	60
43	2005MI5093	1.1112	73272.0194*	2830.55	34
44	2401	1.0597	406132	2830.79	33
45	2004MW6197	1.1859	158557.494*	2594.45	46
46	2005MI5064	0.9451	1057996	2964.41	23
47	2523	0.6313	1131878	2380.03	55
48	04MW 6043	0.8369	1245803	3256.91	9
49	2005MI5057	0.9476	74065.6386*	3190.58	12
50	04MW 6079	1.0097	358134	2799	38
51	14MWLSDT7202	1.067	202160.958*	2803.42	37
52	14MWLSDT7291	1.0136	95315.8035*	2908.82	27
53	2001MS7036	1.0197	172813.299*	2382.12	53
54	90MW5319	1.1087	511415	3169.89	14
55	99MW4047	1.1251	30825.8423**	2589.24	47
56	05MW6026	0.8115	133843	2947.87	25
57	14MWLSDT7421	1.0224	118487.126*	2803.77	36
58	2003MW6053	0.9368	502830	2368.26	56
59	2294	1.2299	392500	2783.55	39
60	2003MW6038	0.8041	26489.915*	2397.01	52

Where bi = Coefficent of regression, S2di = deviation from regression, GY Mean Grain yield, * = Significant ($P \leq 0.05$) and ** = highly significant ($P \leq 0.001$).

4.3.2. AMMI Model

The combined AMMI model ANOVA of the sixty early maturing advanced sorghum genotypes over five sites for grain yield (kg/ha) is presented in Table 10. The ANOVA indicated highly significant differences ($p \leq 0.001$) for treatments (environments, genotypes and GXE). The total variation explained (%) was 99.1 % for treatment and 0.9 % for error. The larger contribution of the treatment than the error reveals the reliability of this multi-location experiment (Table 10). The treatment variation was largely due to among environments variation, genotype and GXE accounted 84.36 %, 4.86 % and 10.78% for the treatment variation, respectively. As stated earlier, the great percentage of the location is an indication that the major factor that affect yield performance of sorghum in drought areas of Ethiopia is the environment. Various authors also reported similar results for other sorghum genotypes tested at different locations (Asfaw (2007, 2008); Hagos and Fetien (2011); Mahnaz *et al.* (2013); Sewagegne *et al.* (2013); Abiy and Firew (2016); Kinde (2016). In the AMMI ANOVA, the GXE was further partitioned by PCA. The Gollob F-test used to measure significant of the GXE components. The number of PCA axis to be retained is determines by testing the mean square of each axis with the estimate of residual through the F-statistics. The result of ANOVA showed that the first two IPCA are significant at 0.001 probability level, this outcome suggests the addition of the first two interactions PCA axes in the model. Hence, the best fit AMMI model for this multi-location yield trial data was AMMI-2 (Table 10).

In particular, the first IPCA captured 49.8 % of the total interaction sum of squares while the second IPCA explained 26.65 % of the interaction sum of squares. Gauch and Zobel (1996) and Yan *et al.* (2002) also proposed that the most accurate model for AMMI can be predicted by using the first two IPCAs. In the present study the first two IPCAs accounted for a total of 76.45 % of the interaction with 122 of the corresponding degrees of freedoms. This indicates that the GXE of the sixty sorghum genotypes with five locations was sufficiently predicted by the first two principal components axes and therefore, most evidence may well to graphically display in AMMI1 and AMMI2 biplot.

Table 10: Genotype x Environment Interaction analysis of variance by AMMI for grain yield (kg/ha) of early maturing advanced sorghum genotypes tested at five locations during 2017 main cropping season.

Source	DF	SS	MS	%Total	%Treatment	%GXE	%Cumulative
Total	899	2376230888	2643193				
Treatments	299	2353974003	7872823**	99.1			
Genotypes	59	114373528	1938534**		4.86		
Environment	4	1985932733	496483183**		84.36		
Replications	10	460154	46015ns				
Interactions	236	253667743	1074863**		10.78		
IPCA 1	62	126333038	2037630**			49.8	49.8
IPCA 2	60	67611000	1126850**			26.65	76.45
Residuals	114	59723705	523892**			23.54	100
Pooled Error	590	21796731	36944	0.9			

DF = degree of freedom, SS =sum of squares, MS = mean of squares, ** = highly significant (P<0.001) and ns = non significant.

The AMMI 1 was used to analyse biplot graph (Fig. 2) using individual environments and mean grain yield performances of sorghum genotypes. As indicated in Figure 2, each environment and genotype main effect was plotted along the abscissa against their respective IPCA1 score as ordinate. The AMMI 1 biplot, showing main effects means of grain yield on the abscissa and IPCA 1 values as the ordinates, genotypes or environments that appear on a vertical line have similar means and those that appear on a horizontal line have similar interaction (similar IPCA 1 value) patterns (Crossa *et al*., 1990) but they have not similar means. According to these authors, genotypes or environments with large IPCA 1 scores (either positive or negative) have high interactions, whereas genotypes or environments with IPCA 1 scores near zero have small interactions. Similarly, in the biplot (Fig. 2) three of the five environments had below average main effects and were unsuitable to the performance of half of the total genotypes as compared to the rest two environments. The remaining two environments (Shaorobit and Sheraro) had the highest main effects and were favorable to the performance of almost half of the genotypes. Similar outcomes have reported by Das *et al*. (2010) and Kulsum *et al.* (2013). On the contrary, environments Mieso, Erer and Kobo were the most unsuitable environments because they had below average main effects. In general Shaorobit showed higher main effect values whereas Erer and Kobo showed below average main effect values. There were high interaction at Kobo due to high IPCA 1 score value and very small interaction (small IPCA 1 score value) at Mieso. Inconsistency in interaction at Kobo present difficulty in producing variety recommendation for that target location. Entries 21, 55, 57, 30, 17, 39, 7, 37, 56, 28, 36, 60, 45, 20 and environments Mieso and Sheraro were least interactive due to low IPCA 1 score value. Similar findings and interpretation have been made by Adugna (2007); Anandan et al. (2009) and Islam *et al.* (2014). Entries 21, 17, 39, 30, 56, 28, 37 and 55 placed closed to the biplot origin and were the most stable but 55 and 30 had below grand mean. Similar result was reported by Anandan *et al*. (2009); Crossa, (1990) and Kempton R A, (1984). Entries 39, 17, 37 21, 56 and 28 had above average main effect and small interaction which makes them the most stable genotypes. On the contrary, entries 19, 27, 13 and 22 had similar and large main effects but 19 showed larger interaction due to high IPCA 1 score and more unstable genotype (Fig. 2).

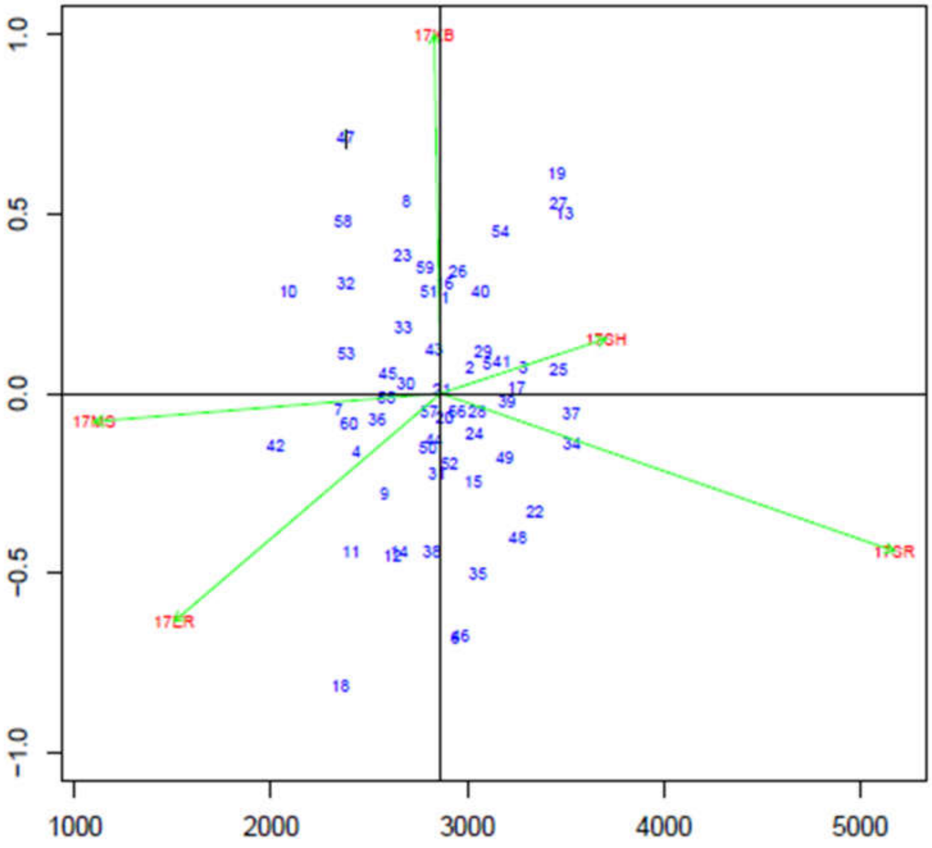


Figure 1: AMMI 1 biplot for grain yield of 60 early maturing sorghum genotypes evaluated across five locations in Ethiopia during 2017 main cropping season.

AMMI 2 biplot presents the pattern of the first two IPCA of the interaction effects and helps in visual interpretation of the G x E interaction patterns and identify genotypes or locations that show small and large interaction effects. In AMMI 2 biplot, environments fell into three sections (Fig 3). Among the environments 17MS (Mieso) had very short spoke and 17SH (Sheraro) had short spokes. They do not exert strong interaction but the environments 17ER (Erer), 17KB (Kobo) and 17SR (Shoarobit) had long spokes and hence indicate the most enfluencing environments. In AMMI 2 biplot, the entries, 38, 47, 19, 3 and 6 are the best or poorest genotypes in some or all environments because they are farthest from the origin where as the best genotype is 6 with respect to the best enhancing environment 17SR and the poor entry is 47 due to its value below average value. On the other hand, the entries 37, 56, 28, 30, 25, 21, 39, 57, 55, 29, 41, 52, 36, 31 and 17 were close to the origin and therefore were less/non-sensitive to environmental interaction. However, entries 57, 55 and 31 were low yielding due to below average grain yield (Fig 3). Hence, entries 28, 56 and 37 were the most yielding and stable due to very close to the origin. Similar outcomes were reported by Sintayehu (2017); Dagnachew *et al.* (2014); Anandan *et al.* (2009); Crossa, (1990) and Kempton R A, (1984).

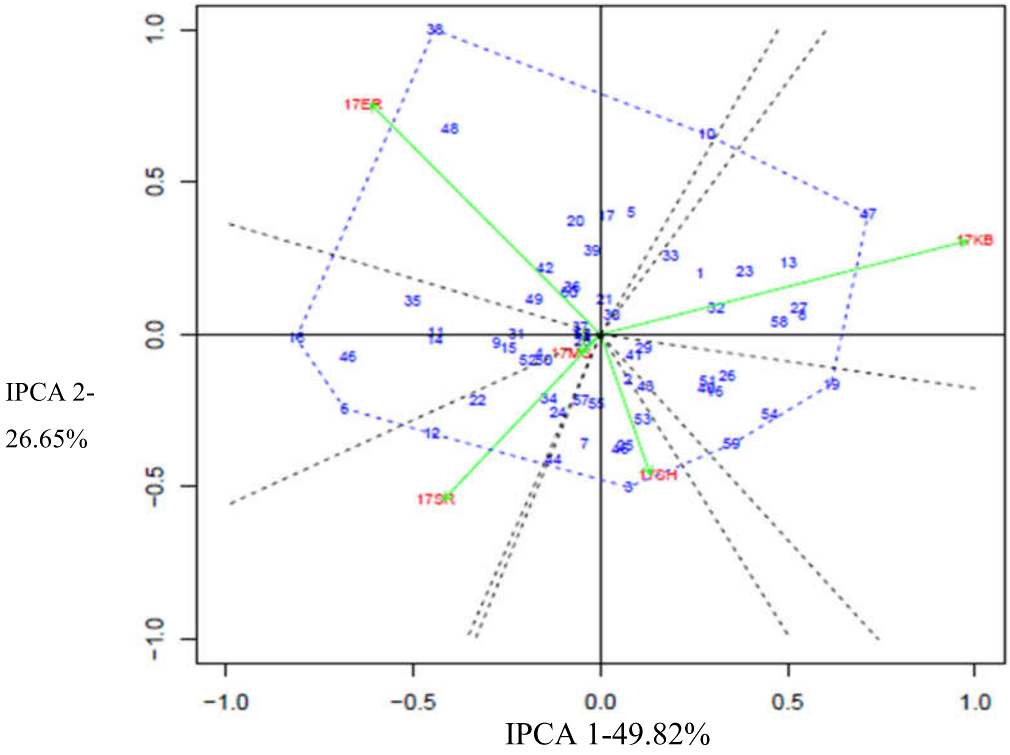


Figure 2: AMMI 2 biplot for grain yield (kg/ha) showing the interaction of IPCA2 against IPCA1 scores of 60 early maturing sorghum genotypes in five environments.

Where 1 = Melkam , 2 = 14MWLSDT7060, 3 = 12MW6251, 4 = 14MWLSDT7410, 5 = 12MW6302, 6 = 14MWLSDT7322, 7 = 14MWLSDT7395, 8 = 14MWLSDT7400, 9 = 14MWLSDT7310, 10 = 13MWF6#6077, 11 = 14MWLSDT7325, 12 = 2005MI5069, 13 = 14MWLSDT7196,14 = 14MWLSDT7311,15 = 14MWLSDT7157, 16 = 14MWLSDT7193, 17 = 14MWLSDT7332,18 = 14MWLSDT7115,19 = 14MWLSDT7176,20 = 14MWLSDT7209,21 = 12MW6440,22 = 14MWLSDT7201,23 = 12MW6146,24 = 14MWLSDT7364, 25 = Pipeline 2, 26 = 14MWLSDT7413, 27 = 13MWF6#6037, 28 = 14MWLSDT7207,29 = 14MWLSDT7040, 30 = 14MWLSDT7036, 31 = 14MWLSDT7324, 32 = 12MW6243, 33 = 12MW6420,34 = 14MWLSDT7238,35= 12MW6444,36 = 14MWLSDT7402,37 = 14MWLSDT7234, 38 = 12MW6471, 39 = 14MWLSDT7042,40 =

14MWLSDT7033, 41 = 14MWLSDT7241,42 = 14MWLSDT7191, 43 = 2005MI5093, 44 = 2401, 45 = 2004MW6197, 46 = 2005MI5064,47 = 2523,48 = 04MW 6043,49 = 2005MI5057, 50 = 04MW 6079, 51 = 14MWLSDT7202, 52 = 14MWLSDT7291, 53 = 2001MS7036, 54 = 90MW5319,55 = 99MW4047,56 = 05MW6026,57 = 14MWLSDT7421, 58 = 2003MW6053, 59 = 2294, 60 = 2003MW6038 and 17ER = Erer, 17MS = Mieso, 17KB = Kobo, 17SR = Shaorobit, 17SH = Sheraro.

4.3.3. GGE biplot model

Stability analysis of the tested genotypes (represented by entry number) based on their IPCA scores using the GGE biplot of analysis is presented in Fig 4 and Fig 5. The polygon of lines in Fig. 4 is formed by connecting vertex genotypes, by connecting straight lines and rest of genotypes (represented by entry number) fall inside the polygon. The vertex entries were 19, 13, 34, 6, 18, 42, 10 and 47 (Fig 4). These entries are either the best or poorest genotypes in some or all environments because they are farthest from the origin (Yan and Kang, 2003).

In the present study, the GGE biplot graphic analysis of the sixty early maturing sorghum genotypes tested at five locations revealed that the first two principal components explained 71.30% of the total variance (Fig 4). This GGE biplot is used to facilitate visual analysis of the genotype by location data. Genotypes close to the origin are not sensitive (unfavorable) to the environments and those distant from the origin are sensitive (favorable) to environments and have large interactions. Accordingly, statistically stable genotypes and locations were located near to the biplot origin, with scores practically zero for the two interaction axis (IPCA1 and IPCA2). The entires, which lie near the origin and practically stable were entries 28, 56, 57, 20 and 21and had wide adaptability. However, entry 57 was below average yield. Hence, entries 28, 56, 20 and 21 were high yielding and stable across the five locations. On the other hand entries 19, 13, 34, 6, 18, 42, 10, 47, 27, 22, 46 and 8 were located far away from the origin, which were more sensitive to environment changes and are considered as specifically adapted genotyypes in agreement with the finding of Abay and Bjornstad (2009); Dehghani *et al*. (2006); Tesfaye *et al*. (2008) and Gasura *et al*. (2015) reported high yielder and stable genotype as well as low yielding and poorly stable ones.

The graphic analysis of the first principal component (IPCA1) represents variety productivity, and the second principal component (IPCA2) variety stability (Yan *et al*., 2000). Therefore, the GGE biplot revealed that the ideal genotype must have a high IPCA1 value (high productivity) and an IPCA2 value near to zero (more stable). Thus based on the graphic interpretation, the present study revealed that entry 34 had the largest IPCA1 score, and hence had the highest average grain yield. The IPCA2 value of this genotype, however, was the largest indicating its specific adaptation. In contrast, 57 yielded poorly at all sites, but was relatively stable, as indicated by its small IPCA1 scores (low yielding) and relatively small IPCA2 scores (stable). Genotypes that had IPCA1 scores >0 were identified as higher yielding and those that had IPCA1 scores <0 were identified as lower yielding. Accordingly, the average yield of 42, 10, 18 and 47 were below average, and the lower yielding genotypes due to highly unstable (large absolute IPCA2 scores). In contrast, entries 19, 27, 13, 34, 22 and 48 had positive IPCA1 scores and were identified as high yielder genotypes.

Figure 5 revealed the relationship among genotypes in biplot analysis, hence; the biplot revealed that 19, 27 and 13 were similar, because the angle between them was smaller. In contrast, genotype 19 and 46 were dissimilar, as their angle was larger. In addition, the positions of the genotypes in opposing quadrants on the Cartesian plan also revealed their dissimilar genetic performance, as observed for 19 and 46, 19 and 6, 27 and 46, 27 and 6, 13 and 46, 13 and 6, 34 and 10, 34 and 42. Moreover, the relationship among testers was also graphically described in the GGE biplot (Fig 5). The cosines of the angle between the testers normally estimated the correlation coefficient between them. Hence, the pair of testers, which were positively correlated had an angle between their vectors less than 90^o (17ER and 17SR, 17ER and 17MS, 17MS and 17SH, 17SR and 17MS, 17SR and 17SH, 17SH and 17KB); while the angle between vectors of tester 17ER and 17KB was approximately 90^o, and were not correlated (Fig 5).

With respect to the contribution of testing locations to the GXE, location mieso (17MS) had least contribution as it lied closest to the origin, but locations Shaorobit (17SR) and Kobo (17KB) were made the highest contribution. The biplot in this trail also indicated that entry 13, 27, 19 and 40 were performed above average in location Kobo (17KB); while 34, 37, 22,25,3,48,24,49,17,21,41,39 and 2 in 17SR (Shoarobit), 17MS (Mieso), 17ER (Erer) and 17SH (Sheraro). Meanwhile, discriminating ability was an important measure of a test environment. Another equally important measure of a test environment was its representativeness of the target environment. An ideal environment should be highly differentiating of the genotypes and at the same time representative of the target environment (Yan *et al*.2000 and Yan etal.2006). Hence in the current experiment, locations 17SR (Shaorobit) and 17KB (Kobo) were most discriminating of the entries as indicated by the longer distance between their markers and the origin. However, due to their relatively large IPCA2 score, genotypic differences observed at both locations did not exactly reflect the genotypes in average yield over all sites. On the other hand, location Mieso (17MS) was not actually the most discriminating as distance of its vector was the smallest, but varietal difference at this site was highly consistent with those averaged over all sites, because it had the lowest IPCA2 scores and IPCA1 scores. In agreement with this finding, Abay and Bjornstad (2009); Dehghani *et al*. (2006); Tesfaye *et al.* (2008) and Gasura *et al.* (2015) reported the existence of a good testing environment for selecting widely adaptable and high yielding cultivar.

To clearly display the ‘which-won-where’ pattern and sensitivity degree between the genotype and environment, polygon view of a GGE biplot based on the IPCA1 and IPCA2 values was displayed in Fig 5. The perpendicular genotypes in the biplot have divided the biplot in to 5 sectors in which each location fell in either of the sectors. Yan and Kang (2003) explained that the polygon view of a biplot was the best way to visualize the interaction patterns between genotypes and environments, and to effectively interpret a biplot. In this study, the ‘which won where’ feature of the biplot identified wining genotypes; i.e., entry 13 for instance was the winning/corner genotype in locations 17SH (Sheraro) and 17KB (Kobo); entry 25 in locations 17MS (Mieso) and 17SH (Sheraro); entry 22 in locations 17ER (Erer) and 17SR (Sheraro). Similarly, entry 34 was the vertex/winning genotype in location 17SR and 17MS. According to the findings of Yan and Tinker (2006), the vertex genotypes were the most responsive genotypes, as they have the longest distance from the origin in their direction. On the other hand, the result also showed some genotypes, which fall in sectors where there were no locations at all; these genotypes are poorly adapted to five of the testing locations (18, 46, 35,38, 11, 9, 31, 52, 36, 4, 42, 10, 32, 58, 47, 45, 50, 44, 24, 7 and 33).

Yan *et al*. (2000) defined mega environments as a cluster of locations or environments that constantly share the same best variety. Hence, the result of this experiment identified two

Sorghum growing mega-environments. The first mega-environment contained locations of (Erer) 17ER, (Shoarobit) 17SR, (Mieso) 17MS and (Sheraro) 17SH with winning entry 34; while the second mega-environment on the other hand, contained location (Kobo) 17KB with winning entry 19.

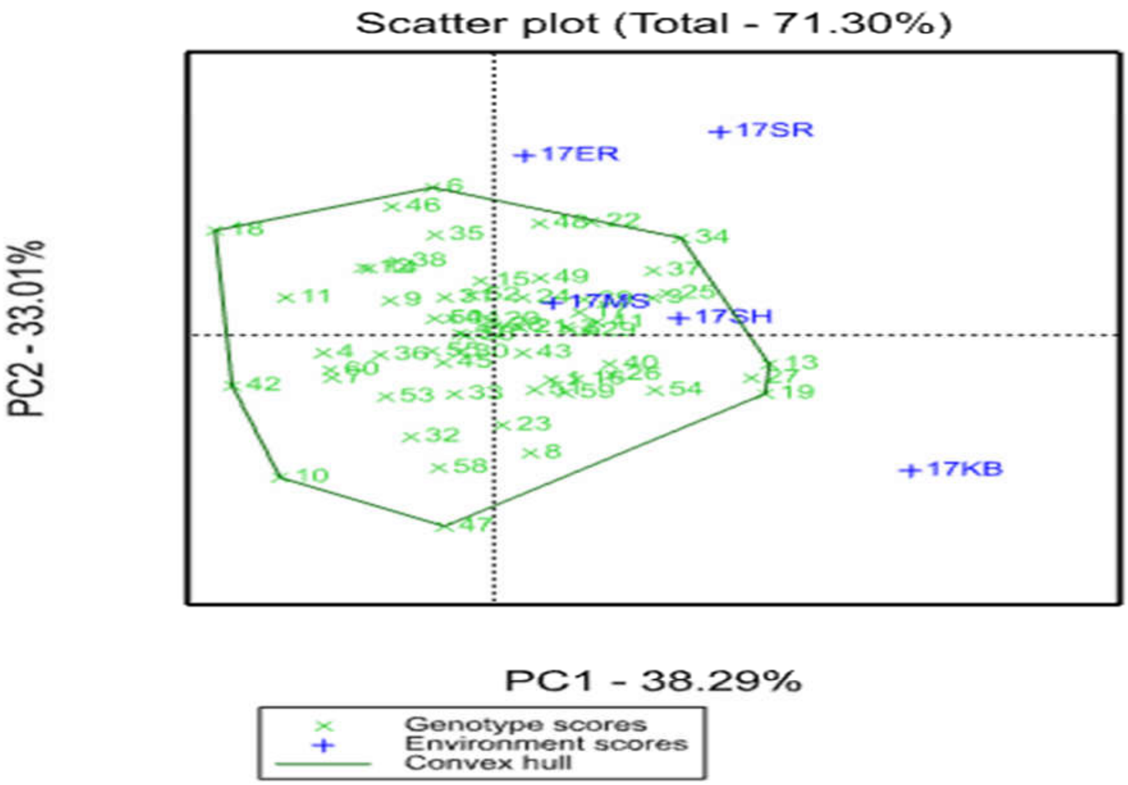


Figure 3: The ‘which-won-where’ feature of the biplot.

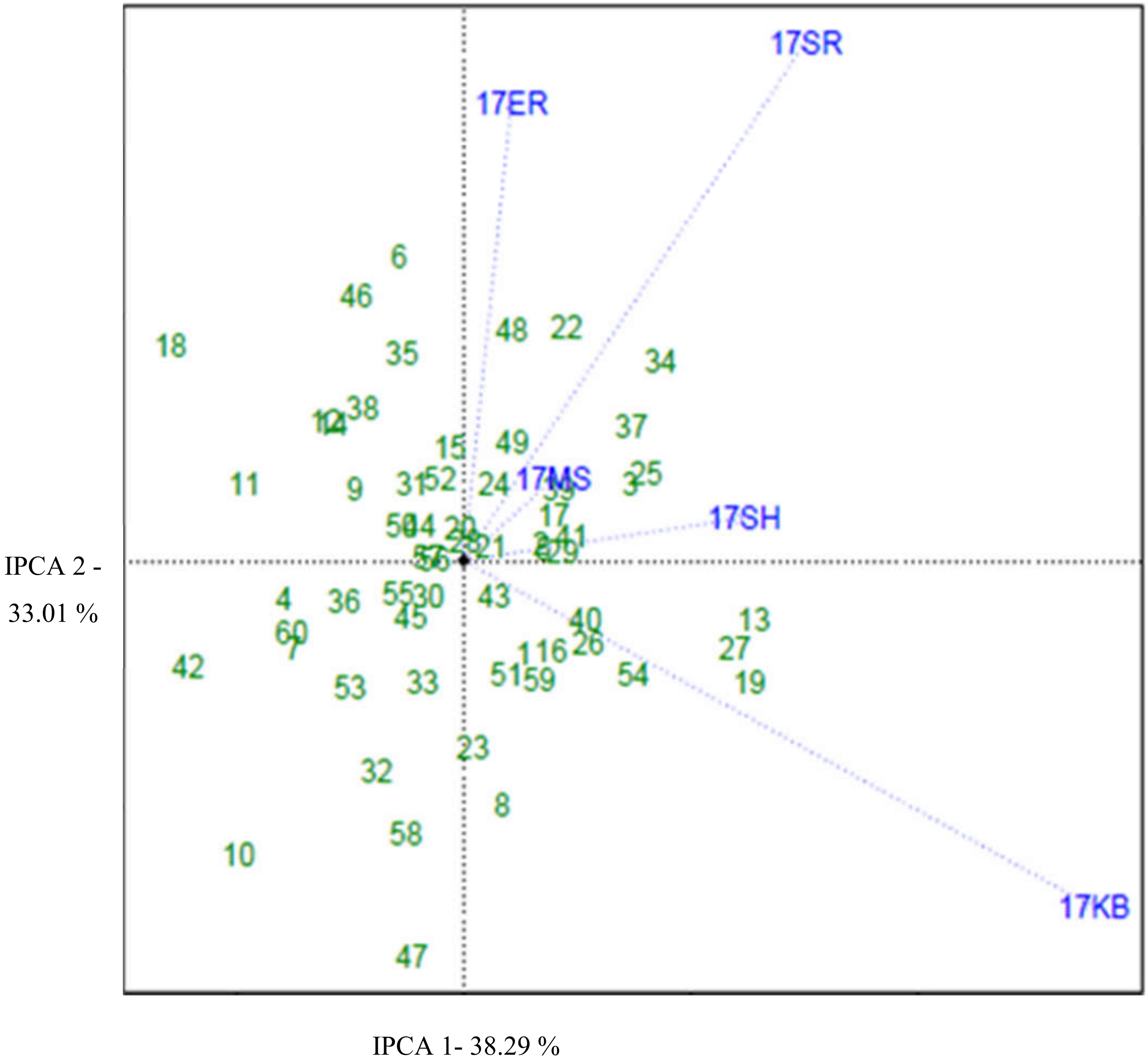


Figure 4: The relationship among testers and mega environments.

Where 1 = Melkam , 2 = 14MWLSDT7060, 3 = 12MW6251, 4 = 14MWLSDT7410, 5 = 12MW6302, 6 = 14MWLSDT7322, 7 = 14MWLSDT7395, 8 = 14MWLSDT7400, 9 = 14MWLSDT7310, 10 = 13MWF6#6077, 11 = 14MWLSDT7325, 12 = 2005MI5069, 13 = 14MWLSDT7196,14 = 14MWLSDT7311,15 = 14MWLSDT7157, 16 = 14MWLSDT7193, 17 = 14MWLSDT7332,18 = 14MWLSDT7115,19 = 14MWLSDT7176,20 = 14MWLSDT7209,21 = 12MW6440,22 = 14MWLSDT7201,23 = 12MW6146,24 = 14MWLSDT7364, 25 = Pipeline 2, 26 = 14MWLSDT7413, 27 = 13MWF6#6037, 28 = 14MWLSDT7207,29 = 14MWLSDT7040, 30 = 14MWLSDT7036, 31 = 14MWLSDT7324,

32 = 12MW6243, 33 = 12MW6420,34 = 14MWLSDT7238,35= 12MW6444,36 = 14MWLSDT7402,37 = 14MWLSDT7234, 38 = 12MW6471, 39 = 14MWLSDT7042,40 = 14MWLSDT7033, 41 = 14MWLSDT7241,42 = 14MWLSDT7191, 43 = 2005MI5093, 44 = 2401, 45 = 2004MW6197, 46 = 2005MI5064,47 = 2523,48 = 04MW 6043,49 = 2005MI5057, 50 = 04MW 6079, 51 = 14MWLSDT7202, 52 = 14MWLSDT7291, 53 = 2001MS7036, 54 = 90MW5319,55 = 99MW4047,56 = 05MW6026,57 = 14MWLSDT7421, 58 = 2003MW6053, 59 = 2294, 60 = 2003MW6038 and 17ER = Erer, 17MS = Mieso, 17KB = Kobo, 17SR = Shaorobit,17SH=Sheraro.

Comparison Biplot of five test environments: The average environments coordinate (AEC) is a line that pass through the average environment (represented by small circle) and biplot origin. A test environment that has a small angle with the AEC is more representative of other test environments (Yan *et al*., 2000 and Yan *et al*., 2006). Thus, 17SR (Shoarobit) was more representative testing location (Figure 6). In agreement with this finding Gasura *et al*., (2015) reported the existence of a good testing environment for high yielding cultivar.

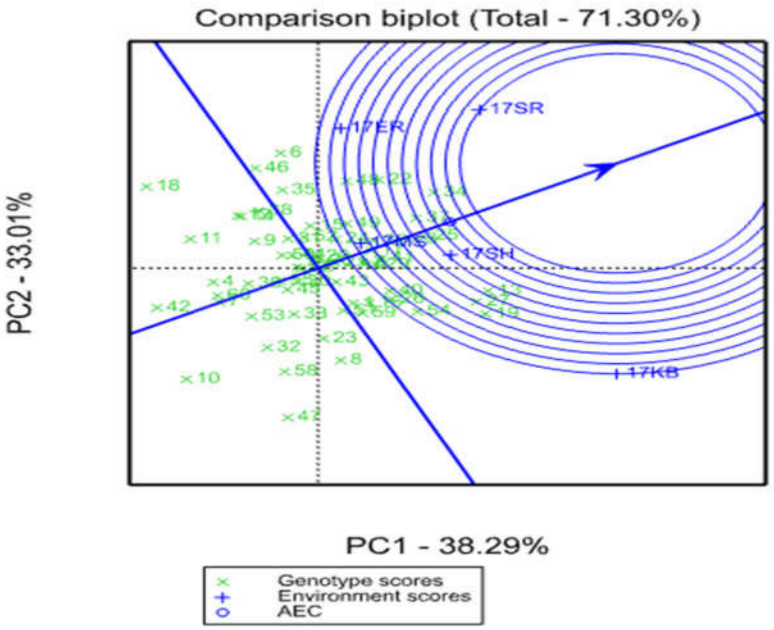


Figure 5: GGE-biplot showing a comparison of five testing environments with in ideal environment for grain yield (kg/ha).

An ideal genotype should have both high mean grain yield performance across environments. It is one which is near or at the centre of the concentric circle, and is also a genotype to be on average environmental coordinate (AEC) on positive direction and has vector length equal to the longest vector of the genotype and indicated by an arrow pointed to it (Yan *et al*., 2006 and Kaya *et al*., 2006). The Biplot indicated that genotype 34 is the most ideal genotypes, where as 37, 25, 3, 22, 41, 17 and 39 were nearest to the ideal genotype (the center of concentric circle). Therefore, these genotypes are more required and ideal genotypes than other tested genotypes. In line with this finding (Gasura *et al*., 2015) found the presence of that ideal genotype.

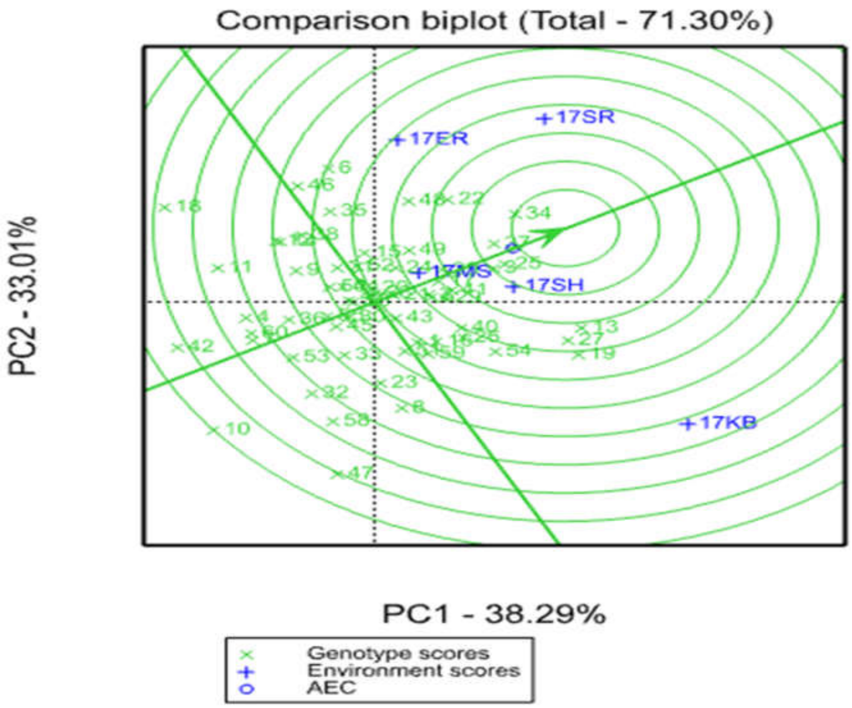


Figure 6: GGE-biplot showing a comparison of all genotypes with in ideal genotypes for grain yield (kg/ha).

4.3.4. AMMI stability value

In additive main effect and multiplicative interaction stability analysis (ASV) method, a genotype with lowest ASV score is the most stable across diverse environments and the higher the ASV value (either negative or positive) the more specifically adapted a genotype is to specific environments (Purchase, 1997). Table 11 shows ASV for each genotype and the ranks of the genotypes according to their ASV values. The results revealed that from the tested early maturing sorghum genotypes fifty one of them had ASV of below one.AccordinglyMelkam,14MWLSDT7060,12MW6251,14MWLSDT7410,12MW6302,14MWLSDT7395,14MWLSDT7310,13MW F6#6077,14MWLSDT7325,2005MI5069,14MWLSDT7196, 14MWLSDT7311, 14MWLSDT7, 14MWLSDT7193, 14MWLSDT733 2,14MWLSDT7209,12MW6440,14MWLSDT7201,14MWLSDT7364,Pipline2,14MWLSDT7413,13MWF6#6037,14MWLSDT7207, 14MWLSDT7040,14MWLSDT7036,14MWLSDT7324,12MW6243,12MW6420,14MWLSDT7238,12MW6444,14MWLSDT7402,1 4MWLSDT7234,14MWLSDT7042,14MWLSDT7033,14MWLSDT7241,14MWLSDT7191,2005MI5093,2401,2004MW6197,2005 MI5057,04MW6079,14MWLSDT7202,14MWLSDT7291,2001MS7036,90MW5319,99MW4047,05MW6026,14MWLSDT7421,200 3MW6053,2294,2003MW6038, were relatively widely stable (Table 11).

In contrary, due to their large ASV genotype 14MWLSDT7322, 14MWLSDT7400, 14MWLSDT7115, 14MWLSDT7176, 12MW6146, 12MW6471, 2005MI5064, 2523 and 04MW 6043 were the most unstable genotypes (Table 11). The mean yield of genotypes is also considered for selection of genotypes as a high yielder and stable genotypes. Among the selected widely stable early maturing genotypes the mean yield of twenty seven genotypes are above the grand mean. Therefore, based on mean yield and ASV, genotypeMelkam,14MWLSDT7060, 12MW6251, 12MW6302, 14MWLSDT7196, 14MWLSDT7157, 14MWLSDT7193,14MWLSD T7332,14MWLSDT7209, 12MW6440, 14MWLSDT7201, 14MWLSDT7364, Pipline 2, 14MWLSDT7413, 13MWF6#6037, 14MWL SDT7207, 14MWLSDT7040, 14MWLSDT7238,12MW6444,14MWLSDT7234,14MWLSDT7042,14MWLSDT7033,14MWLSDT72 41,2005MI50714MWLSDT7291, 90MW5319 and 05MW6026 are relatively high yielder and widely stable genotypes while the remaining twenty four genotypes are below the grand mean due to this they are low yielder and not selected as stable. The six most stable and high yielde early maturing sorghum genotypes obtained using this model were genotype 13MWF6#6037, 05MW6026, 14MWLSDT7207 ,14MWLSDT7234 , 14MWLSDT7042 and 12MW6440 (Table 11).

Table 11: IPCA1 and IPCA 2 scores; and ASV for the sixty early maturing sorghum genotypes sorted on ASV evaluated at five locations during 2017 main cropping season.

Entry#	Genotype Name	GY (kg/ha)	GY Rank	IPCA 1 Score	IPCA 2 Score	ASV	ASV Rank
27	13MWF6#6037	3465.1	4	0.5295	0.0861	0.0073	1
30	14MWLSDT7036	2685.27	41	0.0298	0.0648	0.0599	2
55	99MW4047	2589.24	47	-0.011	-0.2288	0.0735	3
56	05MW6026	2947.87	25	-0.049	-0.0007	0.091	4
28	14MWLSDT7207	3050.93	19	-0.0487	-0.0233	0.0916	5
37	14MWLSDT7234	3528.52	2	-0.054	0.0217	0.1009	6
39	14MWLSDT7042	3200.93	11	-0.023	0.274	0.1178	7
21	12MW6440	2868.93	31	0.0109	0.1171	0.1375	8
57	14MWLSDT7421	2803.77	36	-0.052	-0.2189	0.1459	9
4	14MWLSDT7410	2434.99	50	-0.164	-0.0592	0.155	10
2	14MWLSDT7060	3013.5	22	0.0727	-0.1466	0.1573	11
36	14MWLSDT7402	2540.45	49	-0.076	0.157	0.1666	12
41	14MWLSDT7241	3174.82	13	0.0891	-0.0697	0.1713	13
60	2003MW6038	2397.01	52	-0.083	0.1359	0.1746	14
17	14MWLSDT7332	3249.17	10	0.0151	0.3894	0.1798	15

7	14MWLSDT7395	2343.43	58	-0.043	-0.361	0.2102	16
29	14MWLSDT7040	3080.19	16	0.1148	-0.0436	0.2164	17
45	2004MW6197	2594.45	46	0.0523	-0.3767	0.2397	18
43	2005MI5093	2830.55	34	0.12	-0.1736	0.2543	19
25	Pipline 2	3462.67	5	0.0653	-0.3671	0.2568	20
20	14MWLSDT7209	2884.52	29	-0.067	0.3706	0.2627	21
24	14MWLSDT7364	3034.68	20	-0.113	-0.2562	0.2775	22
53	2001MS7036	2382.12	53	0.1122	-0.2763	0.286	23
50	04MW 6079	2799	38	-0.152	-0.0832	0.2909	24
34	14MWLSDT7238	3533.08	1	-0.138	-0.2093	0.3015	25
5	12MW6302	3099.92	15	0.0807	0.3983	0.3095	26
42	14MWLSDT7191	2024.65	60	-0.148	0.2156	0.3234	27
49	2005MI5057	3190.58	12	-0.178	0.1166	0.3458	28
52	14MWLSDT7291	2908.82	27	-0.195	-0.0825	0.3709	29
3	12MW6251	3284.55	8	0.0742	-0.501	0.3896	30
44	2401	2830.79	33	-0.127	-0.4071	0.4023	31
33	12MW6420	2673.53	42	0.1862	0.259	0.415	32
31	14MWLSDT7324	2847.04	32	-0.224	0.0018	0.4186	33
15	14MWLSDT7157	3028.49	44	-0.247	-0.0463	0.4633	34
9	14MWLSDT7310	2579.09	48	-0.277	-0.0263	0.5187	35
1	Melkam	2885.09	28	0.2653	0.2019	0.5365	36

51	14MWLSDT7202	2803.42	37	0.2858	-0.1505	0.5566	37
40	14MWLSDT7033	3067.98	17	0.2825	-0.1764	0.5591	38
32	12MW6243	2380.68	54	0.3084	0.0863	0.5836	39
16	14MWLSDT7193	2882.85	30	0.305	-0.1885	0.6055	40
26	14MWLSDT7413	2950.72	24	0.3381	-0.1374	0.6506	41
22	14MWLSDT7201	3343.65	7	-0.328	-0.2135	0.6588	42
59	2294	2783.55	39	0.3492	-0.3608	0.7827	43
11	14MWLSDT7325	2408.68	51	-0.44	0.006	0.8222	44
14	14MWLSDT7311	2652.33	21	-0.442	-0.016	0.8268	45
58	2003MW6053	2368.26	56	0.4762	0.0405	0.8915	46
54	90MW5319	3169.89	14	0.451	-0.263	0.9119	47
12	2005MI5069	2617.49	45	-0.451	-0.3249	0.9487	48
35	12MW6444	3052.16	18	-0.502	0.1086	0.9501	49
10	13MWF6#6077	2086.77	59	0.2831	0.6555	0.9586	50
13	14MWLSDT7196	3494.64	3	0.5006	0.2322	0.9892	51
8	14MWLSDT7400	2690.96	40	0.5376	0.0629	1.0084	52
23	12MW6146	2670.21	43	0.3848	0.2066	1.1322	53
19	14MWLSDT7176	3453.1	6	0.6155	-0.164	1.177	54
48	04MW 6043	3256.91	9	-0.402	0.6738	1.2054	55
46	2005MI5064	2964.41	23	-0.674	-0.0712	1.2652	56
6	14MWLSDT7322	2937.86	26	-0.684	-0.2423	1.3361	57

47	2523	2380.03	55	0.7144	0.3957	1.4914	58
18	14MWLSDT7115	2354.53	57	-0.813	-0.012	1.5191	59
38	12MW6471	2818.12	35	-0.443	1	1.8276	60
	Mean	2863.9					

Where GY = Grain yield by AMMI, ASV = AMMI Stability value, IPCA 1 Score = Interaction prinicipal component analysis Score 1 and IPAC 2 Score = Interaction prinicipal component analysis Score 2.

5. SUMMERY AND CONCLUSION

Sorghum (*Sorghum bicolor*) is one of the major important cereal crops which the lives of millions of people depend and grows in areas where other major cereals marginally grown. However, drought becomes the major problem for sorghum production in Ethiopia especially in drought prone areas of the country which needs the development of drought tolerant or resistance varieties. The yield performance of crop varieties is also highly affected by genotype x environment interaction which is the major concern to plant breeders while developing improved varieties. In view of this, the yield performance of 60 early maturing advanced sorghum genotypes were tested for further confirmation with the objectives of estimating the magnitude of GXE for grain yield and other traits and to identify high yielder and stable genotypes across locations.

The experiment was conducted at five locations during 2017 main cropping season. The experiment was carried out using RCBD with Row Column arrangement and three replications. Recommended fertilizer application and agronomic practices were followed at each location. Data on grain yield, phenological and other traits were collected from all locations. The data collected were subjected to spatial analysis and linear mixed model for individual and across locations and stability analysis using various models.

In spatial analysis, plots that are located together in the field are more likely to have similar yield due to shared micro-environment. The spatial analysis for each location revealed that the genotypes were significantly different for grain yield. This showed that there were genetic difference among genotypes for grain yield at each location. The REML combined analysis of variance across locations showed very highly significant ($P \leq 0.0001$) difference among locations, significant ($P \leq 0.05$) among genotypes and highly significant ($P \leq 0.0001$) among interactions for most of the traits studied. Significant component of variation for locations and genotype indicated variation in the performance of genotypes for grain yield, phenological and other traits in different environments. On the other hand, significant GXE interaction showed inconsistency in the performance of sorghum genotypes across locations, that is, the relative performances of genotypes were significantly affected by the varying environmental conditions. The partitioning of the combined analysis of variance component for grain yield indicated that environments, genotypes and G x E interaction contributed 86.4 %, 1.9 % and 10.9 %, respectively, for the total variance. Larger proportion of environment variance indicated the larger effect of environment on yield performance of sorghum genotypes in the test environment than other variances components.

The mean yield of genotypes across location was 2863.9 kg/ha; with genotype means grain yield ranged from 2024.6 kg/ha to 3533.1kg/ha, indicating wide difference in yield potential across locations. The genotype with the lowest mean grain yield was 14MWLSDT7191 (2024.6 kg/ha). The performance of the standard check (Melkam = 2885.1kg/ha) was statistically different to the top fifteen high yielding genotypes but higher than the grand mean (2863.95 kg/ha). Shaorobit and Sheraro were the highest yielding environments with mean values of 5174.0 kg/ha and 3706.7 kg/ha, respectively, indicate the two environments are suitable for sorghum production, whereas Mieso, Erer and Kobo were the poorest yielding environments with mean grain yields of 1099.0 kg/ha, 1508.5 kg/ha and 2832.1 kg/ha, respectively.

Eberhart and Russell's joint regression model, AMMI, GGE biplot model and ASV models were used for grain yield to identify superior and relatively stable genotypes across location. Eberhart and Russell's joint regression ANOVA showed that the performance of genotypes for grain yield was statistically different. The GXE (linear) was not significant and the pooled deviation was significant. The interaction sum square was accounted largely by the pooled deviation (79 %) and only 21 % by the GXE (linear).

The combined AMMI ANOVA showed significant differences among genotypes and the presence of interaction effect. In this study including the IPCA residual both the first two IPCAs were significant. For the total variation the treatment variation accounted about 99.1 % %, and for the treatment variation was attributed to genotype variation 4.86 %, location variation 84.36 %% and interaction 10.78%. In addition 76.46 % of the interaction effect was explained by the first two IPCAs.

Based on Eberhart and Russell's stability analysis, considering their above average mean grain yield, bi value closest to unity and the S^2di value is small, genotype Melkam, 05MW6026, 14MWLSDT7207, 2005MI5064, 12MW6302, 14MWLSDT7332, 12MW6444, and 14MWLSDT7042 were stable genotypes. However, the check (Melkam) genotype was low yielder as compared to these selected stable genotypes. Thus, genotypes 05MW6026, 14MWLSDT7207, 14MWLSDT7332, 12MW6444, 12MW6302 and 14MWLSDT7042 were the most stable and high yielder genotypes. Genotype 14MWLSDT7060, 12MW6251, 14MWLSDT7322, 14MWLSDT7196, 14MWLSDT7193, 14MWLSDT7176, 12MW6440, and 14MWLSDT7201, 14MWLSDT7364, Pipline 2, 14MWLSDT7413,13MWF6#6037, 14MWLSDT7040, 14MWLSDT7238, 14MWLSDT7234, 14MWLSDT7033, 14MWLSDT7241, 14MWLSDT7291, 90MW5319 had b_i value of greater than one and above mean yield performance. Therefore, these genotypes were highly contributed to the GXE and were suitable for conducive environments. In contrary, genotype 2003MW6038, 14MWLSDT7410, 13MWF6#6077, 14MWLSDT7324, 14MWLSDT7325, 12MW6243, 14MWLSDT7402, 12MW6471, 14MWLSDT7191, 2523, and 2003MW6053 had $b_i$value less than one and these genotypes were contributed less to the GXE. Hence, these genotypes are suitable for harsh environments.

AMMI 2 biplot helps in visual interpretation of the G x E interaction patterns and identify genotypes or locations that show small and large interaction effects. Accordingly, environments Erer, Kobo and Shaorobit were the most enfluencing environments due to large interaction while Mieso and Sheraro had less enfluencing environments. In AMMI 2 biplot, the genotypes, 12MW6471, 2523, 14MWLSDT7176, 12MW6251, 14MWLSDT7322 had large interactions due to large IPCA 1 and IPCA 2, and are the best or poorest genotypes in some or all environments because they are farthest from the origin where as the best genotype is 14MWLSDT7322 with respect to the best enhancing environment Shaorobit and the poor genotype is 2523 due to its value below average value. On the other hand, the genotypes 14MWLSDT7234, 05MW6026, 14MWLSDT7207, 14MWLSDT7036, Pipline 2, 12MW6440 ,14MWLSDT7042,14MWLSDT7421,99MW4047,14MWLSDT7040,14MWLSDT7241, 14MWLSDT7291, 14MWLSDT7402, 14MWLSDT7324 and 14MWLSDT7332 were close to the origin and therefore were less/non-sensitive to environmental interaction. However, genotypes 14MWLSDT7421, 99MW4047 and 14MWLSDT7324 were below average yield. Genotypes 14MWLSDT7207, 05MW6026 and 14MWLSDT7234 were the most yielding and stable due to very close to the origin.

GGE biplot is the best method as compared to AMMI biplot to show graphically the 'which-won where' and the relationship between testers and mega environments. Therefore, based on the overall mean grain yield and stability of this multi-location trial, genotype 14MWLSDT7238 could be recommende to locations Erer, Shaorobit, Mieso and Sheraro areas that share similar characteristics. Likewise, genotype 14MWLSDT7176 could be recommended to location Kobo. Genotypes 14MWLSDT7207, 05MW6026, 14MWLSDT7209 and 12MW6440 fortunately, could be grown in all testing locations due to the high yielding and stable genotypes. However, genotype 14MWLSDT7421 was the lower yielding and stable genotype.

Additive Main Effects and Multiplicative Interaction stability value (ASV) was one of the stability models to identify the stable genotype for this study. Accordingly, The six most stable and high yielder early maturing sorghum genotypes on this model were genotype 13MWF6#6037, 05MW6026, 14MWLSDT7207, 14MWLSDT7234, 14MWLSDT7042 and 12MW6440.

The results of genotype x environment interaction and stability analysis methods indicated that, Eberhart and Russell's stability analysis, AMMI 2 biplot, GGE biplot and ASV analysis identified two early maturing sorghum genotypes 05MW6026 and 14MWLSDT7207 that had a high mean performance and high stability for grain yield. Therefore, genotype 05MW6026 and 14MWLSDT7207 can be recommended as a candidate for releasing over a wide range of locations of the lowland Ethiopia.

In general, results from this study gave valuable information for future studies related to allocation of early maturing sorghum genotypes to different growing conditions in the dry lowlands areas of Ethiopia. The sorghum growing dry lowland areas of Ethiopian were various and contributed largely to the changes of genotypes yield performance over locations. Therefore, further study on the GXE effects and stability of early maturing sorghum genotypes is needed in multi locations for a number of years and location to determine the interaction effect of genotypes and select stable genotypes. Since the current study was conducted only for one year, the work should be repeated at least for some more years to give sound conclusions and reliable recommendations.

REFERENCES

Abay Fetien and A. Bjornstad, 2009. Specific adaptation of barley varieties in different locations in Ethiopia. Euphytica, 167:161-195.

Abiy Legesse and Firew Mekbib., 2016. Genotype X Environment Interaction and Stability of Early Maturing Sorghum [*Sorghum bicolor* (L.) Moench] Genotypes in Ethiopia. M.Sc. Thesis, Alemaya University of Agriculture, Ethiopia:2016-01-04T05:19:25Z.

Abush Tesfaye, V P. Gupt and Ketema belete, 2001. Genotype X Environment Interaction in Land Race Derived Advanced Lines of Sorghum (Sorghum bicolor L. Moench). M.Sc. Thesis.

Akcura, M., Kaya, Y., Taner, S. and Ayranci, R., 2006. Parametric stability analyses for grain yield of durum wheat. Plant Soil Environ, 52(6): 254–261.

Ali A., Qamar, I.A, Arshad, M., and Sheikh, S., 2001. Correlation of economically important traits in sorghum bicolor varieties. Ongenotype J of Biolog. Science. 1 (5):330 331.

Alberts, M.J.A., 2004. Comparison of statistical methods to describe genotype x environment interaction and yield stability in multi-location maize trials. M.Sc. Thesis, University of the Free State. Bloemfontein, South Africa.

Allard, R.W. and Bradshaw, A.D., 1964. Implications of Genotype by environment interactions in applied plant breeding. *Crop science,* 4:503-508.

Almeida, F.J.E., Tardin, F.D., Daher, R.F., Barbe, T.C., Paula, C.M., Cardoso, M.J. and Godinho, V.P.C. 2014. Stability and adaptability of grain sorghum hybrids in the off-season. *Genetic and Molecular Research,* DOI http://dx.doi.org/10.4238/.

Al-Temimi, H.N., Al-Shahwany, A.W. and Alsaadawi, I.S., 2013. Screening of bread wheat cultivars (Triticum aestivum L.) to water deficit stress under field conditions. Journal of Science, 54(3): 577-584.

Annicchiarico, P., 1997. Joint regression Vs. AMMI analysis of genotype-environment interactions for cereals in Italy. Euphytica, 94: 53-62.

Anandan, A, R Eswaran, T Sabesan and M Prakash, 2009. Additive main effects and multiplicative interactions analysis of yield performances in rice genotypes under coastal sagenotype environments. Advances in Biological Research, 3:43-48.

Asfaw Adugnua, 2007. Assessment of Yield Stability in Sorghum, African Crop Science Journal, vol.15, No, 2 pp 83-92.

Assar, A. H., R. Uptmoor, A.A. Abdelmula , C. Wagner , M. Salih, A. M. Ali, F. Ordon and W. Friedt, 2009. Assessment of sorghum genetic resources for genetic diversity and drought tolerance using molecular markers and agro-morphological traits. U. of K. J. Agric. Sci. 17(1):1-22.

Baker, R.J., 1990. Crossover genotype by environmental interaction in spring wheat. pp. 42–51. *In:* Kang, M.S. (Ed.) *Genotype by Environment Interaction and Plant Breeding*. Louisiana State University Agricultural Center, Baton Rouge, Louisiana.

Bakheit, B. R., 1990. Variability and correlations in grain sorghum genotypes (Sorghum bicolor [L.] Moench) under drought conditions at different stages of growth. Journal of Agronomy and Crop Science, 165(5): 355–360.

Basford, K. E. and Cooper, M., 1998. Genotype x environment interactions and some considerations of their implications for wheat breeding in Australia. Australian Journal of Agricultural Research, 49:153-174.

Becker, H. C. and Léon, L., 1988. Stability analysis in plant breeding. Plant Breeding, 101:123.

Blum, A., 1983. Genetic and physiological relationship in plant breeding for drought resistance. Agr. Water Mgmt. 7:195-205.

Borrell A, Hammer G, van Oosterom E (2001). Stay-green. A consequence of the balance between supply and demand for nitrogen during grain filling? Ann. Appl. Biol. 138:91-95.

Borrell, A.K., G.L. Hammer and R.G. Henzell, 2000b. Does maintaining green leaf area in Sorghum improve yield under drought? II. Dry matter production and yield. Crop Science, 40: 1037-1048.

Bowman. J. C., 1972. Genotype X Environment Interactions (1), Department of Agriculture, University of Reading, Great Britain, Ann. Genet. Sel. anim., I972,4(I), II7-I23.

Burgueno, J., A. Cadena, J. Crossa, M. Banziger, A.R. Gilmour, B. Cullis., 2000. *User's* Guide for Spatial Analysis of Field Variety Trials Using ASREML. Mexico, D.F.: CIMMYT, ISBN: 970-648-060-9.

Burke, J.J., Franks, C.D., Burow, G. and Xin, Z., 2010. Selection system for the stay-green drought tolerance trait in sorghum germplasm. Journal of Agronomy, 102(4): 1118-1122.

Butler, J. D., Byrne, P. F., Mohammadi, V., Chapman P. L., and Haley, S. D., 2005. Agronomic performance of Rht Alleles in a spring wheat population across a range of moisture levels. Crop Science, 45:939- 947.

Burton, G.W. and E.H. DeVane, 1953. Estimation of heritability in tall Festuca (*Festuca arudindcea*) from replicated clonal material. *Agronomy* J., **45**: 78-481.

Ceccarelli, S. and S. Grando, 2007. growing Areas of Tigray Region, northern Ethiopia. Decentralized-participatory plant breeding:. An example of demand driven research. Euphytica, 155(3): 349-360.

Central Statistical Agency of Ethiopia (CSA), 2017. Agricultural Sample Survey 2016/2017. Stat Bull, 584.

Crossa, J., Gauch, H.G. and Zobel, R.W., 1990. Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. Crop Science, 30: 493 500.

Cruz- Aguado, J., R. Rodes, I. Perez and M. Dorado, 2000. Morphological characteristics and yield components associated with accumulation and loss of dry mass in the internode of wheat. Field Crop Research, 66: 129-139.

Cullis B. R, Gogel B. J, Verbyla A. P, Thompson R., 1998. Spatial analysis of multi-environment early generation trials, Biometrics, vol.54, pp.1-18.

Cullis B.R, Smith A.B, Coombes N.E, 2006. 'On the Design of Early GenerationVariety Trials With Correlated Data', Journal of Agriculture, Biological and Environmental Statistics, vol.11, no.4, pp.381-393.

Dagnachew Lule, Masresha Fetene, Santie de Villiers and Kassahun Tesfaye, 2014. Additive Main Effects and Multiplicative Interactions(AMMI) and genotype by environment interaction (GGE) biplot analyses aid selection of high yielding and adapted finger millet varieties. J. Appl. Biosci., 76:6291–6303.

Das, S, R C Misra, M C Patnaik and S R Das., 2010. G × E interaction, adaptability and yield stability of midearly rice genotypes. Indian J of Agric. Res., 44:104-111.

Dehghani H., A. Ebadi, and A. Yousefi, 2006. Biplot Analysis of Genotype by Environment Interaction for Barley Yield in Iran. Agron. J. 98:388–393.

Dillon SL, Shapter FM, Henry RJ, Cordeiro G, Izquierdo L, Lee LS, 2007. Domestication to Crop Improvement: Genetic Resources for Sorghum and Saccharum Andropogoneae. Ann Bot, 100:975-989.

Ding, M., Tier, B. and Yan, W., 2007. Application of GGE Biplot Analysis to Evaluate Genotype, Environment and GxE Interaction on P. radiata: A Case Study. http://proceedings.com.au/afgc/slides%20(PDF)/thurs%201600%20ding.pdf.

Domitruk, D.R., Duggah, B.L. and Fowler, D.B. 2001. Genotype by environment interaction of no-till winter wheat in Western Canada. Canadian Journal of Plant Science, 81:7-16.

Dugan, W. and Labuschagne, M.T. , 2002. G x E interaction and phenotypic stability analysis of linseed in Ethiopia. *Plant Breed*., 121: 66-71.

Eberhart, S.A. and Russell, W.A. 1966. Stability parameters for comparing varieties. Crop Science, 6: 36-40.

Ethiopian Institute of Agricultural Research (EIAR), 2014. Ethiopian strategy for sorghum. Counry strategy document.

Ezeaku IE, Mohammed SG, 2006. Character association and path analysis in grain sorghum. Afr. J. Biotechnol., 5(14): 1337-1340.

Fantaye Belay and Hintsa Meresa, 2017. Performance evaluation of sorghum [*Sorghum bicolor* (L.) Moench] hybrids in the moisture stress conditions of Abergelle District, Northern Ethiopia. Academic journal, Vol. 8(4), pp. 26-32, April 2017:DOI: 10.5897/JCO2016.0168.

Finlay,G.J., Bullock, P.R., Sapirstein, H.D., Naeem, H.A., Hussain, A., Angadi, S.V., and DePauw, R.M., 2007. Genotypic and environmental variation in grain, flour, dough and bread-making characteristics of western Canadian spring wheat. Can. J. Plant Sci., 87: 679–690.

Finlay, K.W. and Wilkinson, G.N., 1963. The analysis of adaptation in a plant breeding program. Australian Journal of Agricultural Research, 14: 742-754.

Fisher R.A., 1925. Statistical methods for research works. Oliver and Boyd, London.

Francis, T.R. and Kannenburg, L.W., 1978. Yield stability studies in short season maize. A descriptive method for grouping genotypes. Canadian Journal of Plant Sciences, 58:1029-1034.

Freeman, G.H., 1973. Statistical methods for the analysis of genotype-environment interactions. Heredity, 31: 339-354.

Freeman, G.H., 1990. Modern statistical methods for analysing genotype x environment interactions. In: Kang, M.S.(ed.).Genotype-by-environment interaction and plant breeding. Louisiana State University Agricultural Center, Baton Rouge, La. pp.118 125.

Gasura, E., Setimela, P. S. and Souta, C. M., 2015. Evaluation of the performance of sorghum genotypes using GGE biplot. Canadian. Journal of Plant Sci. 95(6): 1205–1214.

Gauch, H.G. 1982a. Noise reduction by eigenvector ordinations. Ecology, 63: 1634-1649.

Gauch, H.G., 1982b. Multivariate analysis in community ecology. 1sted, Cambridge University press, London and New York, ISBN-10: 0521282403.

Gauch, H.G. 1988. Model selection and validation for yield trials with interaction. Biometrics, 44: 705-715.

Gauch, H.G. and Zobel, R.W. 1997. Identifying mega-environments and targeting genotypes. Crop Science, 37(2): 311-326.

Gebeyehu Geremew, Asfaw Adugna, Taye Tadesse, Tesefaye Tesso, Ketema Belete, Hailemichael H, 2004. Development of sorghum varieties and hybrids for dry land areas of Ethiopia. Uga J Agri Sci., 9:594-605.

Gebrekidan H, 2003. Grain Yield Response of Sorghum [*Sorghum bicolor* (L.) Moench] to Tied Ridges and Planting Methods on Entisols and Vertisols of Alemaya Area, Eastern Ethiopian Highlands.

Gleeson, A. C., and Cullis, B. R., 1987. Residual Maximum Likelihood (REML) Estimation of a Neighbour Model for Field Experiments, *Biometrics,* 43, 277-288.

Gilmour, A. R., Cullis, B. R., and Verbyla, A. P., 1997. Accounting For Natural And Extraneous Variation In The Analysis Of Field Experiments,"Journal of Agricultural, Biological, and Environmental Statistics, 2, 269–273.

Gul, I., Saruhan, V., Basbag, M., 2005. Determination of yield and yield components and relationship among the components of grain sorghum cultivars grown as main crop. Asian Journal of Plant Sciences, 4: 613-618.

Hagos T. and Fetien A., 2011. Additive Main Effects and Multiplicative Interactions analysis of yield performance of sesame genotypes across environments in Northern Ethiopia. *Journal of the drylands*, 4(1): 259-266.

Harlan J, De Wet J., 1972. A simplified classification of cultivated sorghum. Crop Science, **12**:172-176.

IBPGR and ICRISAT, 1993. Descriptors for sorghum *[sorghum bicolor*(L.)Moench]. International Board for plant genetic Resources, Rome, Italy; International Crops Research Institute for the Semi -Arid Tropics, Patancheru, India.

Frew Mekbib, 2005. The contribution of farmers' breeders in meeting food security: the case of sorghum (Sorghum bicolor (L.) Moench) in Ethiopia. Journal.

Kang, M.S., 1996. Using genotype-by-environment interaction for crop cultivar development. Advances in Agronomy, 62: 199-252.

Kang, M.S., 1998. Using genotype by environment interaction for crop cultivar development. *Advances in Agronomy, 62*: 199-252.

Kassahun Amare, Habtamu Zeleke and Geremew Bultosa, 2015. Variability for yield, yield related traits and association among traits of sorghum (Sorghum Bicolor (L.) Moench) varieties in Wollo, Ethiopia. M.Sc. Thesis. Haramaya University, College of Agriculture, Department of Plant Sciences, Haramaya, Ethiopia, Vol7(5),pp125-133, May 2015: DOI: 10.5897/JPBCS2014.0469.

Kempton, R A., 1984. The use of biplots in interpreting variety by environment interactions. J of Agric. Sci., 103:123135.

Kenga, R., Alabi, S. and Gupta, O., 2003. Yield stability of sorghum hybrids and parental genotypes. African Crop Science Journal, 11(2): 65-73.

Kinde L., Gebeyehu C., Abubeker T., Dadi G., Shanene H., Abdela U., 2016. Evaluation of Sorghum (Sorghum bicolor (L) Moench) Varieties and Environments for Yield Performance and Stability, Journal of Biology, Agriculture and Healthcare, Vol.6, No.21, 2016.

Kulsum, M U, M Jamil Hasan, A Akter, H Rahman and P Biswas., 2013. Genotype-environment interaction and stability analysis in hybrid rice: an application of additive main effects and multiplicative interaction. Bangladesh J. Bot., 42(1): 73-81.

Leiser, W.L., Rattunde, H.F., Piepho, H.-P., Parzies, H.K., 2012. Getting the most out of sorghum low-input field trials in West Africa using spatial adjustment. J. Agron.Crop Sci. 198, 349–359.

Lin, C.S., Binns, M.R. and Lefkovitch, L.P., 1986. Stability analysis: where do we stand ?.Crop Science, 26: 894-899.

Ludlow, M.M. and Muchow, R.C.,1990. A critical evaluation of the traits for improving crop yield in water limited environments. Advance Agronomy, 43: 107-153.

Lyle F. Friesen, Anita L. Brûlé-Babel, Gary H. Crow, and Patricia A. Rothenburger., 2016. Mixed model and stability analysis of spring wheat genotype yield evaluation data from Manitoba, Canada: Can. J. Plant Sci., 96: 305–320 (2016):dx.doi.org/10.1139/cjps-2015-0252.

Mahalanobis, P.C., 1936. On the generalized distance in statistics. Pro. Nat. Sci India, B 2: 49-55.

Mahnaz, R., Ezatollah, F. and Mohammad, M. J., 2013. Additive Main Effect and Multiplicative Interaction Analysis of phenotypic stability in chickpea genotypes over stress and non-stress environments. *International Journal of Agriculture and Crop Sciences*, 5(36):253-260.

Maposa, D., Mudimu, E. and Ngwenya, O. A., 2010. Multivariate analysis of variance (MANOVA) of the performance of sorghum genotypes in different agro-ecological regions of Zimbabwe. *African Journal of Agricultural Research*, 5(3): 196-203.

McBee GG., 1984. Relation of senescence, nonsenescence, and kernel maturity to carbohydrate metabolism in sorghum. In: Mughogho LK (Ed.) Sorghum root and stalk diseases, a critical review. Proceedings of the consultative group discussion of research needs and strategies for control of sorghum root and stalk diseases. Bellagio, pp. 119-129.

Meckel, L., D.B. Egli, R.E. Phillips, D. Radcliiffe and J.E. Leggett, 1984. Effect of moisture stress on seed growth in soybeans. Agronomy Journal, 76: 647-650.

MOORTHY, S. M., N.K. DAS and K.MANDAL, 2012. Genotype x Environment interaction and stability analysis in bivoltine silkworm genotypes of Bombyx moriL. IJBPAS, 1(10): 1443-1449.

Muez Mehari, Sentayehu Alamerew, Berhane Lakew, Haddis Yirga and Mizan Tesfay. 2014. Parametric stability analysis of malt barley genotypes for grain yield in Tigray, Ethiopia. World Journal of Agricultural Sciences, 10 (5): 210-215.

Parmar D.J., G.N. Motaka, J.S. Patel and S.G. Patel, 2016. Study on different stability procedures for yield of rice genotypes (O*ryza sativa* L.): Department of Agricultural Statistics, B.A. College of Agriculture, AAU, Anand- 388110. International Journal of Science, Environment, ISSN 2278-3687 (O) and Technology, Vol. 5, No 3, 2016, 1503 – 1514

Paterson, A.H., Bowers, J.E., Bruggmann, R., Dubchak, I., Grimwood, J., Gundlach, H., Haberer, G., Hellsten, U., Mitros, T., Poliakov, A. and Schmutz, J., 2009.The Sorghum bicolor genome and the diversification of grasses. Nature, 457(7229), pp.551-556.

Pham, H. N. and Kang, M.S. 1988.Interrelationships among and repeatability of several stability statistics estimated from international maize trials. Crop Science,28: 925-928.

P. O. Kurt Polat, E. A. Cifci, and K. Yagdı, 2016. Stability Performance of Bread Wheat (*Triticum aestivum L.)* Genotypes: J. Agr. Sci. Tech. (2016), Vol. 18: 553-560.

Plant Genetic Resources Centre/Ethiopia, 1986. Ten years of collection, conservation and utilization, 1976-86. PGRC/E, Addis Ababa, Ethiopia.

Purchase, J.L,. 1997. Parametric analysis to describe genotype by environment interaction and stability in winter wheat. PhD. thesis. Department of Agronomy, Faculty of Agriculture, University of the Orange Free State, Bloemfonten, South Africa.

Rakshit S, Hariprasanna K, Gomashe S, Ganapathy KN, Das IK, Ramana OV, Dhandapani A, Patil JV, 2014. Changes in Area, Yield Gains, and Yield Stability of Sorghum in Major Sorghum Producing Countries, 1970 to 2009. Crop Sci., 54:1571–1584.

Richards R. A., 2006. Physiological traits used in the breeding of new cultivars for water-scarce environments. Agric. Water Manage, 80: 197–211.

Sabaghnia, N., Dehghani, H. and Sabaghpour, S.H. 2006. Non-parametric methods for interpreting genotype by environment interaction of lentil genotypes. *Crop Science Journal,* 46: 1100-1106.

Samonte, S.O.P.B., L.T. Wilson, A.M. McClung and J.C. Medley, 2005. Targeting Cultivars on to Rice Growing Environments Using AMMI and SREG GGE Biplot Analyses. Crop Science 45:2414-2424.

Sarah Brumlop and Maria R. Finckh, 2011. Applications and potentials of marker assisted selection (MAS) in plant breeding.

Sewagegne Tariku, Taddesse Lakew, Mulugeta Bitew and Mitiku Asfaw. 2013. Genotype by environment interaction and grain yield stability analysis of rice (*Oryza sativa* L.) genotypes evaluated in north western Ethiopia. Net Journal of Agricultural Science, 1(1): 10-16.

Shrestha, S.P., Asch, F., Dusserre, J., Ramanantsoanirine, A. and Brueck, H. 2012. Climate effects on yield components as affected by genotypic responses to variable environmental conditions in upland rice systems at different altitudes. Field Crops Research, 134:216-228.

Shukla, G.K. 1972. Some statistical aspects of partitioning genotype-environmental components of variability. Heredity, 29: 237-24.

Sintayehu Admas and Kassahun Tesfaye, 2017. Genotype-by-environment interaction and yield stability analysis in sorghum [*Sorghum bicolor* (L.) Moench] genotypes in North Shewa, Ethiopia. Ethiopian Biodiversity Institute, P.O. Box 30726, Addis Ababa, Ethiopia: DOI: 10.1515/ausae-2017-0008.

Smith CW, Frederiksen RA, 2000. History of cultivar development in the United States: From "memories of A.B. Maunder – Sorghum breeder". In: Smith CW, Fredriksen RA (eds) Sorghum: Origin, history, technology and production, pp 191-223.

Suzuki, D., Griffiths, A. and Lewontin, R., 1981. An introduction to genetic analysis. W. H. Freeman and Company. San Francisco, USA.

Tardieu, F., 2013. Plant response to environmental conditions: assessing potential production, water demand, and negative effects of water deficit. Frontiers in physiology, 4:17.

Taye T. Mindaye , Emma S. Mace , Ian D. Godwin , David R. Jordan, 2016. Heterosis in locally adapted sorghum genotypes and potential of hybrids for increased productivity in contrasting environments in Ethiopia. The University of Queensland, Queensland, Alliance for Agriculture and Food Innovation, Hermitage Research Facility. 604 Yangan Rd, Warwick, QLD, 4370, Australia. Journal of crop science: https://doi.org/10.1016/j.cj.2016.06.020

Taye T., T. Tesfaye., and G. Ejeta, 2008. Combining ability of introduced sorghum parental lines for major morpho-agronomic traits. Journal of SAT Agricultural Research.

Taylor, J. R. N., 2003. Overview importance of sorghum in Africa [Ongenotype].Available from: http: WWw.sciencedirect/science.

Tesfaye Letta, M. G. D'Egidio and Mohammed Abinasa. 2008. Analysis of multi-environment yield trials in durum wheat based on GGE-biplot. Journal of Food, Agriculture & Environment Vol.6 (2): 217 – 221.

Thomas H, Rogers LJ., 1990. Turning over an old leaf. Univ. Wales Rev. Sci. Tech. 6:29-38.

Tolk JA, Howell TA, Miller FR, 2013. Yield component analysis of grain sorghum grown under water stress. Field Crop Res., 145:44-51.

USDA, 2017. World Agricultural Production U.S. Department of Agriculture Foreign Agricultural Service / Office of Global Analysis International Production Assessment Division (IPAD): Ag Box 1051, Room 4630, South Building Washington, DC 20250-1051.

Vange, T., Ango I. and Nache A.V., 2014. Stability analysis of six improved sorghum genotypes across four environments in the Southern Guinea Savanna of Nigeria. Internationals Journal of Advances in Agricultural Science and Technology, 2 (2): 01-14.

Van Oosteriom, E.J., R. Jayachandram, and F.R. Bidininger. 1996. Diallel analysis of the stay green traits and its components in sorghum. Crop Sci. 36:549-555.

Vieira, R.D., D.M. Tekrony and D.B. Egli, 1992. Effect of drought stress and defoliation in the field on soybean seed germination and vigor. Crop Science, 32: 471-475.

Wolfe DW, Henderson DW, Hsiao TC, Alvino A., 1988. Interactive water and nitrogen effects on senescence of maize. II. Photosynthetic decline and longevity of individual leaves. Agron. J. 80:865-870.

Wricke, G., 1964. Zur berechnung der ıkovalenz bei sommerweizen und hafer. Z. Pflanzenzuchtg, 52: 127-138.

Yan, W., 2001. GGE biplot: a windows application for graphical analysis of Multi-Environment trial data and other types of two way data. Agronomy Journal 93: 1111-1118.

Yan, W. and Tinker, N.A. 2005. An integrated biplot analysis system for displaying, interpreting and exploring genotype by environment interactions. *Crop Science,* 45: 1004–16.

Yates, F. and Cochran, W.G., 1938. The analysis of group of experiments. Journal of Agricultural Science, 28: 556-580.

Yayeh, Z and P.W. Bosland. 2000. Evaluation of genotype, environment and genotype by environment interaction for capsaicinoids in Capsicumannum L. Euphytica, 111: 185-190.

Younesi, O., and Moradi, A., 2009. The effect of water limitation in the field on sorghum seed germination and vigor. Australian Journal of Basic and Applied Sciences, 3(2): 1156-1159, INSInet Publication.

Zerihun Tadesse, Dagne wagery and Sintayehu Alamrew, 2011. Genotype X Environment Interaction Yield stability analysis of Maize (Zea Mays L) in Ethiopia: M.Sc thesis.

APPENDIX

Appendix Table 1: Variance component estimation by REML of early maturing sorghum genotypes for grain yield, phenological and other traits tested at Erer, Kobo, Mieso, Sheraro and Shewa Robit during 2017 main cropping season.

		Traits							
Site	VarComponent	DTE	PN	PL	PW	PE	DS	STG	PWt
	Genotype	0.08ns	29.81***	3.54***	0.8***	1.56***	0.68***	0.56***	336386***
SR	Replicate	0ns	0.02ns	0.07ns	0.1ns	0ns	0.01ns	0.02ns	766ns
	Error	0.79	1.58	1.41	0.8	0.16	0.36	0.3	41246
	Genotype	0.06ns	59.77***	2.63***	0.3***	0.57***	0.15***	0.32***	303386***
ER	Replicate	0.01ns	0ns	0ns	0.1ns	0ns	0ns	0ns	108.8ns
	Error	0.46	2.21	0.59	0.3	0.06	0.06	0.1	13009
	Genotype	0.12*	42.35***	4.31***	0.1*	0.44***	0.18**	0.2**	200479***
MS	Replicate	0.1ns	0.16ns	0ns	0ns	0ns	0ns	0ns	0ns
	Error	0.51	4.54	2.51	0.2	0.18	0.31	0.3	35254
	Genotype	0.01ns	22.65***	3.94***	0.1ns	0.72***	0.27***	0.4***	506450***
KB	Replicate	0.01ns	0ns	0ns	0ns	0ns	0ns	0ns	0ns
	Error	0.19	11.82	1.04	0.4	0.24	0.23	0.2	24507
	Genotype	0.03*	37.34***	1.91*	1*	0.16***	0.55***	0.93***	175877***
SH	Replicate	0.02ns	0.04ns	0.03ns	0.9ns	0.01ns	0ns	0ns	5284ns
	Error	0.12	7.18	3.79	3.1	0.11	0.21	0.2	48397

Where REML = Residual Maximum Likelihood, DTE = Days to Emergency, PN = Panicle number, PL = Panicle length, PW = Panicle width, PE = Panicle exersion, DS = Drought score, STG = Staygreen, PWt = Panicle weight, SR = Shaorobit, ER = Erer, MS = Mieso, KB = Kobo, SH = Sheraro, *** = vary highly significant ($P\leq 0.0001$), ** = highly significant ($P\leq 0.001$), * = significant ($P\leq0.05$) and ^{ns} = insignificant ($P>0.05$).

Appendix Table 2: Variance component estimation by REM of early maturing sorghum genotypes for grain yield, phonological and other complex traits tested at five locations during 2017 main cropping season.

	Estimate				error
Traits	Gen	Rep/Site	Site	G:S	
GY	61140*	76.11ns	2743000***	346000***	25870
DTE	0.04**	0.02**	1.42ns	0.01ns	0.43
DTF	10.48***	0.08ns	23.15ns	1.49**	8.41
DTM	0.55*	0.54ns	53.95ns	1.8**	9.95
GFP	6.61***	0.46ns	73.55ns	3.31**	19.62
GFR	65.51*	2.07ns	2098.39ns	256.85***	82.54
PHT	491.94***	0ns	1138.56ns	203.7***	41.91
PWt	42903.5*	574.9ns	1849005ns	261291.8***	33091
PN	7.3*	0.03ns	176.72ns	31.05***	5.48
PL	2.56***	0.01ns	4.31ns	0.7***	1.88
PW	0.28***	0.1ns	1.31ns	0.12*	1.06
PE	0.52***	0.00003ns	0.47ns	0.17***	0.15
DS	0.1*	0.0003ns	0.58ns	0.27***	0.241
STG	0.29***	0.002ns	0.24ns	0.19***	0.21
TSW	4.25***	0ns	7.03ns	7.24***	2.61

Where REML = Residual Maximum Likelihood, DTE = Days to Emergency, DTF = Days to flowering, DTM = Days to maturity, GFP = Grain filling period, GFR = Grain filling rate, PHT = Plant heght, PN = Panicle number, PL = Panicle length, PW = Panicle width, PE = Panicle exersion, DS = Drought score, STG = Staygreen, PWt = Panicle weight, TSW = Thousand weight, *** = vary highly significant (P≤ 0.0001), ** = highly significant (P≤ 0.001), * = significant (P≤0.05) and ^{ns} = insignificant (P>0.05).

Appendix Table 3: Predicted mean grain yield (kg/ha) of sixty early maturing sorghum genotypes by spatial model tested at Erer, Kobo, Mieso, Sheraro and Shewa Robit during 2017 main cropping season.

Genotype code	Genotype Name	Expperimental Locations				
		ER	KB	MS	SH	SR
1	Melkam	1358	2851	1048	3661	4857
2	14MWLSDT7060	1341	3193	1189	4300	5506
3	12MW6251	1475	3398	1331	4763	6238
4	14MWLSDT7410	1309	2746	983	3433	4527
5	12MW6302	1622	2684	1080	3489	5145
6	14MWLSDT7322	2184	2655	1289	3741	6413
7	14MWLSDT7395	1024	3088	1019	3928	4546
8	14MWLSDT7400	1145	2854	965	3549	4359
9	14MWLSDT7310	1828	2519	1089	3288	5297
10	13MWF6#6077	589	2742	697	3030	2816
11	14MWLSDT7325	1926	2252	1013	2835	4991
12	2005MI5069	1486	3018	1170	4047	5495
13	14MWLSDT7196	1657	2896	1185	3909	5654
14	14MWLSDT7311	1957	2442	1107	3212	5446
15	14MWLSDT7157	1691	2799	1157	3745	5539
16	14MWLSDT7193	1557	2856	1129	3778	5337
17	14MWLSDT7332	1388	2965	1109	3893	5158
18	14MWLSDT7115	2018	2282	1062	2941	5268
19	14MWLSDT7176	1240	3342	1214	4527	5568
20	14MWLSDT7209	2113	2146	1040	2736	5219
21	12MW6440	1773	2613	1108	3435	5356
22	14MWLSDT7201	1814	3099	1335	4381	6434
23	12MW6146	1101	2897	966	3606	4342
24	14MWLSDT7364	1460	3122	1205	4229	5644
25	Pipline 2	1587	3235	1304	4514	6173
26	14MWLSDT7413	1938	2537	1140	3381	5592
27	13MWF6#6037	1115	3401	1190	4570	5392
28	14MWLSDT7207	1435	2896	1097	3787	5129
29	14MWLSDT7040	1478	3029	1172	4064	5500
30	14MWLSDT7036	1426	2803	1053	3605	4918
31	14MWLSDT7324	1693	2691	1111	3540	5325
32	12MW6243	1269	2621	913	3176	4183
33	12MW6420	835	3153	972	3947	4230
34	14MWLSDT7238	2135	2857	1357	4098	6706

35	12MW6444	1800	2700	1157	3616	5596
36	14MWLSDT7402	1340	2720	984	3401	4549
37	14MWLSDT7234	1436	3283	1266	4522	5913
38	12MW6471	1994	2079	964	2543	4801
39	14MWLSDT7042	1600	2868	1150	3824	5461
40	14MWLSDT7033	1500	2980	1160	3983	5453
41	14MWLSDT7241	1617	2924	1182	3940	5616
42	14MWLSDT7191	1360	2399	853	2802	3947
43	2005MI5093	1689	2721	1122	3594	5377
44	2401	1515	2957	1156	3948	5444
45	2004MW6197	1194	3146	1111	4130	5065
46	2005MI5064	2084	2528	1194	3445	5921
47	2523	733	2774	768	3172	3224
48	04MW 6043	2356	2158	1141	2891	5815
49	2005MI5057	1592	2922	1171	3924	5555
50	04MW 6079	964	3351	1109	4393	4935
51	14MWLSDT7202	1426	2868	1082	3730	5051
52	14MWLSDT7291	1710	2749	1143	3660	5484
53	2001MS7036	1273	2840	1010	3593	4634
54	90MW5319	1273	3205	1167	4285	5370
55	99MW4047	1414	2897	1089	3777	5080
56	05MW6026	1244	3009	1071	3897	4906
57	14MWLSDT7421	1430	2941	1115	3869	5207
58	2003MW6053	988	2862	906	3478	4003
59	2294	1685	2746	1131	3640	5418
60	2003MW6038	1325	2620	935	3204	4313
	Mean	1509	2832	1099	3707	5174

Where ER = Erer, KB = Kobo, MS = Mieso, SH = Sheraro, SR = Shaorobit.

Appendix Table 4: Means for grain yield, phenological and other complex traits of sixty early maturing advanced sorghum genotypes by mixed model tested at Erer during 2017 main cropping season.

Entry#	Genotype Name	DTE	DTF	GFP	DTM	GFR	PHT	PWt	TSW	PN	PL	PW	PE	DS	STG
1	Melkam	7.0	71.7	32.0	103.7	49.3	128.5	1937.1	29.3	33.7	27.8	15.0	2.9	2.8	3.9
2	14MWLSDT7060	6.7	71.0	33.0	104.0	36.0	125.0	1286.9	25.3	44.0	20.9	15.1	2.4	2.5	3.0
3	12MW6251	7.3	72.3	34.7	107.0	35.9	147.4	1769.9	25.7	38.3	23.5	15.1	3.2	2.8	3.2
4	14MWLSDT7410	6.7	72.0	31.3	103.3	36.2	139.3	1536.1	24.3	38.0	28.2	15.5	3.4	3.5	3.0
5	12MW6302	6.7	73.0	28.0	101.0	81.7	125.1	1943.3	24.6	42.0	24.9	14.6	1.9	3.1	4.2
6	14MWLSDT7322	6.7	73.0	33.0	106.0	66.4	175.5	1873.7	23.3	34.7	21.2	14.1	1.9	2.9	2.9
7	14MWLSDT7395	6.7	63.3	43.0	106.3	11.8	125.0	430.2	26.7	35.0	24.4	14.6	1.0	2.7	2.2
8	14MWLSDT7400	6.0	67.7	39.7	107.3	17.1	144.1	653.5	26.5	26.3	23.9	15.4	3.1	3.7	4.3
9	14MWLSDT7310	7.3	72.0	33.7	105.7	46.6	157.8	2226.5	22.2	32.7	22.6	15.5	1.7	3.0	3.4
10	13MWF6#6077	7.0	74.0	26.0	100.0	54.1	107.7	1357.9	19.1	40.3	24.5	14.1	2.1	2.4	2.9
11	14MWLSDT7325	6.7	74.7	30.7	105.3	47.5	144.1	1145.0	25.0	26.0	21.5	14.5	1.9	2.8	3.3
12	2005MI5069	8.0	72.3	31.7	104.0	48.6	163.1	1597.1	29.9	34.3	21.4	14.5	3.3	2.8	3.7
13	14MWLSDT7196	7.3	69.3	35.7	105.0	52.8	140.3	1760.5	27.6	31.3	22.3	15.3	3.8	3.6	4.0
14	14MWLSDT7311	6.7	71.7	33.7	105.3	54.4	192.5	1692.4	25.2	37.3	22.3	14.6	1.3	3.2	3.3
15	14MWLSDT7157	6.7	71.7	31.3	103.0	59.3	154.9	1883.4	28.1	38.7	21.8	14.8	2.0	2.5	3.0
16	14MWLSDT7193	6.0	62.3	45.3	107.7	19.0	135.7	975.5	26.6	53.0	21.0	15.3	3.1	3.4	4.2
17	14MWLSDT7332	7.0	72.3	29.7	102.0	85.7	179.0	2281.7	20.7	36.0	19.3	14.8	3.8	3.0	3.6
18	14MWLSDT7115	7.0	73.0	30.3	103.3	65.0	178.8	1876.0	23.3	38.3	24.0	14.3	3.3	2.9	2.3
19	14MWLSDT7176	7.3	66.3	42.7	109.0	25.2	142.7	1119.0	31.7	31.7	24.2	15.7	1.9	3.0	3.5
20	14MWLSDT7209	7.7	75.3	32.3	107.7	62.6	176.6	2101.1	26.0	35.0	21.5	14.3	1.6	2.1	1.9
21	12MW6440	7.3	70.7	30.7	101.3	56.2	150.9	1975.8	22.4	36.3	23.1	15.0	3.8	3.5	4.0
22	14MWLSDT7201	7.3	70.3	31.3	101.7	73.7	151.0	1312.4	25.7	34.0	22.0	15.3	2.2	2.8	3.3
23	12MW6146	7.3	71.3	38.0	109.3	31.7	110.3	1009.4	25.3	33.3	25.7	15.3	2.1	2.4	3.5
24	14MWLSDT7364	6.3	72.0	31.0	103.0	48.7	167.3	2309.2	25.4	50.7	22.8	15.2	1.9	3.0	3.4
25	Pipline 2	6.3	68.7	35.7	104.3	40.3	166.0	1601.3	23.4	36.0	21.7	16.3	2.1	3.2	3.7

26	14MWLSDT7413	7.7	73.7	30.3	104.0	28.3	137.0	1203.8	24.9	30.0	22.7	15.0	2.7	3.4	3.2
27	13MWF6#6037	7.3	67.7	31.0	98.7	55.4	153.5	1755.3	24.7	42.0	21.2	17.0	2.6	3.0	3.9
28	14MWLSDT7207	5.7	71.7	27.3	99.0	56.4	152.1	1769.8	31.0	37.3	22.9	15.2	1.8	1.9	2.1
29	14MWLSDT7040	6.7	70.0	35.3	105.3	46.6	150.3	1326.3	29.7	29.3	22.1	15.6	2.2	2.8	4.1
30	14MWLSDT7036	7.3	72.0	35.3	107.3	45.5	141.3	1159.3	30.0	25.7	22.3	15.1	3.0	3.3	4.0
31	14MWLSDT7324	7.0	73.0	33.3	106.3	52.7	187.0	1495.3	20.0	35.3	21.4	13.7	1.8	2.5	3.5
32	12MW6243	7.0	70.3	35.7	106.0	19.2	115.0	1563.7	23.5	42.0	24.0	14.7	2.8	2.5	3.8
33	12MW6420	7.0	75.0	29.3	104.3	56.5	123.2	1755.5	19.5	43.0	20.7	15.0	4.2	2.6	2.8
34	14MWLSDT7238	7.0	72.0	33.0	105.0	62.1	160.7	2182.1	24.6	42.0	24.7	14.5	1.9	2.3	2.3
35	12MW6444	6.3	72.3	33.7	106.0	72.6	169.3	2192.5	24.0	43.3	22.1	14.9	2.2	2.7	2.9
36	14MWLSDT7402	6.7	71.0	31.7	102.7	48.9	185.6	1524.1	27.1	27.0	23.0	14.2	1.6	2.6	2.9
37	14MWLSDT7234	6.3	72.0	29.7	101.7	81.9	156.3	2179.7	25.1	50.7	23.4	14.9	1.8	2.1	2.3
38	12MW6471	6.7	75.7	32.7	108.3	111.3	187.8	3063.5	29.5	47.0	21.0	14.4	1.8	2.8	2.5
39	14MWLSDT7042	7.0	71.3	33.0	104.3	72.9	159.0	2188.1	30.9	27.7	23.0	14.9	2.7	2.8	3.9
40	14MWLSDT7033	7.3	68.3	39.0	107.3	27.2	126.6	1042.2	22.7	25.3	23.0	15.5	2.2	2.7	3.9
41	14MWLSDT7241	7.0	73.0	35.3	108.3	44.5	162.7	1791.2	30.9	41.7	24.1	15.1	1.9	2.2	2.5
42	14MWLSDT7191	6.0	76.3	31.0	107.3	38.0	143.3	1204.8	25.2	27.0	20.9	14.7	4.1	2.9	3.1
43	2005MI5093	7.0	72.0	34.0	106.0	29.6	138.0	1138.3	26.2	39.0	20.4	14.6	1.8	3.2	3.8
44	2401	6.7	62.3	47.7	110.0	19.0	136.3	986.4	26.3	48.0	22.1	14.3	1.5	2.9	2.7
45	2004MW6197	7.0	70.0	35.0	105.0	20.7	167.9	1080.0	26.3	56.0	21.8	14.3	2.1	3.4	3.3
46	2005MI5064	7.3	73.3	30.7	104.0	73.2	150.8	2500.8	30.0	50.0	21.6	14.2	1.6	2.6	3.2
47	2523	7.0	62.7	42.3	105.0	14.2	136.4	674.7	28.4	48.0	22.7	14.0	3.6	2.9	3.1
48	04MW 6043	7.7	62.0	41.7	103.7	92.6	176.2	2434.5	25.0	38.0	24.4	14.6	2.9	3.8	3.5
49	2005MI5057	6.3	71.7	35.3	107.0	63.9	163.0	2122.8	32.3	46.3	24.1	14.5	1.9	2.7	2.9
50	04MW 6079	7.3	72.0	32.3	104.3	52.5	139.3	2160.2	24.7	41.7	22.2	13.9	3.0	2.7	3.2
51	14MWLSDT7202	7.3	68.7	35.3	104.0	23.4	148.3	1016.2	22.3	45.7	20.5	14.4	2.3	2.3	2.7
52	14MWLSDT7291	6.7	70.3	36.3	106.7	44.8	177.4	1765.4	28.2	39.3	22.5	14.2	1.4	2.8	2.6
53	2001MS7036	6.7	63.0	48.3	111.3	8.9	155.5	876.5	30.2	44.0	25.3	14.1	1.3	3.0	3.0

54	90MW5319	6.3	62.3	41.0	103.3	19.4	129.0	873.3	24.0	53.0	22.6	15.4	1.7	2.3	2.8
55	99MW4047	6.7	67.7	39.0	106.7	24.6	120.4	1088.9	27.8	43.0	22.7	14.1	2.5	3.3	3.5
56	05MW6026	6.7	65.7	38.3	104.0	40.8	144.3	1676.6	27.3	53.0	22.3	13.8	1.8	2.2	3.1
57	14MWLSDT7421	6.7	68.7	31.3	100.0	36.4	154.9	1626.8	32.5	38.3	21.5	13.8	1.9	2.6	2.7
58	2003MW6053	7.3	68.0	37.7	105.7	13.0	149.1	587.9	26.4	44.3	25.7	14.8	2.9	2.4	2.8
59	2294	6.7	62.0	44.7	106.7	8.3	113.0	523.1	31.0	26.7	22.1	14.8	1.4	2.7	2.4
60	2003MW6038	6.7	68.7	35.3	104.0	36.6	147.7	1328.5	25.4	40.0	23.3	14.9	2.8	2.7	3.2
	Mean	6.9	70.1	34.8	104.9	45.8	149.8	1558.5	26.2	38.8	22.8	14.8	2.4	2.8	3.2

Where, DTE = Days to Emergency, DTF = Days to flowering, DTM = Days to maturity, GFP = Grain filling period, GFR = Grain filling rate, PHT = Plant heght, PN = Panicle number, PL = Panicle length, PW = Panicle width, PE = Panicle exersion, DS = Drought score, STG = Staygreen, PWt = Panicle weight, TSW = Thousand weight.

Appendix Table 5: Means for grain yield, phonological and other complex traits of sixty early maturing advanced sorghum genotypes by mixed model tested at Kobo during 2017 main cropping season.

Entry#	Genotype Name	DTE	DTF	GFP	DTM	GFR	PHT	PWt	TSW	PN	PL	PW	PE	DS	STG
1	Melkam	7.7	80.3	51.0	117.3	70.0	149.4	3638.2	32.4	39.3	22.2	13.4	4.0	3.0	4.3
2	14MWLSDT7060	8.7	83.0	51.3	120.3	60.5	178.4	3681.0	32.8	45.3	18.7	13.9	2.3	3.7	3.7
3	12MW6251	8.0	81.7	53.7	121.3	60.2	190.8	3568.0	34.7	44.3	19.6	13.7	4.3	3.7	3.7
4	14MWLSDT7410	8.0	86.7	50.3	123.0	36.5	204.5	2872.1	26.3	43.0	25.4	14.0	4.0	4.3	3.3
5	12MW6302	7.7	81.3	49.0	116.3	73.2	138.3	3427.4	24.0	51.0	23.2	13.6	2.7	3.3	5.0
6	14MWLSDT7322	8.0	86.3	48.3	120.7	33.4	231.0	2146.1	35.7	45.7	18.5	13.9	2.7	4.3	3.3
7	14MWLSDT7395	8.0	78.0	58.3	122.3	30.2	163.8	2256.4	31.5	42.7	20.7	13.8	1.0	3.3	2.3
8	14MWLSDT7400	8.0	80.7	51.3	118.0	72.9	180.1	4218.3	31.7	48.0	20.4	14.3	3.7	3.3	5.0
9	14MWLSDT7310	8.0	82.7	51.7	120.3	40.1	219.6	2408.1	31.0	51.3	19.3	13.9	2.7	4.0	4.7
10	13MWF6#6077	7.7	81.0	46.7	113.7	57.1	131.3	3031.1	19.2	51.3	21.2	14.3	3.3	3.7	4.0
11	14MWLSDT7325	8.3	89.3	43.3	118.7	33.4	225.6	1722.9	31.9	40.7	18.2	13.5	2.3	4.0	4.3
12	2005MI5069	7.3	86.7	46.0	118.7	30.6	178.5	1907.1	34.3	26.7	18.4	14.4	3.7	4.3	4.3
13	14MWLSDT7196	8.3	80.0	54.3	120.3	90.4	176.1	4854.8	33.3	47.3	19.7	14.6	4.0	3.0	4.0
14	14MWLSDT7311	8.0	83.0	53.3	122.3	33.2	229.8	2332.9	29.0	47.0	17.1	13.6	1.3	4.3	3.0
15	14MWLSDT7157	8.0	84.0	50.3	120.3	48.1	201.8	2953.8	34.6	42.7	16.3	13.4	3.0	3.3	4.0
16	14MWLSDT7193	7.7	72.0	57.0	115.0	61.5	150.9	3534.1	38.9	43.3	15.8	13.9	3.3	3.3	5.0
17	14MWLSDT7332	8.0	84.0	53.0	123.0	65.2	171.7	4198.8	34.7	46.0	14.0	13.6	4.3	3.0	3.3
18	14MWLSDT7115	8.0	91.7	51.0	128.7	12.7	215.4	1833.8	23.2	40.7	21.7	13.6	4.7	5.0	2.0
19	14MWLSDT7176	7.7	76.0	59.3	121.3	78.4	191.7	3481.1	37.7	45.3	20.1	14.4	3.0	3.7	4.3
20	14MWLSDT7209	8.0	79.3	54.3	119.7	57.8	186.1	3402.3	31.1	41.3	18.9	14.1	1.7	3.7	2.7
21	12MW6440	8.0	79.7	52.0	117.7	59.9	185.0	3399.0	31.4	48.7	19.6	13.8	4.3	4.3	4.3
22	14MWLSDT7201	8.3	80.7	53.0	119.7	50.5	181.8	3079.7	35.6	39.0	19.9	13.5	2.7	4.3	4.3
23	12MW6146	8.3	80.3	51.3	117.7	67.9	150.7	3692.0	27.1	44.3	23.0	14.8	3.0	3.3	4.3
24	14MWLSDT7364	7.7	81.7	55.3	123.0	47.3	193.2	2919.9	32.1	44.0	20.2	13.9	2.3	3.7	4.3
25	Pipline 2	8.0	76.0	55.7	117.7	60.5	207.8	3644.1	33.7	49.0	17.8	14.8	2.0	3.7	4.7

26	14MWLSDT7413	8.0	79.0	53.7	118.7	70.9	200.5	3898.1	29.9	46.7	17.6	13.2	3.3	3.7	4.3
27	13MWF6#6037	8.0	77.3	54.7	118.0	84.6	160.8	4804.8	34.8	45.7	17.9	15.2	3.0	2.3	3.3
28	14MWLSDT7207	7.7	79.7	54.7	120.3	49.7	184.5	2859.9	30.7	42.7	18.9	14.2	2.3	4.0	3.7
29	14MWLSDT7040	7.7	77.3	53.7	117.0	62.8	187.6	3681.5	33.0	41.0	20.1	14.1	2.7	3.3	4.7
30	14MWLSDT7036	8.0	80.7	51.0	117.7	54.6	181.9	3344.3	34.8	41.3	18.8	14.3	2.7	3.3	4.3
31	14MWLSDT7324	8.0	83.0	46.0	115.0	51.0	243.9	2656.6	31.0	50.0	18.8	13.9	2.3	3.7	4.7
32	12MW6243	8.7	84.0	48.0	118.0	63.3	139.4	3890.2	28.8	47.3	21.5	14.2	3.7	3.0	5.0
33	12MW6420	7.7	84.3	50.0	120.3	59.7	142.2	3634.1	22.6	50.3	17.8	14.4	4.7	4.3	3.7
34	14MWLSDT7238	8.0	83.7	50.7	120.3	66.8	190.8	3777.8	29.5	49.7	22.9	14.4	2.7	3.3	2.7
35	12MW6444	8.0	82.3	52.0	120.3	38.8	206.1	2749.0	32.6	48.7	18.8	13.9	3.3	4.3	4.0
36	14MWLSDT7402	8.0	80.7	55.3	122.0	42.3	258.1	3068.6	33.7	47.0	18.0	13.8	1.3	3.7	3.3
37	14MWLSDT7234	8.0	81.7	54.3	122.0	62.8	186.2	3481.5	28.6	45.0	20.0	13.9	2.3	3.0	3.3
38	12MW6471	8.0	85.7	50.3	122.0	52.9	211.5	3347.3	34.8	42.0	19.7	13.8	2.3	2.7	3.3
39	14MWLSDT7042	8.0	79.0	53.0	118.0	64.1	196.4	4368.7	35.0	50.7	19.9	14.3	2.7	3.3	4.3
40	14MWLSDT7033	8.0	79.7	57.3	123.0	62.6	188.2	4079.3	35.6	49.0	21.5	14.5	3.3	3.0	4.3
41	14MWLSDT7241	8.3	86.0	45.7	117.7	74.5	210.7	3693.9	28.4	48.3	20.0	13.7	2.7	3.3	3.7
42	14MWLSDT7191	8.0	86.7	48.7	121.3	34.9	170.4	2519.6	29.9	45.0	18.6	14.5	5.0	4.3	4.0
43	2005MI5093	8.3	82.0	50.7	118.7	60.5	215.9	3351.9	31.3	51.7	16.1	14.1	2.3	3.7	4.7
44	2401	7.7	70.7	61.3	118.0	35.3	180.2	2959.8	32.7	50.3	17.9	13.2	2.0	3.7	3.7
45	2004MW6197	8.3	85.0	48.7	119.7	48.4	179.7	2096.4	32.8	45.0	19.6	14.3	2.7	4.7	3.7
46	2005MI5064	8.0	87.3	44.7	118.0	34.0	185.1	1718.3	31.4	26.7	19.1	13.3	1.7	4.7	4.0
47	2523	8.0	70.7	62.0	118.7	61.0	155.5	3831.4	32.0	49.0	20.0	14.2	3.7	3.0	2.7
48	04MW 6043	8.7	82.3	49.3	117.7	63.3	190.1	4055.8	28.0	37.3	20.6	14.2	3.7	3.7	5.0
49	2005MI5057	8.3	82.0	52.3	120.3	55.4	211.4	3305.8	36.7	43.0	21.7	13.7	2.0	3.7	3.7
50	04MW 6079	7.7	83.7	50.0	119.7	43.9	189.6	2718.5	25.7	42.3	19.3	14.0	2.7	4.0	4.0
51	14MWLSDT7202	8.0	74.0	62.3	122.3	52.6	194.1	3389.3	35.6	45.3	15.0	14.1	2.7	3.0	4.0
52	14MWLSDT7291	8.0	80.0	56.0	122.0	43.7	249.0	3251.3	34.0	46.7	18.5	13.4	1.3	5.0	2.7
53	2001MS7036	8.0	80.7	55.0	121.7	41.8	211.6	2514.4	27.4	48.0	22.3	13.3	2.0	5.0	4.3

54	90MW5319	8.0	69.3	63.7	119.0	61.2	167.7	3728.7	32.8	44.7	17.7	13.8	2.3	3.0	4.3
55	99MW4047	8.0	82.3	48.7	117.0	48.7	147.1	2817.5	33.3	38.0	18.2	13.6	3.0	3.7	3.7
56	05MW6026	8.0	77.7	52.3	116.0	49.2	195.2	2560.2	34.0	48.0	17.9	13.5	2.3	3.7	3.7
57	14MWLSDT7421	8.0	78.0	54.7	118.7	45.2	213.0	2766.4	30.1	46.3	17.6	13.1	3.0	4.0	4.0
58	2003MW6053	8.3	73.3	59.3	118.7	54.3	182.7	3470.7	32.0	33.3	22.8	14.0	3.0	3.0	3.7
59	2294	8.0	68.3	67.0	121.3	51.0	175.4	3308.2	32.3	44.3	18.9	14.3	2.0	3.7	3.0
60	2003MW6038	7.7	77.3	58.0	121.3	36.3	206.7	2489.8	34.7	39.7	18.8	14.2	3.7	4.3	4.0
	Mean	8.0	80.7	52.9	119.6	53.6	189.0	3206.5	31.6	44.6	19.4	14.0	2.9	3.7	3.9

Appendix Table 6: Means for grain yield, phonological and other complex traits of sixty early maturing advanced sorghum genotypes by mixed model tested at Mieso during 2017 main cropping season.

Entry#	Genotype Name	DTE	DTF	GFP	DTM	GFR	PHT	PWt	1000GW	PN	PL	PW	PE	DS	STG
1	Melkam	6.7	78.7	36.0	114.7	21.7	126.3	920.3	34.7	13.3	32.8	14.8	2.7	3.3	3.3
2	14MWLSDT7060	5.7	76.0	34.0	110.0	18.7	129.2	1034.0	34.8	17.0	22.4	13.4	2.0	3.0	3.0
3	12MW6251	6.7	75.7	34.7	110.3	26.8	148.7	1444.7	35.3	24.3	24.8	14.0	2.7	3.3	2.7
4	14MWLSDT7410	6.3	79.0	32.7	111.7	40.5	159.2	1671.1	31.7	25.7	31.8	14.1	3.0	2.3	2.3
5	12MW6302	6.7	80.3	33.3	113.7	31.2	120.5	1106.8	30.9	24.7	25.1	13.2	1.7	3.7	3.7
6	14MWLSDT7322	6.3	80.0	31.3	111.3	22.6	180.3	1491.0	30.0	23.0	21.4	13.4	1.7	3.0	3.0
7	14MWLSDT7395	6.3	75.0	39.7	114.7	25.4	138.9	1355.5	30.0	22.7	25.8	13.6	1.0	2.3	2.7
8	14MWLSDT7400	5.7	77.0	34.0	111.0	34.1	164.4	1550.9	28.7	37.0	24.7	13.1	2.0	3.3	3.7
9	14MWLSDT7310	6.3	80.7	36.7	117.3	17.0	170.5	967.6	28.9	31.3	22.3	13.2	1.3	3.3	3.3
10	13MWF6#6077	6.0	79.3	38.0	117.3	17.2	111.8	1646.5	29.7	23.7	28.1	13.6	2.0	2.3	2.3
11	14MWLSDT7325	5.7	81.0	33.3	114.3	39.6	178.4	1835.2	31.7	31.3	22.6	13.8	1.3	2.3	3.0
12	2005MI5069	7.3	78.0	35.0	113.0	18.0	139.8	1271.0	29.4	16.3	22.6	13.3	2.7	3.0	3.3
13	14MWLSDT7196	6.7	79.0	31.3	110.3	36.8	148.2	2059.2	28.7	32.0	23.3	13.2	3.3	3.3	3.7
14	14MWLSDT7311	5.7	79.3	33.7	113.0	29.8	200.6	1648.7	32.0	38.0	24.0	13.3	1.0	3.7	3.7
15	14MWLSDT7157	5.3	76.7	33.3	110.0	49.1	168.7	1789.8	33.8	34.3	25.8	13.7	2.0	3.3	2.7
16	14MWLSDT7193	5.7	69.7	37.7	107.3	23.9	135.3	1726.4	33.0	20.7	23.0	13.4	2.3	3.3	3.3
17	14MWLSDT7332	6.0	79.0	32.7	111.7	39.9	138.8	2046.9	35.3	32.3	21.1	14.0	3.0	2.7	3.0
18	14MWLSDT7115	6.3	78.7	35.7	114.3	26.5	165.1	1734.3	42.0	23.0	27.7	13.6	2.7	2.7	2.3
19	14MWLSDT7176	6.3	76.0	34.0	110.0	42.7	143.8	2111.2	39.7	26.7	26.7	14.0	1.7	3.3	3.3
20	14MWLSDT7209	6.0	79.0	34.0	113.0	38.3	165.1	2219.2	32.3	32.0	23.3	13.4	1.3	2.7	2.7
21	12MW6440	7.0	80.0	31.0	111.0	22.6	142.9	1452.0	33.7	16.7	25.2	13.3	3.3	3.3	4.0
22	14MWLSDT7201	6.7	78.7	32.0	110.7	30.9	147.3	2211.6	39.7	27.3	22.4	13.3	1.7	3.0	3.7
23	12MW6146	7.0	80.3	31.0	111.3	24.5	131.8	988.2	39.9	22.0	26.4	13.4	2.0	2.7	3.3
24	14MWLSDT7364	5.3	77.3	34.7	112.0	35.5	144.2	1570.2	41.0	29.7	23.9	14.0	1.3	3.0	2.7
25	Pipline 2	6.0	75.7	34.3	110.0	53.5	165.9	1968.6	35.3	34.3	24.0	14.2	2.0	2.7	3.0

26	14MWLSDT7413	6.7	77.3	34.3	111.7	29.9	127.1	1947.0	30.1	36.7	23.6	13.1	2.7	3.3	3.0
27	13MWF6#6037	7.3	77.7	33.3	111.0	32.6	138.6	1324.4	29.2	22.7	23.6	14.4	2.0	3.3	3.7
28	14MWLSDT7207	5.9	76.0	33.7	109.7	63.8	195.9	2503.2	31.7	34.3	26.0	13.6	1.3	1.3	1.7
29	14MWLSDT7040	6.0	77.7	34.0	111.7	25.7	142.6	1343.1	29.8	25.7	22.9	13.4	1.7	3.3	4.0
30	14MWLSDT7036	6.3	81.3	31.7	113.0	20.4	171.0	1124.6	32.1	16.0	23.7	13.2	2.3	3.7	3.7
31	14MWLSDT7324	6.0	81.3	32.3	113.7	40.3	201.3	2019.9	30.3	36.0	24.8	13.4	1.3	2.3	3.3
32	12MW6243	6.7	80.0	30.3	110.3	29.4	96.0	2027.6	28.7	27.7	26.2	13.6	2.7	3.7	3.3
33	12MW6420	6.7	83.0	34.3	117.3	19.0	123.1	1093.3	30.4	22.0	22.2	13.2	4.0	3.3	2.7
34	14MWLSDT7238	6.0	77.3	34.7	112.0	40.8	162.0	2080.9	33.3	31.0	28.0	13.9	1.7	3.0	2.3
35	12MW6444	5.7	79.0	35.7	114.7	46.5	152.0	2539.0	32.0	32.7	24.2	13.2	2.0	2.7	3.0
36	14MWLSDT7402	6.7	78.0	36.0	114.0	25.3	174.1	1744.2	36.0	27.7	24.3	13.1	1.0	2.7	3.3
37	14MWLSDT7234	5.3	75.3	34.3	109.7	44.4	162.0	1153.5	43.1	37.3	24.4	13.4	1.7	2.7	2.3
38	12MW6471	6.0	82.0	35.0	117.0	15.5	152.6	1290.2	39.7	18.7	22.0	13.6	1.3	3.0	2.7
39	14MWLSDT7042	6.3	77.3	35.3	112.7	28.0	160.0	1405.5	38.0	22.3	24.8	13.6	2.0	3.3	3.7
40	14MWLSDT7033	6.0	77.3	34.7	112.0	35.7	179.5	2240.5	33.7	32.0	24.8	13.3	2.0	2.7	3.3
41	14MWLSDT7241	6.3	75.3	34.0	109.3	40.9	156.0	1899.8	29.7	33.0	27.6	13.6	1.7	2.3	2.7
42	14MWLSDT7191	5.0	82.0	35.3	117.3	14.7	140.7	1223.8	32.1	18.0	22.6	13.6	3.3	3.3	3.3
43	2005MI5093	6.7	78.3	32.0	110.3	33.8	155.8	1966.1	31.7	22.3	22.1	13.0	1.3	3.7	3.3
44	2401	6.0	74.7	37.3	112.0	45.3	148.2	2477.8	39.2	32.3	23.2	13.8	1.0	1.7	1.7
45	2004MW6197	6.3	76.7	34.0	110.7	20.0	135.6	1425.1	36.0	21.7	25.0	13.4	2.0	3.7	4.0
46	2005MI5064	6.0	75.3	35.3	110.7	49.4	160.5	1773.3	31.8	31.3	22.7	13.4	1.0	2.3	2.7
47	2523	6.3	75.7	36.0	111.7	33.2	150.8	1156.8	34.0	33.3	23.2	13.1	3.0	3.7	4.0
48	04MW 6043	6.7	79.3	34.0	113.3	30.9	152.6	2068.0	29.8	22.3	26.1	13.3	2.3	3.3	3.7
49	2005MI5057	5.0	73.3	36.7	110.0	38.0	151.5	2020.7	28.0	31.0	26.7	13.7	1.7	2.7	3.3
50	04MW 6079	6.7	82.7	33.3	116.0	25.2	147.6	1342.5	30.8	16.0	24.8	14.2	2.7	2.3	2.7
51	14MWLSDT7202	6.0	77.3	35.7	113.0	31.4	172.5	1506.5	32.3	27.7	23.7	13.3	2.0	3.3	3.3
52	14MWLSDT7291	6.3	76.7	33.3	110.0	39.8	190.3	2229.6	31.4	37.0	25.0	13.3	1.0	2.7	3.0
53	2001MS7036	6.0	77.3	35.7	113.0	25.7	158.1	1169.0	33.3	27.7	27.8	13.1	1.0	2.7	3.3

54	90MW5319	5.0	69.0	39.3	108.3	38.3	135.1	1217.4	30.3	37.0	23.8	13.4	1.0	2.3	2.3
55	99MW4047	6.7	78.7	32.7	111.3	22.0	103.3	1521.4	32.6	22.3	26.0	13.2	2.0	3.3	3.3
56	05MW6026	5.7	76.7	32.7	109.3	58.0	191.2	2883.7	36.0	37.0	23.8	13.0	1.3	2.0	2.7
57	14MWLSDT7421	6.0	77.7	34.0	111.7	40.6	147.0	1769.4	37.6	33.3	22.1	13.1	1.7	2.3	2.7
58	2003MW6053	7.0	75.3	35.3	110.7	18.7	133.6	972.4	29.4	20.7	26.1	13.3	2.0	2.7	2.7
59	2294	5.7	67.3	44.3	111.7	22.5	134.7	995.2	36.1	27.3	21.9	13.1	1.0	3.3	3.0
60	2003MW6038	6.7	80.3	32.7	113.0	33.7	147.9	1329.1	35.7	24.0	25.9	13.2	2.0	2.3	3.3
	Mean	6.2	77.7	34.5	112.1	32.1	151.9	1643.4	33.3	27.3	24.6	13.5	1.9	2.9	3.1

Where, DTE = Days to Emergency, DTF = Days to flowering, DTM = Days to maturity, GFP = Grain filling period, GFR = Grain filling rate, PHT = Plant heght, PN = Panicle number, PL = Panicle length, PW = Panicle width, PE = Panicle exersion, DS = Drought score, STG = Staygreen, PWt = Panicle weight, TSW = Thousand weight.

Appendix Table 7: Means for grain yield, phonological and other complex traits of sixty early maturing advanced sorghum genotypes by mixed model tested at Sheraro during 2017 main cropping season.

Entry#	Genotype Name	DTE	DTF	GFP	DTM	GFR	PHT	PWt	1000GW	PN	PL	PW	PE	DS	STG
1	Melkam	5.0	70.0	27.7	97.7	133.0	204.3	4038.3	27.3	48.3	27.3	15.3	2.0	1.3	4.0
2	14MWLSDT7060	5.0	69.3	32.0	101.3	134.9	198.3	4521.7	26.3	68.0	21.0	15.1	1.0	1.0	2.7
3	12MW6251	5.0	70.0	30.7	100.7	156.5	239.5	4265.6	27.7	58.0	26.2	15.8	1.7	1.7	3.7
4	14MWLSDT7410	5.0	70.0	30.7	100.7	113.6	218.7	4007.8	26.8	72.0	26.4	16.2	1.3	2.7	2.7
5	12MW6302	5.0	70.0	30.0	100.0	117.5	186.7	3792.8	25.5	55.7	25.9	14.7	1.0	1.7	4.0
6	14MWLSDT7322	5.0	71.7	31.3	103.0	119.6	248.4	3982.8	33.5	64.7	24.2	13.1	1.0	1.0	2.0
7	14MWLSDT7395	5.0	65.0	36.0	101.0	109.7	185.6	3661.7	29.6	63.7	25.2	14.7	1.0	1.3	1.3
8	14MWLSDT7400	5.0	67.7	28.3	96.0	125.5	202.4	4192.0	24.3	52.7	26.7	16.7	1.0	3.7	4.0
9	14MWLSDT7310	5.0	70.3	34.3	104.7	95.7	272.8	3551.7	26.0	70.3	25.9	16.9	1.0	1.3	1.7
10	13MWF6#6077	5.0	73.0	28.7	101.7	108.3	153.2	3387.2	20.7	56.3	24.0	14.0	1.0	1.3	2.7
11	14MWLSDT7325	5.0	75.3	28.3	103.7	99.8	258.2	2906.1	31.3	54.3	23.0	14.4	1.0	1.0	2.3
12	2005MI5069	5.0	71.0	30.3	101.3	136.0	236.1	4182.1	34.8	50.3	22.9	14.7	1.3	1.0	3.7
13	14MWLSDT7196	4.7	69.0	29.7	98.7	132.3	207.7	4087.0	31.3	46.0	22.6	14.9	2.3	3.0	4.0
14	14MWLSDT7311	4.0	72.0	30.0	102.0	107.2	229.8	3906.1	25.8	68.3	26.2	15.3	1.0	1.0	2.7
15	14MWLSDT7157	4.7	71.7	32.0	103.7	117.3	240.9	4239.6	29.5	69.3	22.9	14.9	1.0	1.0	2.3
16	14MWLSDT7193	5.0	62.3	35.7	98.0	106.1	179.1	3626.1	33.8	51.0	23.9	16.2	1.3	3.3	4.0
17	14MWLSDT7332	4.7	72.0	30.0	102.0	131.4	216.9	4029.3	27.6	56.0	24.3	15.8	2.0	2.7	4.0
18	14MWLSDT7115	4.7	72.0	26.0	98.0	113.3	233.7	3497.7	26.5	57.0	22.0	13.6	1.0	1.3	1.7
19	14MWLSDT7176	4.7	68.7	29.0	97.7	156.5	228.2	4348.4	32.7	57.0	26.1	16.9	1.0	2.7	3.0
20	14MWLSDT7209	5.0	75.3	26.0	101.3	105.3	229.4	3108.0	26.0	50.3	22.2	13.8	1.0	1.0	1.0
21	12MW6440	4.7	69.7	30.3	100.0	113.4	180.6	3634.5	28.3	49.3	24.0	15.8	2.0	2.3	3.7
22	14MWLSDT7201	4.7	68.3	30.3	98.7	144.8	226.5	4448.9	30.3	56.7	23.4	16.7	1.7	1.0	2.0
23	12MW6146	5.0	71.3	30.3	101.7	121.7	210.8	4377.2	22.2	51.3	28.6	17.1	1.3	1.7	4.0
24	14MWLSDT7364	4.3	69.7	31.3	101.0	136.7	208.3	4291.7	32.5	53.7	23.8	16.2	1.0	1.0	3.0
25	Pipline 2	5.0	71.3	24.7	96.0	188.4	242.4	4666.1	28.9	61.7	22.4	18.0	1.0	2.7	4.0

26	14MWLSDT7413	4.7	74.3	27.7	102.0	121.7	206.2	3664.1	27.8	59.3	27.2	16.4	2.0	3.3	2.7
27	13MWF6#6037	5.0	68.0	33.0	101.0	142.7	187.9	4298.7	30.0	59.0	21.4	19.6	1.3	1.7	4.0
28	14MWLSDT7207	4.7	72.0	33.7	105.7	112.5	214.6	3797.3	25.2	59.0	24.2	16.4	1.0	1.0	1.3
29	14MWLSDT7040	5.0	69.3	33.7	103.0	120.9	186.3	4222.0	30.0	54.7	22.2	16.7	1.0	1.3	3.7
30	14MWLSDT7036	4.7	70.3	29.7	100.0	121.6	222.1	3785.2	33.0	48.7	25.7	16.2	1.3	1.7	2.7
31	14MWLSDT7324	4.7	71.7	29.3	101.0	120.9	192.8	3465.9	28.3	62.3	22.8	12.7	1.0	1.0	2.7
32	12MW6243	4.7	70.3	28.3	98.7	112.0	135.0	3602.3	21.1	61.7	23.8	15.3	2.0	1.3	4.0
33	12MW6420	4.7	75.7	31.3	107.0	127.3	198.3	3948.4	28.5	62.7	22.4	15.8	3.0	1.3	1.7
34	14MWLSDT7238	5.0	72.7	28.3	101.0	147.0	230.8	4075.9	26.0	65.0	23.8	13.3	1.0	1.3	1.7
35	12MW6444	4.7	72.3	29.3	101.7	123.9	240.2	3765.0	28.0	63.7	23.0	15.1	1.0	1.0	1.7
36	14MWLSDT7402	5.0	70.0	30.0	100.0	114.4	289.5	3530.0	29.7	55.3	26.6	14.4	1.0	1.0	1.7
37	14MWLSDT7234	4.7	70.7	28.3	99.0	160.4	194.7	4455.0	27.0	63.7	25.7	17.3	1.0	1.7	1.7
38	12MW6471	5.0	78.0	29.3	107.3	86.8	243.8	2410.7	32.0	60.3	20.6	14.4	1.0	2.7	1.3
39	14MWLSDT7042	5.0	69.3	32.0	101.3	119.7	228.3	3788.3	31.8	61.7	25.7	16.1	1.3	1.0	3.3
40	14MWLSDT7033	5.0	69.7	28.7	98.3	139.6	225.2	4116.0	32.2	56.3	23.8	16.7	1.3	1.0	3.3
41	14MWLSDT7241	5.0	71.3	29.7	101.0	132.9	221.1	3887.8	26.3	69.3	24.4	16.0	1.0	1.3	1.0
42	14MWLSDT7191	5.0	77.0	30.0	107.0	93.7	205.2	3056.8	32.7	53.3	22.2	14.9	2.3	1.3	2.3
43	2005MI5093	4.3	72.0	31.0	103.0	116.2	251.5	3650.0	31.3	58.7	22.2	16.0	1.0	2.0	3.7
44	2401	4.7	62.3	33.7	96.0	117.4	240.6	3799.4	33.5	59.0	25.3	15.3	1.0	3.3	2.0
45	2004MW6197	5.0	68.7	30.7	99.3	135.9	206.6	4210.0	32.8	45.3	22.8	15.0	1.3	1.7	2.3
46	2005MI5064	4.3	70.7	34.0	104.7	101.9	217.7	4350.0	34.3	55.0	23.0	14.3	1.0	1.3	3.0
47	2523	4.3	63.3	33.0	96.3	96.1	192.2	3323.3	27.7	55.7	25.0	14.0	2.0	1.7	2.7
48	04MW 6043	5.0	75.0	58.0	108.0	65.1	235.3	3140.2	27.0	51.7	26.6	14.7	1.3	3.7	1.0
49	2005MI5057	4.3	72.0	29.7	101.7	133.6	200.0	3801.1	35.5	56.3	23.8	14.3	1.0	1.0	1.0
50	04MW 6079	5.0	72.0	31.0	103.0	143.3	226.7	4491.7	27.8	59.0	22.3	11.3	1.7	1.0	1.7
51	14MWLSDT7202	5.0	67.0	29.7	96.7	125.5	228.9	3685.6	25.2	58.3	23.1	14.7	1.0	1.0	1.0
52	14MWLSDT7291	4.0	69.7	29.0	98.7	126.3	253.1	3750.0	29.3	62.7	25.8	14.5	1.0	1.0	1.7
53	2001MS7036	5.0	64.0	34.0	98.0	105.8	205.8	3416.7	26.2	45.0	25.4	14.6	1.0	1.3	2.3

54	90MW5319	4.7	61.7	34.3	96.0	124.7	199.6	4426.7	32.0	58.7	25.6	17.3	1.0	1.0	2.0
55	99MW4047	5.0	67.0	32.7	99.7	115.7	208.9	4021.1	30.3	62.3	24.2	14.0	1.0	3.0	3.3
56	05MW6026	5.0	63.3	33.0	96.3	118.3	205.6	3728.3	34.2	57.0	24.3	12.3	1.0	1.3	2.7
57	14MWLSDT7421	4.7	69.0	32.0	101.0	123.8	256.7	4274.3	32.7	63.0	23.8	13.7	1.0	1.7	1.7
58	2003MW6053	5.0	67.3	32.3	99.7	108.2	180.2	3701.7	29.0	55.0	27.4	15.6	1.0	1.0	1.3
59	2294	4.7	61.7	35.3	97.0	102.5	188.0	3883.9	35.5	58.3	26.4	15.0	1.0	1.0	1.0
60	2003MW6038	4.7	68.3	29.3	97.7	109.5	230.8	3546.7	32.7	50.3	25.4	15.3	1.0	1.3	2.3
	Mean	4.8	69.9	31.1	100.6	121.5	216.5	3863.7	29.3	57.8	24.3	15.3	1.3	1.6	2.5

Where, DTE = Days to Emergency, DTF = Days to flowering, DTM = Days to maturity, GFP = Grain filling period, GFR = Grain filling rate, PHT = Plant heght, PN = Panicle number, PL = Panicle length, PW = Panicle width, PE = Panicle exersion, DS = Drought score, STG = Staygreen, PWt = Panicle weight, TSW = Thousand weight.

Appendix Table 8: Means for grain yield, phonological and other complex traits of sixty early maturing advanced sorghum genotypes by mixed model tested at Shaorobit during 2017 main cropping season.

Entry#	Genotype Name	DTE	DTF	GFP	DTM	GFR	PHT	PWt	1000GW	PN	PL	PW	PE	DS	STG
1	Melkam	7.0	74.7	37.7	112.3	129.4	188.0	4473.3	30.9	51.0	28.8	16.4	2.7	3.3	4.0
2	14MWLSDT7060	7.3	74.3	39.0	113.3	142.3	193.9	4649.7	24.0	45.7	21.6	17.9	4.0	2.3	2.7
3	12MW6251	7.3	76.0	36.7	112.7	171.7	247.4	5420.0	29.0	62.0	23.5	16.9	3.7	2.7	2.7
4	14MWLSDT7410	7.0	75.3	37.7	113.0	119.6	239.1	4540.0	27.1	56.3	29.0	17.8	5.0	4.7	3.7
5	12MW6302	5.7	77.3	36.3	113.7	141.4	163.2	4545.0	26.0	59.7	25.2	17.1	2.0	4.3	4.0
6	14MWLSDT7322	6.3	76.3	37.3	113.7	173.6	281.3	4535.0	35.0	57.0	20.6	16.0	2.0	3.3	3.3
7	14MWLSDT7395	6.7	63.7	47.3	111.0	96.0	188.5	4170.0	27.6	58.7	25.8	16.4	1.0	3.7	2.3
8	14MWLSDT7400	6.0	69.0	42.0	111.0	104.1	197.2	4320.0	27.6	53.0	23.9	17.4	4.7	4.7	4.3
9	14MWLSDT7310	8.0	75.3	36.3	111.7	147.5	271.3	4906.7	29.3	62.0	22.9	17.8	1.7	3.7	3.7
10	13MWF6#6077	7.7	76.3	40.3	116.7	66.6	143.8	3430.0	18.3	59.0	24.7	14.6	2.0	2.7	2.7
11	14MWLSDT7325	7.3	75.0	38.7	113.7	130.0	253.8	4393.3	31.2	59.3	22.4	16.1	2.3	4.0	3.7
12	2005MI5069	7.7	75.0	38.7	113.7	142.4	220.7	5035.0	34.6	54.7	21.9	15.6	5.0	3.3	3.7
13	14MWLSDT7196	7.3	71.0	40.0	111.0	142.0	211.3	5158.3	29.0	57.7	23.7	18.5	5.0	5.0	4.3
14	14MWLSDT7311	7.7	73.0	39.3	112.3	139.3	274.3	4757.8	27.8	68.0	21.9	16.1	1.7	4.3	3.7
15	14MWLSDT7157	7.0	73.0	39.0	112.0	142.5	246.4	4390.0	32.4	63.3	22.3	17.1	2.0	2.7	3.0
16	14MWLSDT7193	6.3	64.0	47.3	111.3	114.4	180.3	4762.6	35.3	60.7	21.3	17.6	4.7	3.7	4.3
17	14MWLSDT7332	7.3	73.7	39.0	112.7	129.7	193.8	5025.4	27.8	62.7	17.6	15.9	5.0	3.7	4.0
18	14MWLSDT7115	7.3	75.7	36.7	112.3	144.2	230.8	5010.0	25.0	56.7	24.5	16.4	4.3	3.0	3.3
19	14MWLSDT7176	7.3	66.0	46.3	112.3	120.6	233.4	5412.2	28.4	61.0	23.7	17.5	1.7	3.0	3.3
20	14MWLSDT7209	8.3	76.7	35.7	112.3	148.1	232.8	4476.7	30.9	61.3	21.4	15.8	2.0	1.3	1.3
21	12MW6440	7.3	73.3	38.7	112.0	139.7	222.1	4798.3	27.8	51.0	23.7	17.1	5.0	4.0	3.7
22	14MWLSDT7201	7.0	73.7	38.3	112.0	169.2	243.5	5608.9	27.5	64.3	22.4	17.6	2.3	3.0	3.3
23	12MW6146	7.3	73.3	39.7	113.0	109.0	165.1	3582.2	26.1	41.3	24.7	15.9	2.0	2.0	2.3
24	14MWLSDT7364	7.0	76.0	35.3	111.3	160.1	225.0	5063.3	27.9	64.3	23.5	16.6	2.3	4.3	3.7
25	Pipline 2	6.3	67.7	43.7	111.3	142.0	242.6	5593.3	31.2	61.3	22.7	18.3	3.3	3.7	3.7

26	14MWLSDT7413	8.3	74.3	38.7	113.0	148.6	209.9	5446.4	28.7	59.3	22.4	17.2	2.7	3.0	2.7
27	13MWF6#6037	7.0	69.0	42.0	111.0	128.3	188.6	4937.4	27.4	64.3	22.0	18.6	3.3	5.0	4.7
28	14MWLSDT7207	7.0	73.3	38.0	111.3	133.3	220.9	5029.8	26.6	61.3	22.6	16.5	2.0	1.7	1.7
29	14MWLSDT7040	6.3	72.0	40.7	112.7	135.9	225.2	4865.8	33.7	52.0	23.3	18.1	2.7	3.3	4.0
30	14MWLSDT7036	7.3	75.0	36.7	111.7	135.3	227.9	4913.2	35.9	61.7	21.2	16.8	5.0	4.7	5.0
31	14MWLSDT7324	7.7	76.3	36.0	112.3	147.9	264.6	4330.9	32.1	58.7	19.3	14.9	2.0	3.3	3.3
32	12MW6243	7.0	72.0	40.0	112.0	105.2	139.7	3322.1	27.5	52.7	24.4	15.5	2.7	2.3	2.7
33	12MW6420	7.0	75.3	40.0	115.3	103.7	148.9	3973.3	26.9	59.7	20.6	16.6	5.0	2.0	3.0
34	14MWLSDT7238	7.3	73.0	38.7	111.7	175.3	221.4	5575.6	27.9	68.7	23.9	16.5	2.0	2.0	2.7
35	12MW6444	6.7	73.3	38.0	111.3	146.0	236.3	5048.9	29.0	62.7	22.5	17.5	2.0	3.0	3.0
36	14MWLSDT7402	6.3	73.0	39.3	112.3	115.4	284.0	4465.0	33.0	57.0	23.1	15.4	2.7	3.3	3.3
37	14MWLSDT7234	7.3	75.0	37.3	112.3	157.3	223.8	5246.7	31.1	61.7	23.5	15.1	2.0	1.3	1.3
38	12MW6471	7.3	74.3	39.0	113.3	121.2	243.7	4647.2	32.2	65.0	21.5	15.9	2.0	3.0	2.7
39	14MWLSDT7042	7.7	74.7	38.7	113.3	140.3	227.5	4251.9	33.4	51.3	21.8	15.7	4.0	3.7	4.3
40	14MWLSDT7033	8.0	68.3	43.7	112.0	125.9	222.0	5696.3	31.7	57.3	21.9	17.6	2.0	4.3	4.3
41	14MWLSDT7241	6.7	76.3	37.0	113.3	152.3	238.2	5083.3	33.0	61.0	24.3	17.0	2.0	2.0	2.3
42	14MWLSDT7191	6.3	77.0	37.3	114.3	106.0	212.0	3949.1	31.9	61.7	20.2	15.7	5.0	3.0	2.7
43	2005MI5093	7.0	73.7	38.3	112.0	143.6	251.8	5116.7	27.5	66.3	21.3	15.2	2.0	4.0	3.7
44	2401	6.7	64.0	47.7	111.7	114.5	214.6	4419.3	33.4	66.0	22.1	14.9	1.3	3.0	3.3
45	2004MW6197	7.0	73.0	40.3	113.3	127.8	192.6	4422.2	32.9	47.0	19.9	14.5	2.3	4.0	3.3
46	2005MI5064	8.3	77.3	36.3	113.7	163.2	237.5	4912.8	29.6	61.0	21.7	15.7	2.0	2.7	2.7
47	2523	6.7	63.3	48.0	111.3	65.9	166.0	3283.3	28.1	54.3	22.5	14.6	5.0	3.7	3.0
48	04MW 6043	7.7	75.7	38.0	113.7	153.0	247.8	5260.0	29.3	55.3	24.3	16.2	3.7	4.7	4.7
49	2005MI5057	7.0	73.0	38.3	111.3	143.9	236.4	4873.3	37.1	60.0	24.3	16.3	2.7	3.3	3.7
50	04MW 6079	7.3	73.7	38.7	112.3	125.9	221.9	4460.0	28.9	57.7	22.3	16.1	4.7	4.0	4.3
51	14MWLSDT7202	7.7	72.3	40.0	112.3	127.9	243.6	4450.0	29.5	63.0	20.2	15.4	3.3	2.3	2.3
52	14MWLSDT7291	6.7	72.7	39.0	111.7	142.6	258.2	5047.3	32.3	64.3	20.9	15.7	2.0	2.3	3.0
53	2001MS7036	6.3	63.3	48.3	111.7	97.0	242.8	4120.0	28.8	63.7	25.9	15.2	1.0	2.7	2.3

54	90MW5319	7.0	64.7	47.0	111.7	114.6	211.3	5220.0	32.0	62.0	23.1	17.1	1.7	3.0	2.3
55	99MW4047	6.3	69.7	41.7	111.3	123.2	154.4	3358.9	26.1	52.3	22.3	15.8	3.3	3.3	3.7
56	05MW6026	6.7	69.3	42.7	112.0	114.7	219.1	4187.4	29.9	61.3	23.3	16.5	2.0	2.0	3.3
57	14MWLSDT7421	7.0	70.0	41.3	111.3	126.9	257.0	4520.0	36.3	59.0	22.6	15.5	1.7	3.0	2.3
58	2003MW6053	7.3	70.0	41.7	111.7	97.8	209.4	3693.5	33.1	53.0	26.4	16.3	4.7	3.0	3.3
59	2294	7.3	63.7	47.7	111.3	116.3	192.5	4630.0	32.4	66.3	21.2	16.7	1.3	2.7	2.7
60	2003MW6038	6.0	70.3	41.3	111.7	103.7	222.7	3936.7	31.9	54.0	23.2	16.9	3.7	3.0	3.0
	Mean	7.1	72.3	40.1	112.4	130.8	220.1	4645.9	30.0	58.9	22.8	16.4	2.9	3.2	3.3

Where, DTE = Days to Emergency, DTF = Days to flowering, DTM = Days to maturity, GFP = Grain filling period, GFR = Grain filling rate, PHT = Plant heght, PN = Panicle number, PL = Panicle length, PW = Panicle width, PE = Panicle exersion, DS = Drought score, STG = Staygreen, PWt = Panicle weight, TSW = Thousand weight.

Appendix Table 9: Means for grain yield, phenolgical and other complex traits of sixty early maturing advanced sorghum genotypes at Erer, Kobo, Mieso, Sheraro and Shewa Robit during 2017 main cropping season.

	Traits														
Locations	DTE	DTF	GFP	DTM	GFR	PHT	GY	PWt	1000GW	PN	PL	PW	PE	DS	STG
Erer	6.9	70	35	105	45.8	150	1508	1559	26.1836	39	23	15	2	3	3.2
Kobo	8	81	53	120	53.6	189	2831	3207	31.6309	45	19	14	3	4	3.9
Mieso	6.2	78	34	112	32.1	152	1099	1643	33.3028	27	25	13	2	3	3.1
Sheraro	4.8	70	31	101	122	216	3707	3864	29.2672	58	24	15	1	2	2.5
Shaorobit	7.1	72	40	112	131	220	5174	4646	29.9823	59	23	16	3	3	3.3

Where, DTE = Days to Emergency, DTF = Days to flowering, DTM = Days to maturity, GFP = Grain filling period, GFR = Grain filling rate, PHT = Plant heght, PN = Panicle number, PL = Panicle length, PW = Panicle width, PE = Panicle exersion, DS = Drought score, STG = Staygreen, PWt = Panicle weight, TSW = Thousand weight.

Appendix Table 10: Means for grain yield, phonological and other traits of sixty early maturing advanced sorghum genotypes tested at five sites during 2017 main cropping season.

Entry#	Genotype Name	DTE	DTF	GFP	DTM	GFR	PHT	GY	PWt	1000GW	PN	PL	PW	PE	DS	STG
1	Melkam	6.7	75.1	36.9	109.1	80.7	159.3	2885.1	3001.5	30.9	37.1	27.8	15.0	2.9	2.8	3.9
2	14MWLSDT7060	6.7	74.7	37.9	109.8	78.5	165.0	3013.5	3034.6	28.7	44.0	20.9	15.1	2.3	2.5	3.0
3	12MW6251	6.9	75.1	38.1	110.4	90.2	194.7	3284.6	3293.6	30.5	45.4	23.5	15.1	3.1	2.8	3.2
4	14MWLSDT7410	6.6	76.6	36.5	110.3	69.3	192.2	2435.0	2925.4	27.3	47.0	28.2	15.5	3.4	3.5	3.0
5	12MW6302	6.3	76.4	35.3	108.9	89.0	146.8	3099.9	2963.1	26.2	46.6	24.9	14.6	1.8	3.2	4.2
6	14MWLSDT7322	6.5	77.5	36.3	110.9	83.1	223.3	2937.9	2805.7	31.5	45.0	21.2	14.1	1.8	2.9	2.9
7	14MWLSDT7395	6.5	69.0	44.9	111.1	54.6	160.3	2343.4	2374.8	29.1	44.5	24.4	14.6	1.0	2.7	2.2
8	14MWLSDT7400	6.1	72.4	39.1	108.7	70.7	177.6	2691.0	2987.0	27.8	43.4	23.9	15.4	2.9	3.7	4.3
9	14MWLSDT7310	6.9	76.2	38.5	111.9	69.4	218.4	2579.1	2812.1	27.5	49.5	22.6	15.5	1.7	3.1	3.3
10	13MWF6#6077	6.7	76.7	35.9	109.9	60.6	129.5	2086.8	2570.5	21.4	46.1	24.5	14.1	2.1	2.5	2.9
11	14MWLSDT7325	6.6	79.1	34.9	111.1	70.1	212.0	2408.7	2400.5	30.2	42.3	21.5	14.5	1.8	2.8	3.3
12	2005MI5069	7.1	76.6	36.3	110.1	75.1	187.6	2617.5	2798.4	32.6	36.5	21.4	14.5	3.2	2.9	3.8
13	14MWLSDT7196	6.9	73.7	38.2	109.1	90.9	176.7	3494.6	3584.0	30.0	42.9	22.3	15.3	3.7	3.6	4.0
14	14MWLSDT7311	6.4	75.8	38.0	111.0	72.8	225.4	2652.3	2867.6	28.0	51.7	22.3	14.6	1.3	3.3	3.3
15	14MWLSDT7157	6.3	75.4	37.2	109.8	83.3	202.5	3028.5	3051.3	31.7	49.7	21.8	14.8	2.0	2.6	3.0
16	14MWLSDT7193	6.1	66.1	44.6	107.9	65.0	156.2	2882.9	2924.9	33.5	45.7	21.0	15.3	3.0	3.4	4.2
17	14MWLSDT7332	6.6	76.2	36.9	110.3	90.4	180.0	3249.2	3516.4	29.2	46.6	19.3	14.8	3.6	3.0	3.6
18	14MWLSDT7115	6.7	78.2	35.9	111.3	72.3	204.7	2354.5	2790.4	28.0	43.1	24.0	14.3	3.2	3.0	2.3
19	14MWLSDT7176	6.7	70.6	42.3	110.1	84.7	187.9	3453.1	3294.4	34.0	44.3	24.2	15.7	1.8	3.1	3.5
20	14MWLSDT7209	7.0	77.1	36.5	110.8	82.4	198.0	2884.5	3061.5	29.3	44.0	21.5	14.3	1.5	2.2	1.9
21	12MW6440	6.9	74.7	36.5	108.4	78.4	176.3	2868.9	3051.9	28.7	40.4	23.1	15.0	3.7	3.5	3.9
22	14MWLSDT7201	6.8	74.3	37.0	108.5	93.8	190.0	3343.6	3332.3	31.7	44.3	22.0	15.3	2.1	2.8	3.3
23	12MW6146	7.0	75.3	38.1	110.6	71.0	153.7	2670.2	2729.8	28.1	38.5	25.7	15.3	2.1	2.4	3.5
24	14MWLSDT7364	6.1	75.3	37.5	110.1	85.6	187.6	3034.7	3230.9	31.8	48.5	22.8	15.2	1.8	3.0	3.4
25	Pipline 2	6.3	71.9	38.8	107.9	96.9	204.9	3462.7	3494.7	30.5	48.5	21.7	16.3	2.1	3.2	3.8

26	14MWLSDT7413	7.1	75.7	36.9	109.9	79.9	176.1	2950.7	3231.9	28.3	46.4	22.7	15.0	2.7	3.4	3.2
27	13MWF6#6037	6.9	71.9	38.8	107.9	88.7	165.9	3465.1	3424.1	29.2	46.7	21.2	17.0	2.4	3.1	3.9
28	14MWLSDT7207	6.2	74.5	37.5	109.2	83.1	193.6	3050.9	3192.0	29.0	46.9	22.9	15.2	1.7	2.0	2.1
29	14MWLSDT7040	6.3	73.3	39.5	109.9	78.4	178.4	3080.2	3087.8	31.2	40.5	22.1	15.6	2.0	2.8	4.1
30	14MWLSDT7036	6.7	75.9	36.9	109.9	75.5	188.9	2685.3	2865.3	33.1	38.7	22.3	15.1	2.9	3.3	3.9
31	14MWLSDT7324	6.7	77.1	35.4	109.7	82.5	217.9	2847.0	2793.7	28.4	48.5	21.4	13.7	1.7	2.6	3.5
32	12MW6243	6.8	75.3	36.5	109.0	65.8	125.0	2380.7	2881.2	25.9	46.3	24.0	14.7	2.8	2.6	3.8
33	12MW6420	6.6	78.7	37.0	112.9	73.2	147.1	2673.5	2880.9	25.6	47.5	20.7	15.0	4.2	2.7	2.8
34	14MWLSDT7238	6.7	75.7	37.1	110.0	98.4	193.1	3533.1	3538.5	28.3	51.3	24.7	14.5	1.8	2.4	2.3
35	12MW6444	6.3	75.9	37.7	110.8	85.6	200.8	3052.2	3258.9	29.1	50.2	22.1	14.9	2.1	2.7	2.9
36	14MWLSDT7402	6.5	74.5	38.5	110.2	69.3	238.2	2540.4	2866.4	31.9	42.8	23.0	14.2	1.5	2.7	2.9
37	14MWLSDT7234	6.3	74.9	36.8	108.9	101.4	184.6	3528.5	3303.3	31.0	51.7	23.4	14.9	1.8	2.2	2.2
38	12MW6471	6.6	79.1	37.3	113.6	77.6	207.9	2818.1	2951.8	33.6	46.6	21.0	14.4	1.7	2.8	2.5
39	14MWLSDT7042	6.8	74.3	38.4	109.9	85.0	194.2	3200.9	3200.5	33.8	42.7	23.0	14.9	2.5	2.8	3.9
40	14MWLSDT7033	6.9	72.7	40.7	110.5	78.2	188.3	3068.0	3434.8	31.2	44.0	23.0	15.5	2.2	2.7	3.8
41	14MWLSDT7241	6.7	76.4	36.3	109.9	89.0	197.7	3174.8	3271.2	29.6	50.7	24.1	15.1	1.8	2.2	2.4
42	14MWLSDT7191	6.1	79.8	36.5	113.5	57.5	174.3	2024.6	2390.8	30.3	41.0	20.9	14.7	4.0	3.0	3.1
43	2005MI5093	6.7	75.6	37.2	110.0	76.7	202.6	2830.6	3044.6	29.6	47.6	20.4	14.6	1.7	3.3	3.8
44	2401	6.3	66.8	45.5	109.5	66.3	184.0	2830.8	2928.6	33.0	51.1	22.1	14.3	1.4	2.9	2.7
45	2004MW6197	6.7	74.7	37.7	109.6	70.6	176.5	2594.4	2646.7	32.2	43.0	21.8	14.3	2.1	3.5	3.3
46	2005MI5064	6.8	76.8	36.2	110.2	84.3	190.3	2964.4	3051.1	31.4	44.8	21.6	14.2	1.4	2.7	3.1
47	2523	6.5	67.1	44.3	108.6	54.1	160.2	2380.0	2453.9	30.0	48.1	22.7	14.0	3.4	3.0	3.1
48	04MW 6043	7.1	74.6	44.2	111.3	81.0	200.4	3256.9	3391.7	27.8	40.9	24.4	14.6	2.8	3.8	3.6
49	2005MI5057	6.2	74.4	38.5	110.1	87.0	192.4	3190.6	3224.7	33.9	47.3	24.1	14.5	1.9	2.7	2.9
50	04MW 6079	6.8	76.8	37.1	111.1	78.2	185.0	2799.0	3034.6	27.6	43.3	22.2	13.9	2.9	2.8	3.2
51	14MWLSDT7202	6.8	71.9	40.6	109.7	72.2	197.5	2803.4	2809.5	29.0	48.0	20.5	14.4	2.3	2.4	2.7
52	14MWLSDT7291	6.3	73.9	38.7	109.8	79.4	225.6	2908.8	3208.7	31.0	50.0	22.5	14.2	1.4	2.8	2.6
53	2001MS7036	6.4	69.7	44.3	111.1	55.9	194.8	2382.1	2419.3	29.2	45.7	25.3	14.1	1.3	2.9	3.1

54	90MW5319	6.2	65.4	45.1	107.7	71.6	168.5	3169.9	3093.2	30.2	51.1	22.6	15.4	1.5	2.3	2.8
55	99MW4047	6.5	73.1	38.9	109.2	66.9	146.8	2589.2	2561.6	30.0	43.6	22.7	14.1	2.4	3.3	3.5
56	05MW6026	6.4	70.5	39.8	107.5	76.2	191.1	2947.9	3007.2	32.3	51.3	22.3	13.8	1.7	2.2	3.1
57	14MWLSDT7421	6.5	72.7	38.7	108.5	74.6	205.7	2803.8	2991.4	33.8	48.0	21.5	13.8	1.8	2.7	2.7
58	2003MW6053	7.0	70.8	41.3	109.3	58.4	171.0	2368.3	2485.2	30.0	41.3	25.7	14.8	2.7	2.4	2.8
59	2294	6.5	64.6	47.8	109.6	60.1	160.7	2783.6	2668.1	33.5	44.6	22.1	14.8	1.4	2.7	2.4
60	2003MW6038	6.3	73.0	39.3	109.5	64.0	191.2	2397.0	2526.1	32.1	41.6	23.3	14.9	2.6	2.7	3.2
	Mean	6.6	74.1	38.7	109.9	76.8	185.5	2863.9	2983.6	30.1	45.5	22.8	14.8	2.3	2.9	3.2

Where, DTE = Days to Emergency, DTF = Days to flowering, DTM = Days to maturity, GFP = Grain filling period, GFR = Grain filling rate, PHT = Plant heght, PN = Panicle number, PL = Panicle length, PW = Panicle width, PE = Panicle exersion, DS = Drought score, STG = Staygreen, PWt = Panicle weight, TSW = Thousand weight.

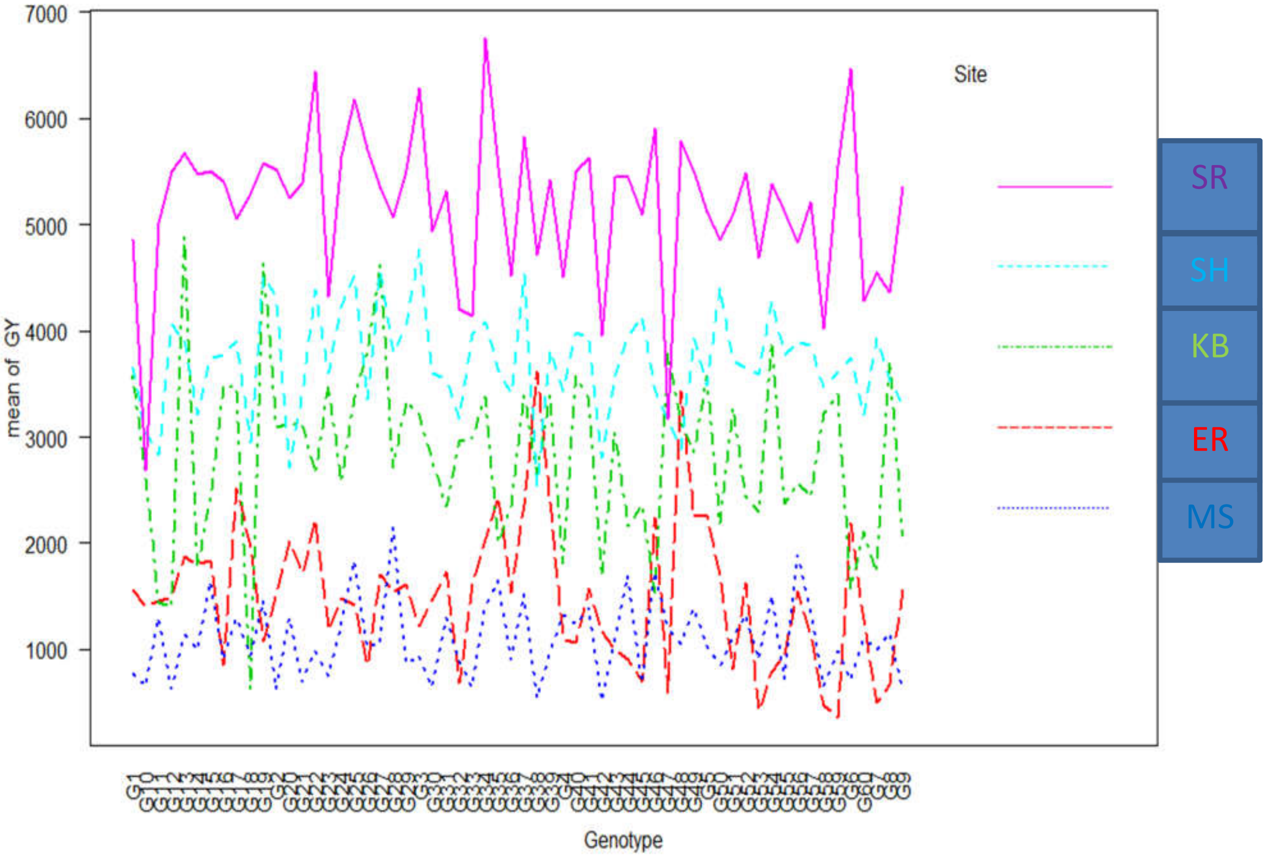
Appendix Table 11: The IPCA 1 and IPCA 2 scores for the five sites, sorted on environmental mean yield, used in the study.

Location	Environment Mean	IPCA - 1	IPCA - 2
Errer	1508.48	-0.6346	-0.07441
Kobo	2831.281	1	-0.28507
Mieso	1099.278	-0.07839	0.656635
Sheraro	3706.683	0.152699	0.267812
Shaorobit	5174.024	-0.43971	-0.56497

Where IPCA - 1 = Interaction Principal Component Analysis Score 1 and IPCA – 2 = Interaction Principal Component Analysis Score 2.

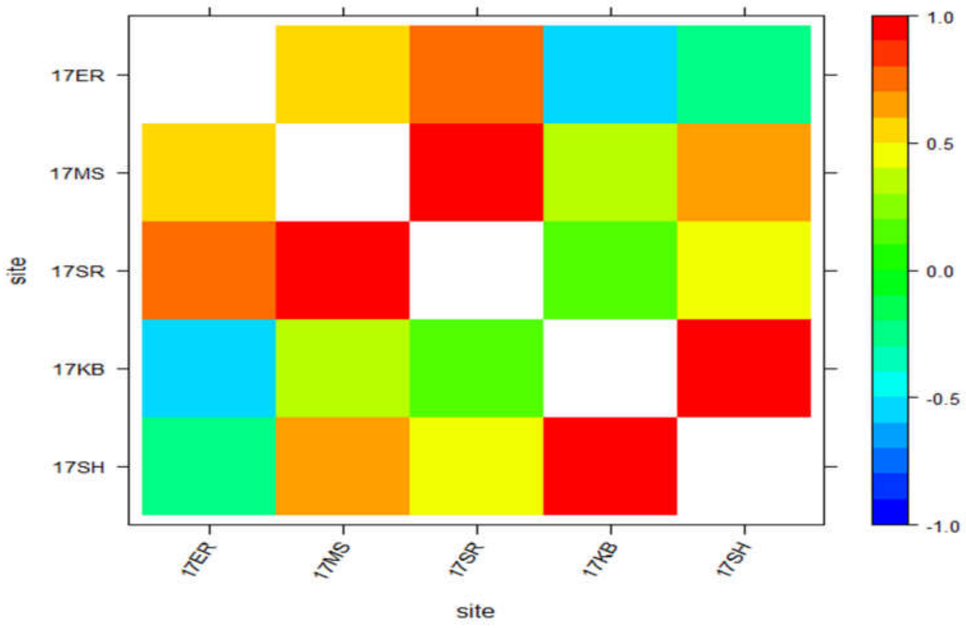
Appendix Table 12: Total monthly rainfall (mm) and mean monthly temperature (°C) of the four tested locations during 2014 main cropping season.

Month	Total Rain fall (mm)					Mean Temperature (°C)									
	Errer	Kobo	Mieso	Shaorobit	Sheraro	Errer		Kobo		Mieso		Shaorobit		Sheraro	
						Min.	Max.	Min.	Max	Min	Max	Min	Max.	Min	Max.
June	95	4.5	13.9	14.9	60.9	16.9	32.3	13.7	31.8	16.7	35	19.2	36.2	21.7	36.2
July	115	154	154.2	244.9	140	16.8	31.3	16.1	33.9	18.8	33.2	19.3	34.3	20.7	32.4
Aug.	110	256	90.1	188.1	253.9	17	30.8	17.1	34	18	31.2	18.6	31.8	20.3	29.7
Sept.	90	160	158.7	98.2	152.5	16.7	31.5	14.5	30.9	16.7	30.6	18	32	19.6	32
Oct.	70	97	147.5	141.9	6.5	13.8	32.1	13.4	30.7	14	29	16.1	30.8	21.2	35.8
Nov.	30	6.3	7.5	25	1.2	11.9	28.6	14.2	31.2	11.8	29.8	14.7	30.3	19.1	36.3

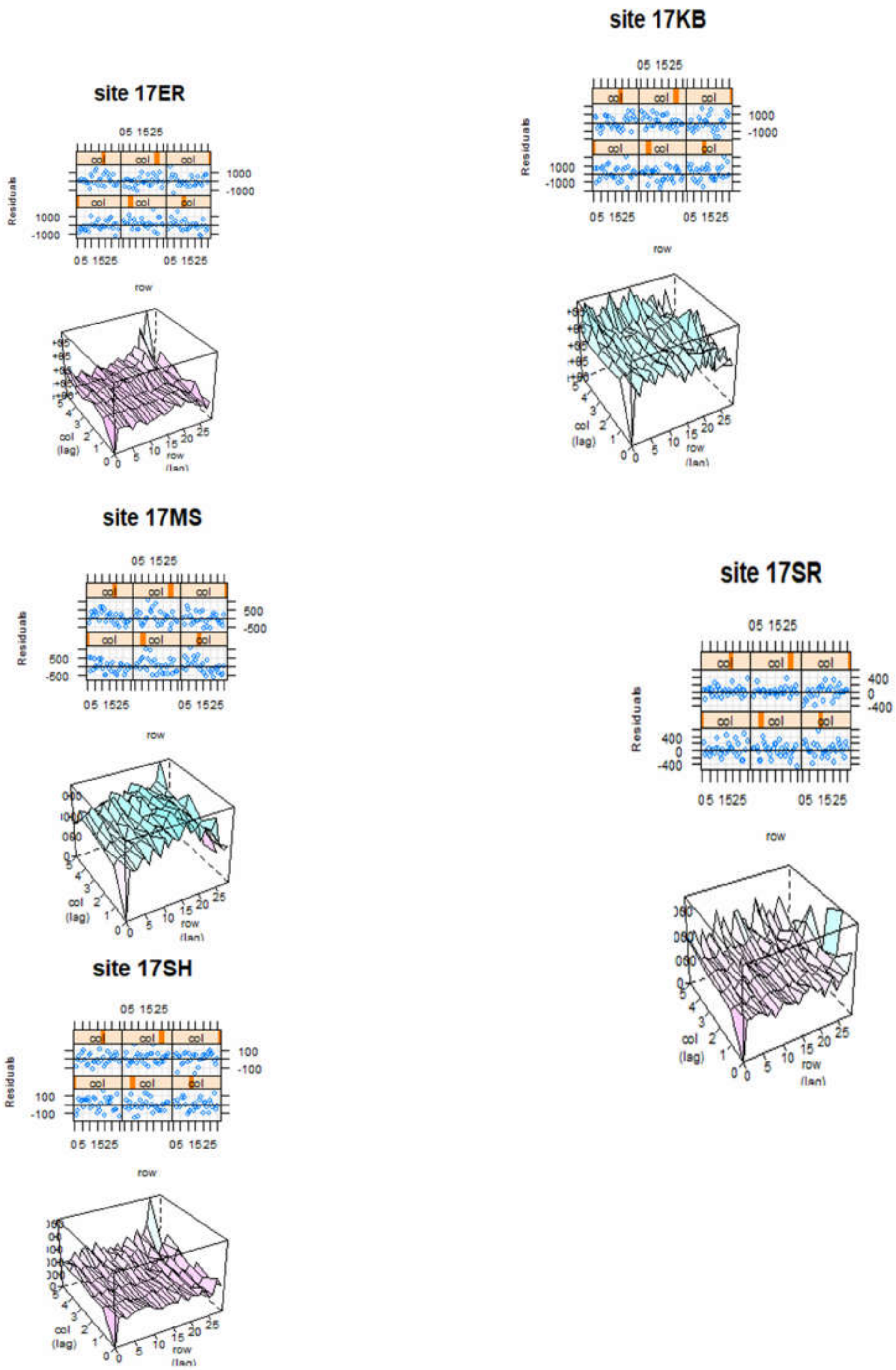


1Appendix Figure 1: Mean grain yield graphical display of genotype by environment interaction.

Where G1 = Melkam , G2 = 14MWLSDT7060, G3 = 12MW6251, G4 = 14MWLSDT7410, G5 = 12MW6302, G6 = 14MWLSDT7322, G7 = 14MWLSDT7395, G8 = 14MWLSDT7400, G9 = 14MWLSDT7310, G10 = 13MWF6#6077, G11 = 14MWLSDT7325, G12 = 2005MI5069, G13 = 14MWLSDT7196, G14 = 14MWLSDT7311, G15 = 14MWLSDT7157, G16 = 14MWLSDT7193, G17 = 14MWLSDT7332, G18 = 14MWLSDT7115, G19 = 14MWLSDT7176, G20 = 14MWLSDT7209, G21 = 12MW6440, G22 = 14MWLSDT7201, G23 = 12MW6146, G24 = 14MWLSDT7364, G25 = Pipeline 2, G26 = 14MWLSDT7413, G27 = 13MWF6#6037, G28 = 14MWLSDT7207, G29 = 14MWLSDT7040, G30 = 14MWLSDT7036, G31 = 14MWLSDT7324, G32 = 12MW6243, G33 = 12MW6420, G34 = 14MWLSDT7238, G35= 12MW6444, G36 = 14MWLSDT7402, G37 = 14MWLSDT7234, G38 = 12MW6471, G39 = 14MWLSDT7042, G40 = 14MWLSDT7033, G41 = 14MWLSDT7241, G42 = 14MWLSDT7191, G43 = 2005MI5093, G44 = 2401, G45 = 2004MW6197, G46 = 2005MI5064, G47 = 2523, G48 = 04MW 6043, G49 = 2005MI5057, G50 = 04MW 6079, G51 = 14MWLSDT7202, G52 = 14MWLSDT7291, G53 = 2001MS7036, G54 = 90MW5319, G55 = 99MW4047, G56 = 05MW6026, G57 = 14MWLSDT7421, G58 = 2003MW6053, G59 = 2294, G60 = 2003MW6038, GY = mean of grain yield and 17ER = Erer, 17MS = Mieso, 17KB = Kobo, 17SR = Shaorobit, 17SH = Sheraro



2Appendix Figure 2: Graphical display of Correlation between locations with heat map (MET analysis) on grain yield performance of early maturing sorghum genotypes.



3**Appendis Figure 3: Spatial trend and spatially independent residuals from the spatial model for grain yield (kg/ha) in each location plotted against row and column positions.**