GENOTYPE x ENVIRONMENT INTERACTION AND YIELD STABILITY OF *STRIGA* RESISTANT SORGHUM [*Sorghum bicolor* (L.) MOENCH] HYBRIDS IN ETHIOPIA

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FANTAYE BELAY MARYE

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Genotype x Environment Interaction and Yield Stability of *Striga* Resistant Sorghum [*Sorghum bicolor* (L.) Moench] Hybrids in Ethiopia

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Fantaye Belay Marye

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POSTGRADUATE PROGRAMS DIRECTORATE

As Thesis advisors, we hereby certify that we have read and evaluated this Thesis entitled **"Genotype x Environment Interaction and Yield Stability of *Striga* Resistant Sorghum (*Sorghum bicolor* (L.) Moench) Hybrids in Ethiopia"** prepared under our guidance by Fantaye Belay. We recommend that it be submitted as fulfilling the Thesis requirement.

Firew Mekbib (PhD)	_____	_____
Major Advisor	Signature	Date
Taye Tadesse (PhD)	_____	_____
Co-advisor	Signature	Date

As members of the Board of Examining of the Final MSc Thesis Open Defense Examination, We certify that we have read and evaluated the Thesis prepared by Fantaye Belay, and examined the candidate. We recommend that the Thesis be accepted as fulfilling the Thesis requirement for the degree of Master of Science in Agriculture (Plant Breeding).

_____	_____	_____
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I dedicate this Thesis manuscript to **MY PARENTS** for their consistent and unreserved encouragement, and their dedicated partnership in the success of my life.

STATEMENT OF THE AUTHOR

By my signature below, I declare and affirm that this Thesis is my own work and that all sources of materials used for Thesis have been duly acknowledged. I have followed all ethical and technical principles of scholarship in the preparation, data collection, data analysis and compilation of this Thesis. Any scholarly matter that is included in the Thesis has been given recognition through citation.

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Name: Fantaye Belay

Signature: _____

Place: Haramaya University

Date of Submission: August 2017

BIOGRAPHICAL SKETCH

The author, Fantaye Belay, was born in December 29, 1987 in Ofla district, South Tigray zone, Ethiopia. He attended his Elementary education at Fala and Korem Elementary and Junior High School, respectively. The author attended his Secondary and Preparatory School at Korem Comprehensive Secondary School. After successful completion of his Ethiopian Higher Education Entrance Examination in 2004, he joined the then Alemaya University, now Haramaya University in January 2005 and graduated with Bachelor of Science Degree in Plant Sciences in July 2007. After graduation, he worked at Samre and Enderta Woreda Agricultural and Rural Development Offices of Southeast zone, Tigray Regional State as Crop production (agronomy) and protection expert from 2008 to 2012.

Then, he was employed by Tigray Agricultural Research Institute at Abergelle Agricultural Research Center in January 2013 and served there as Junior researcher in low land cereal crop improvement until he joined the School of Graduate Studies at Haramaya University in September 2015 to pursue his Master of Science degree (MSc) in Agriculture (Plant Breeding).

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ACRONOMYS AND ABBREVIATIONS

AATF	African Agricultural Technology Foundation
AEZ	Agro Ecological Zones
AMMI	Additive Main effect and Multiplicative Interaction
ASV	AMMI Stability Value
CSA	Central Statistical Agency
EIAR	Ethiopian Institute of Agricultural Research
FARC	Fedis Agricultural Research Center
G x E	Genotype by Environment
GEI	Genotype by Environment Interaction
GGE	Genotype main effect and Genotype by Environment Interaction effects
HuARC	Humera Agricultural Research Center
IBPGR	International Board for Plant Genetic Resources
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
IPCA	Interaction Principal Component Analysis
JLR	Joint Linear Regression
MARC	Melkasa Agricultural Research Center
MhARC	Mehoni Agricultural Research Center
MoA	Ministry of Agriculture
NARS	National Agricultural Research System
S^2di	deviation from Regression
SARC	Sirinka Agricultural Research Center
SAS	Statistical Analysis System
SAT	Semi-Arid Tropics
SSA	Sub-Saharan Africa
TARI	Tigray Agricultural Research Institute
UNDP	United Nations Development Programme
USDA	United States of Department of Agriculture
YSI	Yield Stability Index

TABLE OF CONTENTS

TABLE OF CONTENTS (Continued)

LIST OF TABLES

LIST OF FIGURES

LIST OF TABLES IN THE APPENDICES

Genotype x Environment Interaction and Yield Stability of Striga Resistant Sorghum [*Sorghum bicolor* (L.) Moench] Hybrids in Ethiopia

ABSTRACT

Sorghum known as a Camel crop of cereals, is among the dominant staple food grains for the majority of Ethiopians. In spite of biotic and abiotic stress tolerance, the procedures in the selection of good performing and stable genotypes are complicated by the phenomenon of genotype by environment interaction; therefore, interaction is the major concern to plant breeders to develop improved varieties/hybrids. Forty nine sorghum genotypes (hybrids and open pollinated varieties) were evaluated at five environments during the 2016 main cropping season. The objectives of this study were to estimate the magnitude and nature of GEI for yield and yield related traits and to determine yield stability of striga resistant sorghum genotypes in the dry lowland areas of Ethiopia. The study was conducted using a simple lattice design with two replications at each environment. The result of the combined analysis of variance for grain yield revealed very highly significant (P≤0.001) difference among environment (E), genotype (G) and genotype × environment interaction (GEI). Environment explained 76.13% of the total (G + E +GE) variation, whereas G and GE explained 11.21% and 12.66% of the total variation, respectively. The magnitude of the environment used was 6.8 times greater than the genotype, implying that most of the variation in grain yield was due to the environment. Based on the combined analysis of variance over locations, the mean grain yield of environments ranged from 588 kg ha^{-1} in Humera to 4508 kg ha^{-1} in Sheraro. The highest yield was obtained from ESH-1 (3278 kg ha^{-1}), while the lowest was from K5136 (735 kg ha^{-1}) and the average grain yield of genotypes was 2184 kg ha^{-1}. Different stability models: AMMI Stability Value (ASV), Yield Stability Index (YSI), Regression coefficient (bi) and Deviation from Regression (S^2di) were used to identify stable genotypes. Yield was significantly correlated with bi (0.91), r^2 (0.55) and ASV (-0.56) while it was not correlated with S^2di (-0.26). Generally, AMMI model and GGE biplot were better for partitioning the GEI into the causes of variation and the best multivariate models in this study. Thus, AMMI model was used to identify superior genotypes for specific and wide adaptation. Accordingly, K7439, K7252 and K7437 were specifically adapted to low environments of Humera, Kobo and Fedis, whereas, ESH-1 and K7233 were were the better hybrids for favorable environments of Mehoni and Sheraro, respectively. Moreover, the GGE biplot identified two different sorghum growing mega-environments for grain yield. The first mega environment includes higher (Mehoni) to low yielding (Humera, Kobo and Fedis) environments, respectively, with the winner genotype ESH-1 and the second mega environment containing the highest yielding environment in Sheraro area with winner genotype K7233. Thus, the which-won-where biplot showed two winning genotypes in two mega environments. However, the standard hybrid check, ESH-1 won in most of the environments. In order to give more reliable recommendation this experiment should be repeated at least for one year.

Key words: AMMI, ASV, GEI, Genotype, GGE biplot, Mega environment, YSI

1. INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench] belongs to the grass family Poaceae, is the fifth most important cereal crop globally and occupies the second position among the staple food grains in semi-arid tropics. Sorghum is called as camel of crops and due to the high tolerance of water and temperature stress and also high photosynthesis efficiency; it is considered an important plant in arid and semi-arid regions (Anagholi, 2000). Sorghum is naturally self-pollinated monocotyledon crop plant with the degree of spontaneous cross pollination, in some cases, reaching up to 30%, depending on panicle type (Poehlman and Sleper, 1995). The annual wild and domesticated sorghums are diploid (2n =2x = 20) and are of tropical origin C4 crop. Ethiopia is said to be center of origin and diversity for sorghum (House, 1985; FAO, 1995; Tesfaye *et al*., 2011), which indicates the availability of enormous genetic variability in both cultivated and wild sorghums (Taye *et al*., 2016; Tesfaye *et al*., 2016). Thus, the Ethiopian sorghum collections have been used as a main sources of several genes for important agronomic traits globally (Tesfaye *et al*., 2017), including stay green genes for post flowering drought tolerance (Kebede *et al*., 2001; Haussmann *et al*., 2002), disease resistance, better grain quality and increased yield potential (Prasada and Mengesha, 1981) and have been used widely in many national and international sorghum breeding programs.

Sorghum is a staple crop for more than 500 million people in 30 sub-Saharan Africa and Asian countries (Kumar *et al*., 2011). Hence, more than 80% of the world areas of sorghum production is found in these two continents and primarily grown for human consumption, whereas, in the developed world the total production is used for the feed industries. It remains a critical component of food security for more than 300 million people in Africa; over 100 million people depend on sorghum as staple in Sub-Saharan Africa (SSA) (Serna-Saldivar and Rooney, 1995; Smith and Frederickson, 2000). Sorghum is primarily a crop of resource-poor small-scale farmers and is grown predominantly in low-rainfall, arid to semi-arid environments, typically cultivated across the world in the warmer climatic areas (Olatunji, 1993). In Ethiopia, sorghum is produced by five million small holder farmers and its production is estimated to be four million metric tons from nearly two million hectares of land, giving the potential average grain yield of around two tons per hectare. It is ranked third in

area coverage and fourth in total production (CSA, 2016). However, low yields of sorghum have been recorded due to a number of biotic and abiotic constraints. Among the biotic constraints, *striga* is becoming the major epidemic in most of sorghum growing areas, where soil fertility (nutrient deficiency) and moisture stress are limiting factors, *i.e*. *striga* is rapidly expanding in areas where the soil has low fertility and drought is frequent. Nationally, *striga* causes annual yield loss as high as 65-70% and, at times, leaves plots uncultivated (Gebisa, 2007).

Many researchers (Bayu *et al*., 2001; Omanya *et al*., 2004; Rodenburg *et al*., 2005) have reported variability in sorghum responses to *striga* infestation. The presence of a wide range of variability in *striga* resistant and/or tolerance traits among sorghum genotypes suggests an opportunity to develop high yielding and resistant/tolerant genotypes through hybridization (Mesfin *et al.,* 2014). In a bid to address the constraints embodying sorghum, and to make production a reality, the National Agricultural Research Systems (NARS) in collaboration with international research centers like, ICRISAT and Purdue University are developing and attaching valued importance to hybrid sorghums.

The numerous importances attached to sorghum hybrids stems from the fact that there has been a yield advantage of sorghum hybrids whenever they are compared to the improved and landrace cultivars, commonly in order of 20 to 60% (Atokple, 2003). Sorghum hybrids have been shown to yield 15 to 41% higher than open pollinated varieties under small holder conditions in India and West Africa (Bidinger *et al*., 2005; Toure *et al*., 2007). Reports from research has shown that sorghum hybrids holds a lot of importance and appear to be more reliable than inbred varieties in erratic environments, typically of sorghum growing regions in the semi-arid tropics (Axtell *et al*., 1999).

To date, the total sorghum production area in USA and Australia is planted to hybrids and in China and India more than 85% of sorghum growing areas is planted with improved varieties including hybrids (Reddy *et al*., 2006; Rakshit *et al*., 2014). Beside yield superiority over open-pollinated varieties, hybrids are more stable across different environments (House, 1995) and more tolerant to moisture stress. In Ethiopia, hybrids give 27-30% more grain yield advantage as compared to check varieties and proved to be early maturing than their parental lines (Taye *et al*., 2008; Hailu, 2012; Taye *et al*., 2016).

The yield advantage in sorghum hybrid is due to the complementarity effect of the two inbred lines on the F1 hybrid (Xin *et al*., 2015). It is thus presumed that inbred lines that have *striga* resistant genes complement each other and the F1 hybrids express superiority in reaction to *striga* and could give better yield. Abebe *et al*. (2012) also reported that most resistant sorghum hybrids produced consistently higher grain yields under *S.hermonthica* infestation, supported fewer emerged parasites, and less sustained minimal parasite damage symptoms across locations.

Yield is a complex quantitative character and is greatly influenced by environmental fluctuations, hence, the selection of superior genotype based on yield *per se* at a single location in a year may not be very effective (Shrestha *et al*., 2012). High and stable performance of crop under wider environmental conditions is a desirable attribute of cultivars. Information on the genotype by environment interaction leads to the successful evaluation of stable genotype, which could be used for general cultivation and establishment of strong seed system; consequently, to select a cultivar with high yielding ability. Hence, high attention should be given to the importance of stability in performance for the genotypes under different environment and their interactions (Ghazy *et al*., 2012).

Stability across environments is one of the most desirable properties of a genotype to be recommended for wide cultivation (Benti *et al*., 1996). Stability usually refers to the genotypes ability to perform consistently over wide range of environments. To enhance superior and stable sorghum hybrid development information on nature and magnitude of genotype by environment interaction is extremely important. However, there is no information on genotype by environment interaction and yield stability of *striga* resistant sorghum hybrids in Ethiopia.

Therefore, the specific objectives of the study were to:

1. Estimate the magnitude and nature of genotype by environment interaction for yield and yield related traits, and
2. Determine grain yield stability of *striga* resistant sorghum hybrids in dry lowland areas of Ethiopia.

2. LITERATURE REVIEW

2.1. Origin, Botany and Importance of Sorghum

The geographic place of origin and initial domestication of sorghum [*Sorghum bicolor* (L.) Moench] is in Africa. Ethiopia is believed to be the center of origin and domestication of sorghum (Vavilov, 1951). This is owing to the existence of the largest diversity of sorghum in northeast Africa, in the region bordering Ethiopia and Sudan (Doggett, 1988). Conversely, Stemler *et al*.(1975) argued that none of the bio-geographical, morphological, historical, or evolutionary evidence supported the claim that sorghum was domesticated or originated in Ethiopia, between 5000 and 7000 years ago (Ast *et al.*, 2000; ICRISAT, 2005).

The basic races of cultivated sorghum are: bicolor, vulgare, caudatum, kafir, guinea and durra (Deu *et al*., 1994; BSTID-NRC, 1996). All cultivated sorghum belongs to *Sorghum bicolor* subsp. *bicolor* (Dicko *et al.*, 2006). Common names of sorghum vary from continent to country levels. The most encountered names are *kafferkoren*, *soedangras*, *suikergierst*, or *suiker*-sorghum (The Netherlands), *kaoliang* (China), *mashela* in Ethiopia and Eritrea, *mtatam*, *shallu* or *feterita* (East Africa), *durra* (Egypt and Sudan), chicken corn, sorghum or *guinea* corn (United Kingdom), *jola, jowar, jawa, cholam, bisinga, durra* or *shallu* (India), *kaffir* corn (South Africa), *milo, sorgo*, sudan grass or sorghum (USA), *milo* (Middle East Africa) and great millet, *guinea* corn, *feterita* sorghum or *sorgho* (West Africa) (Dicko *et al*., 2006).

Sorghum is a vigorous grass that reaches up to 6 m in height (Dicko *et al*., 2006). It has deep and spread roots with a solid stem. Leaves are long (0.3-1.4 m), and wide (1-13 cm), with flat or wavy margins. The flower is a panicle, usually erect, but sometimes recurved to form a goose neck. Grain is usually covered by glumes. Glumes are the maternal plant tissues in the panicle that holds the developing caryopsis after pollination. The caryopsis is rounded and bluntly pointed, from 4–8 mm in diameter and varying in size, shape and color with genotype**.** Caryopsis color is an important trait that affects grain quality in sorghum. Sorghum caryopsis is composed of three main parts: seed coat (testa or pericarp), germ (embryo) and endosperm (storage tissue).

Sorghum is one of the main staple food crops for the world's poorest and most food insecure people. Sorghum has high nutritive value, with 70-80% carbohydrate, 11-13% protein, 2-5% fat, 1-3% fiber, and 1-2% ash (Prasad and Staggenborg, 2009). Protein in sorghum is gluten-free and, thus, it is a specialty food for people who suffer from celiac disease (intolerant to food with gluten), including diabetic patients and is a good substitute for cereal grains, such as wheat, barley and rye (Dial, 2012). Its importance is ever increasing as the source of food for rural masses, animal feed and raw material for the industries (Godbharle *et al*., 2010). It is a staple food crop on which the livelihood of millions of Ethiopian depends and it remains to be the primary source of food in Ethiopia. Besides, it has tremendous uses for the Ethiopian farmers and no parts of this plant are ignored (Asfaw, 2007).

Sorghum accounts for an average 10% of daily caloric intake of households living in the eastern and northwestern areas of Ethiopia (USDA, 2012). In Ethiopia, one third of the cereal diet comes from sorghum, and it is the second most important crop for "injera" quality next to tef (Asfaw, 2012). It is utilized in various ways. The grain is used for human food such as porridge, *Kitta*, *Nifro*, infant food, syrup, and local beverage known as *Tella* and A*reke*. The sweet sorghum types are also eaten green as *Eshet* (row grain) or roasted as *Enkuto* (roasted panicle). Sorghum stalks and leaves are also an important source of dry season feed for livestock, source of energy for cooking daily foods, for construction of houses and fences, and as fuel wood (MoA, 2010).

2.2. Sorghum Production in Ethiopia

Sorghum is grown throughout the arid and semiarid tropics and performs better than many other crops under adverse soil and weather conditions (Smith and Frederiksen, 2000; Ejeta and Knoll, 2007). Better adaptation to marginal environments (low soil fertility and drought), in comparison with other cereals, sorghum makes a crop of outstanding potential to meet the increased global food demand. The total grain production from all sorghum producing countries globally was estimated at 63.89 million tons in 2016. The world average annual yield for sorghum reaches 1.5 tons per hectare. FAO reported that the United States of America as the top sorghum producer with a harvest of 15.16 million tons (24.68%), followed by Nigeria (10.01%), Mexico (9.01%), India (6.9%) and Ethiopia (6.35) (USDA, 2016).

Nigeria is the leading sorghum producer in Africa, followed by Ethiopia. However, in productivity, Egypt achieves the highest yield of 5.36 tons per hectare, followed by Ethiopia and South Africa (USDA, 2016). Sorghum is cultivated in Ethiopia between 400 m to 2500 m altitude and it is a staple food crop widely cultivated in different agro-ecological zones (AEZ), predominantly in dry areas where other crops can survive least and food insecurity is widespread. These areas cover nearly 66% of the country (Geremew *et al*., 2004; Asfaw, 2007). In Ethiopia, cereals comprise of 79.88% (9.97 million ha) cultivated area and 86.68% (23.13 million tons) total grain production of the field crops, of which sorghum accounts for 14.85% (1.85 million ha) and 16.20% (4.32 million tons). It ranks third in total area coverage next to tef and maize and fourth in total production next to maize, tef and wheat (CSA, 2016).

Sorghum is grown in almost all regions in Ethiopia. The Oromia, Amhara and Tigray regions are the three major producers of sorghum covering 86% of the total area and 89% of the total annual production in the last 9 years (EIAR, 2014). Oromia took a share of 40.98% (759,954.42 hectares), Amhara, 34.74% (644,263.75 hectares) and Tigray 12.91% (239,371.58 hectares), and the estimated production was 43.59% (1,884,630.071 tons), 31.62% (1,366,961.233 tons) and 14.45% (624,644.832 tons), respectively. From Oromia region, East Hararghe and from Amhara region North Wolo and from Tigray region South, West and North west zones are among the major producers, that cover 134,708.26, 67,182.93, 47,327.94, 72,332.65 and 73,292.14 hectares of land; and 265,278.144, 103,485.647, 93,598.82, 230,257.273 and 220,199.879 tons of annual sorghum production, respectively. The national sorghum productivity is still low (2.33 ton/ha) and in major sorghum growing regions of Oromia 2.48 ton/ha, Amhara 2.12 ton/ha and Tigray 2.61 ton/ha were obtained (CSA, 2016).

2.3. Sorghum Production Constraints

The livelihoods of millions of subsistence farmers depend on sorghum production. However, the national average sorghum productivity in Ethiopia, <2.5 t/ha (CSA, 2016) is low because of a number of factors. Several production constraints were identified as hindrance for sorghum production and productivity enhancement. These include the lack of stable, well-adapted, disease and insect pests tolerant varieties/hybrids.

Sorghum production constraints vary from region to region within Ethiopia. However, drought and *striga* are reported to be important sorghum production constraints in the north and northeastern parts of the country (Wortmann *et al*., 2006). Over 80% of sorghum in Ethiopia is produced under severe to moderate drought stress conditions. Most farmers grow long maturing local landraces, some of which take 7-8 months to mature further complicating the drought problem. Although the extent of yield loss due to drought was not studied in Ethiopia, complete yield loss was observed in some parts of the country, such as Mehoni area (EIAR, 2014). Hybrids have been found better suited than varieties to such stress environments as a result of earliness, better adaptation and stability (Yilma and Abebe, 1986; Fantaye and Hintsa, 2017).

S. hermonthica, the dominant *striga* species, is the most severe in the highly degraded north, northwestern and eastern parts of the country, *viz.* Tigray, Wollo, Gonder, Gojam, North Shewa and Hararghe (AATF, 2011). In spite of biotic and abiotic stress tolerance, it is largely affected by genotype × environment interaction (GEI), making it difficult and expensive to select and recommend new sorghum genotypes for different environments. Yield stability is also one of the setbacks facing sorghum breeders in developing widely adapted varieties with superior yield (Habte *et al*., 2016).

2.4. Genotype x Environment Interaction

The genotype x environment interaction is important for plant breeding because it affects the genetic gain, recommendation and selection of cultivars with wide adaptability (Deitos *et al*., 2006, Souza *et al*., 2009). On the contrary, different genotypes have different performance in each region that can be capitalized to maximize productivity (Souza *et al*. 2008). The differential response of a genotype across environments is defined as the genotype (G) × environment (E) interaction (GEI). Beyene *et al*. (2011) and Bernardo (2002) indicated that it is the rule for quantitative characters. GEI makes it difficult to select the best performing and most stable genotypes. It is an important consideration in plant breeding programs because it impedes progress from selection in any given environment (Yau, 1995). In breeding programs, genotype stability for yield and agronomic performance is an important breeding objective. Previous research suggests that selection of superior genotypes for grain yield and agronomic

traits in maize hybrid performance trials is impacted by GEI (Butron *et al*., 2004). The phenotype of an individual is determined by the effects of its genotype and the environment surrounding it. The effects of genotype and environment on phenotype may not be always independent. The phenotypic response to change in environment is not the same for all genotypes, the consequences of variation in phenotype depend upon the environment. Very often breeders encounter situations where the relative rankings of varieties change from location to location and/or from year to year. GEI is of major consequence to breeders in the process of developing improved varieties. When varieties are grown at several locations for testing their performance, their relative rankings usually do not remain the same. This causes difficulty in demonstrating significant superiority of any variety. GEI is present whether varieties are pure lines, single crosses, double crosses, top-crosses, S1 lines or any other material with which the breeder is working (Dabholkar, 1999).

This differential yield response of cultivars from one environment to another is called genotype x environment interaction (GEI) and can be studied, described and interpreted by statistical models (Crossa, 1990; Vergas *et al*., 1999). Developing crop cultivars that perform well across a wide range of environmental conditions has long been a major challenge to plant breeders. In practice, genotype x environment interaction complicates the identification of superior genotypes (Allard and Bradshaw, 1964). For plant breeders, large genotype x environment interaction impedes progress from selection and has important implications for testing and cultivar release.

An understanding of environmental and genotypic causes of GEI is important at all stages of plant breeding, including ideotype design, parent selection based on traits, and selection based on yield (Jackson *et al.*, 1998). The presence of a large GEI may necessitate establishment of additional testing sites, thus increasing the cost of developing commercially important varieties (Kang, 1996). Understanding of the causes of GEI can be used to establish breeding objectives, to identify ideal test conditions, and to formulate recommendations for areas of optimal cultivar adaptation. It can also help to reduce the cost of extensive genotype evaluation by eliminating unnecessary testing sites and by fine tuning the breeding programs.

There are many reports on G × E and stability studies in sorghum. A study conducted by Habte *et al*. (2016) consisted of 25 sorghum genotypes were evaluated over three years and

seven locations revealed highly significant variations for location, genotype, year and genotype by environment interaction effect and suggested that breeders should deal with the genotype by location type over a fixed number of seasons. Studying G × E for yield using 15 sorghum genotypes in three moisture stressed areas of Ethiopia, Asfaw (2007) found that 12% of the variation was due to genotypes, 61% due to environment while G × E accounted for 27%. The large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield.

In multi evvironment trial, environment explains 80% or higher of the total yield variation (Yan and Hunt, 2002). The environment factors that are contributing to the differences in mean grain yield across environments and years may include soil types, sowing dates, sunshine hours and amount of rainfall during the crop cycle (Dagnachew *et al*., 2014). Generally, information on genotype by environment interaction in the Ethiopian sorghum improvement program for yield stability of striga resistant sorghum hybrids in particular was limited. Hence, conducting a study on genotype by environment interaction and yield stability of striga resistant sorghum hybrids was very important.

2.5. The Concept of Stability and Adaptability

The term “yield stability” is crucial to all types of analysis of genotype by environment interaction, especially with reference to the plant breeding. Yield stability has been reported in diverse ways over the years and there has been different concept of stability (Lin *et al*., 1986). The terms adaptation, phenotypic stability and yield stability have been used by scientists in different ways (Becker and Léon, 1988). Stability in common usage connotes uniformity in performance of the genotype which explains minimum variation among environments for particular genotypes (Chahal and Gosal, 2002). When assessing grain yield of a set of cultivars in a multi-environment trial, changes are commonly observed in the relative yield performance of cultivars with respect to each other across sites.

If the variation in the environment is small, a genotype is considered to be stable. This is called a biological concept of stability or stability statistics. The concept of stability is very important for the assessment of quality traits, stress characters and for disease resistance

(Becker and Léon, 1988). Caccarelli (1989) in his suggestion pointed out two main approaches for selection when significant genotypes by environment interaction were present. The first involved selection for low genotype by environment interaction and high mean yields. This approach recognizes genotypes that are widely adapted to all but most severe stress environment. The second approach is based on the use of genotype by environment interaction by breeding for maximum yields and stability within specific macro-environment (Becker and Léon, 1988).

Eskridge (1990) concluded that selection based on these stability parameters mostly include mean yield, yet more of these methods have clearly illustrated it use. The stability concept is extensively not clear in plant breeding literature, partly due to the myriad of definitions that have been used to represent this concept (Basford and Cooper, 1998), it is an important tool to partition genotype by environment interaction in to mean squares responsible for it occurrence. High yield stability usually refers to the genotypes ability to perform consistently whether at high or low yield levels across a wide range of environment (Annicchiarico, 2002). The ultimate reason for differential stability among genotypes and differential results from various test environments is non-repeatable genotype by environment interaction (Yang and Hunt, 2002).

Adaptability of a given cultivar or hybrid is defined as inherent genetic ability of a cultivar to be stable and high yielding in various environments (Zivanovic *et al*., 2004). Byth (1981) and Clements *et al*. (1983) argued that the term adaptation is applied to both a “condition” and a “process”. The interpretation of their definition requires further considerations. The condition or level of adaptation possessed by individual or a population refers to the genetic constitution and how these match the plant and the environment it occupies. Ultimately, this is the function of the gene possessed by the plant, the regulation of biochemical and physiological processes by these genes during growth and development and how well these match with the available environmental resources and possible hazards (Bindiger *et al*., 1987); therefore, a difference in “condition” of adaptation between individual result from genetic difference, which influences the matching of their growth and development process with the environment. The “process” of adaptation is viewed as a change in the genetic constitution of individuals as they accumulate genes or a change in gene frequencies with populations which better match growth and

development with the environment. A variety that is adaptable over diverse environment is normally tested by the extent of how well they interact with different growing environments. A genotype or variety is considered to be more stable or adaptive if it has a high mean yield but low degree of fluctuation in yielding ability when grown over diverse environments (Falconer, 1981). Living organisms in their own way are able to undergo physiological adjustment enabling them to dispatch changes in their immediate environments. These adjustments themselves are known as adaptation.

There are many statistical methods available to analyze GEI and stability analysis including Yates and Cochran (1938) linear regression analysis, which has been widely used and revised by a number of authors (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Lin and Thompson, 1975; Becker and Leon, 1988; Crossa, 1990); Pinthus (1973) coefficient of determination; Wricke (1962, 1964) ecovalence; Shukla (1972) stability variance parameter; Multivariate analysis methods (Principal component analysis, Principal coordinate analysis, Factor analysis, cluster analysis and Additive main effects and multiplicative interaction (AMMI). Combined ANOVA is more often used to identify the existence of G x E interactions in multi-environmental experiments. An investigation conducted by Mihret (2012) using 13 sorghum varieties in the drought stressed areas (Melkasa and Mieso) of Ethiopia revealed significant interaction effects. Thus, the study result showed the performance of varieties across locations was different, implying that the need for testing the sorghum varieties at multiple locations.

2.6. Analysis of GEI

2.6.1. Regression coefficient (bi) and deviation mean square

Joint linear regression (JLR) is a model used for analyzing and interpreting the non-additive structure (interaction) of two-way classification data. According to Ramagosa and Fox (1993) simple linear regression provides a conceptual model for genotypic stability and is the most widely used statistical technique in plant breeding. This model is also called the Finlay and Wilkinson (1963) approach. It is determined by the regression coefficient by regressing variety mean on the environmental mean, and plotting the obtained genotype regression coefficients against the genotype mean yields.

Finlay and Wilkinson (1963) defined a genotype with bi = 0 as stable, while Eberhart and Russell (1966) defined a genotype with bi = 1 to be stable. Perkins and Jinks (1968) proposed an equivalent statistical analysis where by the observed values are adjusted for environmental effects before the regression. Eberhart and Russell (1966) proposed pooling the sum of the mean square attributable to environments and GEI are partitioned into environments (linear), GE (linear) and deviation from regression (pooled deviation over all the genotypes). This model uses the marginal means of the environments as independent variables in the regression analysis and restricts the interaction to additive form. The method divides the (g-1) (e-1) degree of freedom (DF) for interaction into g-1 degree of freedom for heterogeneity among genotype regressions and the remainder (g-1) (e-2) for deviation.

Kenga *et al.* (2003) conducted the multi environment trial on sorghum hybrids and parental lines, and obtained significant mean square due to environment (linear), significant G x E (linear) interaction, and also significant pooled deviations from regressions. Therefore, the fluctuation in performance of genotypes grown in various environments is not fully predictable. In addition to this, they observed that the large portion of the sum of squares of GEI effects was accounted for by the deviations from regression than linear regression. Therefore, they noted that the magnitudes of GEI effects in this set of materials are largely due to differential non-linear responses of genotypes to varying environment; thus S^2di parameters become important.

The regression approach has been shown to be the most useful for geneticists (Freeman and Perkins, 1971; Freeman, 1973; Hill, 1975; Westcott, 1986), but it should be noted that these authors have pointed out several statistical and biological limitations and criticisms. Crossa (1990) concluded that in trying to determine which genotype is superior with the regression approach, plant breeders have difficulty reaching a compromise between the mean yield, slope and deviation from regression, because the genotype's response to environments is intrinsically multivariate and regression tries to transform it into a univariate problem (Lin *et al*., 1986).

Frequently yield trials have both significant main effects of genotype and environment and GEI (Zobel *et al*., 1988). The existence of GEI necessitates that breeders evaluate genotypes in more than one environment to obtain repeatable rankings of genotypes (Hallauer and Miranda,

1988). However, GEI becomes of practical significance only when crossover interactions occur (Cornelius *et al.*, 1996). Crossover interactions occur in evaluation trials when ranks of cultivars change in different environment. In varying environments, genotypes that provide high average yields with minimum GEI have been gaining importance over increased yields (Caccarelli 1989; Gauch and Zobel, 1997). The definition of a stable cultivar varies with the type of stability analysis used, but generally breeders want cultivars with high mean yield that respond to improved environments (Hallauer and Miranda, 1988).

As per Becker and Leon (1988) the result of the analysis could be non-linear type of interaction, because of insignificant GE (linear), reflecting lack of genetic differences among genotypes for their response to varying environments. While pooled deviations were highly significant against pooled error they show that the differences in stability were due to deviation from linear regression only Khan *et al.* (1988) on sorghum; Ashraf *et al.* (2001) on wheat. In these situations, the above method detect the most suitable and stable varieties over different environments based on b_i value of genotypes which is almost near to unity, non-significant deviation from regression and above average grain yield of genotypes.

2.6.2. Coefficient of determination

Pinthus (1973) proposed the coefficient of determination (r^2) instead of deviation mean squares to estimate stability of genotypes, because r^2 is strongly related to S^2di. Previous findings on sorghum genotypes reported by Showemimo (2007) ranged between 41.8% to 92.0% values of coefficient of determination; suggesting that linear regression accounted from 42–92% variation in sorghum yield. It was also observed in two sets of maize varieties studied that the most stable varieties were associated with high coefficient of determination (Ogunbodede *et al*., 2001).

The effectiveness of the use of r^2 as an index of stability was demonstrated by the observation made by Eberhart and Russell (1966). Coefficient of determination is used to estimate predictable performance of genotypes (Pinthus, 1973). A number of workers, Mekonen *et al*. (2015), Yirga (2017) on sesame and Workie *et al*. (2013) and Lalise (2015) on maize have used it. Coefficient of determination is a relative parameter not dependent on measurement units.

$$r^2 = 1 - \frac{S^2 di}{S^2 xi}$$

Where: r^2=coefficient of determination of genotype i,

$S^2 di$=deviation from regression of genotype i,

$S^2 xi$ =environmental variance of genotype i

$S_{xi}^2 = \frac{\Sigma(x_{ij} - \bar{x}_{i.})2}{E-1}$ Where, X_{ij} is the performance of the i^{th} genotype in the j^{th}environment, $\bar{X}_{i.}$ is the mean performance of the i^{th}genotype and E is the number of environments.

2.6.3. Additive main effects and multiplicative interaction

The development of high yielding cultivars with wide adaptability is the ultimate aim of plant breeders. However, attaining this goal is made more complicated by genotype-environment interactions (GEI) (Gauch and Zobel 1996). Combined analysis of variance can quantify G x E interactions and describe the main effects, but it does not explain the interaction effect (Yuksel *et al*., 2002; Asnake *et al*., 2013). Additive main effects and multiplicative interaction (AMMI) model and genotype main effects and genotype x environment interaction (GGE) biplot analysis are the most commonly used analytical and statistical tools to determine the pattern of genotypic responses across environments (Gauch and Zobel 1996; Yan *et al*., 2000; Yuksel *et al*., 2002). Different methods are presented for statistical analysis including parametric and non-parametric, to estimate the nature of genotype interactions with the environment and their control, but a method that has been approved by every one has not still been introduced (Kaya *et al*., 2006). The AMMI model combines analysis of variance for the genotype and environment main effects with principal components analysis of the genotype by environment interactions (Gauch and Zobel, 1996)

AMMI is multi environmental trials (MET) data analysis, which partitions the GEI matrix into individual genotypic and environmental scores, an example was provided by Zobel *et al.*, (1988). Purchase *et al.* (2000) developed a quantitative stability value to rank genotypes through the AMMI model, namely the AMMI Stability Value (ASV). In analysis of cultivar stability, they found a significant correlation between the stability measures ASV, Shukla and Eberhart and Russel (S^2di), but Finlay and Wilkinson (bi) and Linn and Binns (Pi) showed limited association with any of the other methods. The developed ASV was considered to be the most appropriate single method of describing the stability of genotypes. The difference

from AMMI is that GGE biplot analysis is based on environment-centered PCA, whereas AMMI analysis refers to double-centered PCA. For the research purpose of delineating mega-environments, both AMMI and GGE are suitable, and comparisons so far indicate similar results, as expected. For the research purpose of gaining accuracy, AMMI and GGE (as well as the shifted multiplicative model, etc.) are all equally capable (Gauch *et al.,* 2008).

Gruneberg *et al*. (2005) showed that AMMI, the multivariate tool, was highly effective for the analysis of MET. The additive main effects and multiplicative interaction (AMMI) method integrates analysis of variance and principal components analysis into a unified approach (Gauch, 1988). According to Zobel *et al*. (1988) and Crossa (1990), it can be used to analyze multiplication trials. Zobel *et al*. (1988) pointed out that, considering the three traditional models, analysis of variance (ANOVA) fails to detect a significant interaction component, principal component analysis (PCA) fails to identify and separate the significant genotype and environment main effects, linear regression models account for only a small portion of the interaction sum of squares.

The AMMI method is used for three main purposes. The first is model diagnoses. AMMI is more appropriate in the initial statistical analysis of yield trial, because it provides an analytical tool of diagnosing other models as sub cases when these are better for particular data sets (Gauch, 1988). Secondly, AMMI clarifies the G x E and summarizes patterns and relationships of genotypes and environments (Zobel *et al*., 1988; Crossa, 1990). The third use is to improve the accuracy of yield estimates. Gains have been obtained in the accuracy of yield estimates that are equivalent to increasing the number of replicates by a factor of two to five (Zobel *et al*., 1988; Crossa, 1990). Such gains may be used to reduce testing cost by reducing the number of replications or to include more treatments in the experiments, or to improve efficiency in selecting the best genotypes.

The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the genotype environment interaction (Kaya *et al*., 2002). It has proven useful for understanding complex G x E. The results can be graphed in a useful biplot that shows both main and interaction effects for both the genotypes and environments (Annicchiarico, 2002). In order to determine stability and identify superior genotype across environment, genotype and genotype x environment (GGE) biplot analysis

was conducted using biplot software (Yan and Kang, 2002). The regression analysis was also performed to determine stability and identify superior genotype across environment; on the basis of regression coefficient. An ideal genotype should have the highest mean performance and be absolutely stable. An environment is more desirable and discriminating when located closer to the center circle or to an ideal environment (Dagnachew *et al*., 2014; Naroui *et al*., 2013). AMMI combines analysis of variance (ANOVA) into a single model with additive and multiplicative parameters.

AMMI is ordinarily the model of first choice when main effects and interaction effects are both important, which is the most common cause with yield trials. If, for example, only main effects (additive structure) are present in the data, then the AMMI can be reduced to an ANOVA model. Whereas, if no additive structure is only present then the PCA model is reflected. AMMI results can be readily used to diagnose these and others sub cases (Gabriel, 1978). The pattern portion of G x E sum of squares captured by the regression approach (heterogeneity among regressions) can at best capture only the amount of G x E sum of squares modeled by the simplest AMMI model. Therefore, AMMI analysis can potentially glean more patterns from the G x E than the regression approach (Sneller *et al*., 1997).

Currently, plant breeders widely use AMMI stability model for the purpose of classifying environments to be either favorable or unfavorable group for that specific crop to allocate genotypes to either widely or specifically adaptation and to direct the countries breeding strategy. Accordingly, Asfaw *et al*. (2011) and Molla *et al*. (2013) on finger millet; Alemida *et al*. (2014); Gezahegn *et al*. (2017) on napier grass; Human *et al*. (2011) and Kinde *et al*. (2016) on sorghum were conducted multi environment yield trial and analyzed their yield data using AMMI stability model.

2.6.4. Genotype main effects and genotype x environment interaction effects

The GGE biplot analyses are used in many cultivars x environments interaction studies. Eberhart and Russell (1966) developed a methodology for identifying cultivars with greater adaptability and stability that has been widely used in the identification of genotypes for this purpose (Miranda *et al*. 1998, Grunvald *et al*. 2008). However, other methods for identifying cultivars with adaptability and stability have been developed and many multivariate techniques

are available such as GGE (Genotype main effects and Genotype x Environment interaction) and AMMI (Additive Main effects and Multiplicative Interaction) with new information for cultivars, environmental stratification and cultivar x environment interaction (Miranda *et al*., 2009).

Yan *et al.* (2007) compared the GGE biplot analysis and AMMI analysis with three aspects of genotype by-environment data (GED) analysis, namely mega environment analysis, genotype evaluation, and test environment evaluation. Yan *et al*. (2007) concluded that both GGE biplot analysis and AMMI analysis combine rather than separate G and GE in mega-environment analysis and genotype evaluation. The authors maintain that the GGE biplot is superior to the AMMI-1 graph in mega-environment analysis and genotype evaluation because it better explains G+GE and has the inner product property of the biplot. Moreover, the discriminating power vs. representativeness view of the GGE biplot is effective in evaluating test environments, which is not possible with AMMI analysis. Mega-environments were first defined as environments with similar "biotic and abiotic stresses, cropping system requirements, consumer preferences, and volume of production" (Braun *et al*., 1996). A cluster of environments or locations which constantly share the same best cultivar(s) are called mega-environments (Yan and Rajcan, 2002). Different environments with similar climatic, edaphic and other characteristics can be described by using different data of the environments and METs data to group under homogenous sub regions. Division of the target environments into meaningful mega-environments and deploying different cultivars for different mega-environments is the only way to utilize positive GEI and avoid negative GEI and sole purpose for GEI analysis (Yan, *et al*., 2007).

Therefore, GGE biplot is an effective tool for: 1) mega-environment analysis (e.g. "which-won-where" pattern), where by specific genotypes can be recommended to specific mega-environments (Yan, 2003), 2) genotype evaluation (the mean performance and stability), and 3) environmental evaluation (the power to discriminate among genotypes in target environments). Yan (2000) reported that the first two PCs captured the most useful variation in a biplot. Zobel *et al*. (1988) studied on 20 sorghum genotypes evaluated in 10 environments was best predicted by the first two PCAs based on Gollob's F-test. Hence, a biplot with two PCAs was used to describe the GGE.

2.6.5. AMMI stability value

Quantitative stability measure is essential in order to quantify and rank genotypes according to their yield stability. However, the AMMI model does not provide measure for a quantitative stability. Purchase (1997) developed the AMMI stability value (ASV) based on the AMMI model's IPCA1 and IPCA2 (interaction principal components axis 1 and 2, respectively) scores for each genotype. ASV is the distance from the coordinate point to the origin in a two dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model. Differences in genotype stability and adaptability to environment can be qualitatively assessed using the biplot graphical representation that scatters the genotypes according to their principal component values (Vita *et al*., 2010). In AMMI, the additive portion is separated from interaction by analysis of variance. Then the principal components analysis (PCA) provides a multiplicative model, which is applied to inspect the interaction effect from ANOVA model.

In effect, the ASV is the distance from zero in a two dimensional scatter-gram of IPCA 1 scores against IPCA 2 scores. Since the IPCA 1 score contributes more to GEI sum square, to compensate for the relative contribution of IPCA 1 and IPCA 2 to the total GEI sum square, it has to be weighted by the proportional difference between IPCA 1 and IPCA 2 scores. The distance from zero is then determined by using the theorem of Pythagoras. The larger the ASV value, either negative or positive, the more specifically adapted a genotype is to certain environments. The lower the ASV value, the lower the contribution of a genotype to the interaction and, consequently, the more stable is the genotype (Purchase, 1997).

2.6.6. Yield stability index

Farshadfar *et al.* (2011) developed yield stability index (YSI) which is similar to genotype selection index developed by Farshadfar (2008) is recommended as a measure of stability. YSI is calculated by summing the rank of mean grain yield across environments and rank of AMMI stability value of genotypes. The lowest ASV takes the rank one, while the highest yield mean takes the rank one and then the ranks are summed in a single simultaneous selection index of yield and yield stability. The genotypes with lowest value of this parameter are desirable genotypes with high mean yield and stability.

3. MATERIALS AND METHODS

3.1. Description of the Study Sites

The field experiment was conducted in 2016 main cropping season in five locations representing the major sorghum growing dry lowland areas of Ethiopia (Figure 1), namely Fedis, Kobo, Mehoni, Sheraro and Humera research stations. They are found in East Hararghe zone (Oromia region), North Wello zone (Amhara region) and South, Northwest and West zones of Tigray region, respectively. Drylands in Ethiopia cover about 75% of the total land mass of the country. These drylands harbor one third of the population of Ethiopia and this number is continuously increasing as more and more people migrate from highly degraded highland areas into the dry lowlands (UNDP, 2015). Thus, the livelihood of the population is dependent on sorghum in these dry lowland areas.

The agro-ecology of the locations are described as semi-arid belt of the eastern lowlands of Hararghe (Fedis), sub-moist hot warm low lands (Kobo, Mehoni and Sheraro) and hot to warm semiarid plain (Humera) sub agro-ecology (SA1-1) (EIAR, 2011) with a variation in elevation. The detailed agro-ecological features of the locations are presented on Table 1.

Table 1. Description of the study sites

Location	Geographic position			Rain fall	Temperature (ºC)		Soil type	Location code
	Altitude	Latitude	Longitude	(mm)	Min	Max		
Humera	609	14° 06’N	39° 38’E	576.4	27.0	42.0	*Vertisol*	E1
Kobo	1468	12° 09’N	39° 38’E	673.4	15.36	30.24	*Vertisol*	E2
Fedis	1600	9° 07’N	42° 04’E	724.5	10.5	28.1	*Alfisols*	E3
Mehoni	1578	12° 41’N	39°42’E	600	18.0	32	*Vertisol*	E4
Sheraro	1028	14° 24’ N	37° 45’ E	700	19.3	34.8	*Vertisol*	E5

Source: FARC, MyARC, SARC, MhARC and HuARC, 2016

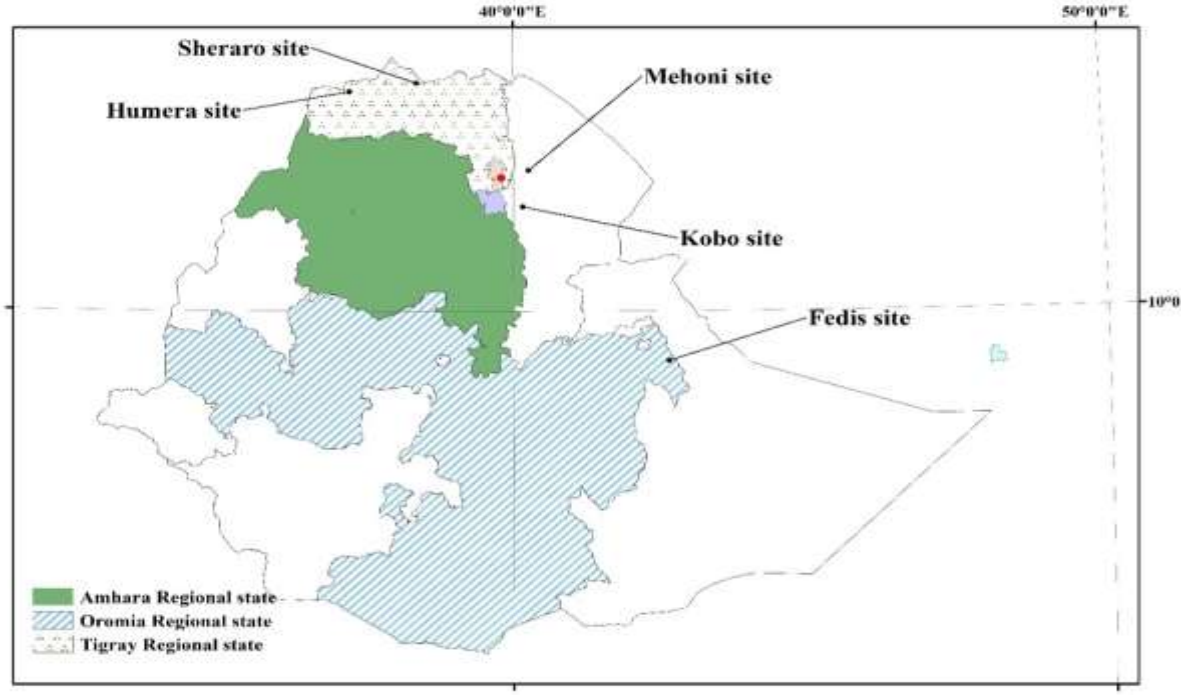

Figure 1. Map of the study sites

3.2. Experimental Materials

Experimental materials comprised of 49 sorghum genotypes that include three *striga* resistant check varieties, Gobye (P9401), Abshir (P9403) and Birhan; two hybrids, ESH-1 and ESH-4 released by the national program and 44 striga resistant sorghum hybrids introduced from Purdue University. The majority of the introduced hybrids were derived from the locally adapted striga resistant sorghum inbred lines with best performing seed parent developed at Purdue. The detailed information of the tested genotypes is presented on Table 2.

Table 2. Description of the experimental materials

SN	Genotypes	Pedigree	Code	Source
1	K7416	P140895A x P9401	G1	Purdue University
2	K7417	P140895A x P9405	G2	Purdue University
3	K7418	P140895A x BRHAN	G3	Purdue University
4	K7437	P140919A x P9401	G4	Purdue University
5	K7438	P140919A x P9405	G5	Purdue University
6	K7439	P140919A x BRHAN	G6	Purdue University
7	K7445	P140927A x BRHAN	G7	Purdue University
8	5136	P111535A x PSL985066	G8	Purdue University
9	5151	P111539A x P9401	G9	Purdue University
10	5152	P111539A x P9405	G10	Purdue University

Table 2. (continued)

SN	Genotypes	Pedigree	Code	Source
11	5153	P111539A x P9406	G11	Purdue University
12	5155	P111539A x PSL985062	G12	Purdue University
13	5156	P111539A x PSL985066	G13	Purdue University
14	5160	P111539A x PSL985369	G14	Purdue University
15	K7229	P111043A x P9401	G15	Purdue University
16	K7230	P111045A x P9401	G16	Purdue University
17	K7231	P111047A x P9401	G17	Purdue University
18	K7232	P111051A x P9401	G18	Purdue University
19	K7233	P111055A x P9401	G19	Purdue University
20	K7234	P111073A x P9401	G20	Purdue University
21	K7235	P111107A x P9401	G21	Purdue University
22	K7236	P111125A x P9401	G22	Purdue University
23	K7237	P111131A x P9401	G23	Purdue University
24	K7242	P111163A x P9401	G24	Purdue University
25	K7244	P111173A x P9401	G25	Purdue University
26	K7245	P111183A x P9401	G26	Purdue University
27	K7249	P111209A x P9401	G27	Purdue University
28	K7251	P111225A x P9401	G28	Purdue University
29	K7252	P111269A x P9401	G29	Purdue University
30	K7255	P111339A x P9401	G30	Purdue University
31	K7256	P111371A x P9401	G31	Purdue University
32	K7259	P111021A x BRHAN	G32	Purdue University
33	K7260	P111043A x BRHAN	G33	Purdue University
34	K7263	P111051A x BRHAN	G34	Purdue University
35	K7265	P111073A x BRHAN	G35	Purdue University
36	K7266	P111107A x BRHAN	G36	Purdue University
37	K7267	P111125A x BRHAN	G37	Purdue University
38	K7268	P111131A x BRHAN	G38	Purdue University
39	K7270	P111143A x BRHAN	G39	Purdue University
40	K7273	P111163A x BRHAN	G40	Purdue University
41	K7274	P111169A x BRHAN	G41	Purdue University
42	K7276	P111183A x BRHAN	G42	Purdue University
43	K7277	P111187A x BRHAN	G43	Purdue University
44	K7280	P111209A x BRHAN	G44	Purdue University
45	BRHAN	Check variety	G45	MARC
46	GOBYE	Check variety	G46	MARC
47	ABSHIR	Check variety	G47	MARC
48	ESH-4	PU207 x PU304	G48	MARC
49	ESH-1	P9401A x ICSR14	G49	MARC

3.3. Experimental Design and Crop Management

The trial was laid out using a 7x7 lattice design with two replications in each location. Each plot consisted of two rows of 5 m length with row-to-row distance of 0.75 m and plant-to-plant distance of 0.20 m, and no land was lost to border effect. The total area of each plot and the harvestable rows had a size of 7.5 m^2 (1.5 m x 5 m), separated by a distance of 1.5 m between replications. All plots were fertilized uniformly with 100 kg ha^{-1} Di-ammonium Phosphate (DAP) and 50kg ha^{-1} Urea. Full dose of P (18 % N and 46 % P_2O_5) and half of N (46 % N) were applied at the time of planting and the remaining half was side dressed at vegetative (knee height) stage of the crop. All of the other agronomic management practices were applied as required at all locations as per the recommendations for sorghum in dry lowland areas of Ethiopia.

3.4. Data Collection and Sampling Techniques

Data were collected both on plot and plant basis, based on the descriptors list for sorghum (IBPGR/ICRISAT, 1993). Phenological data (days to emergence, flowering, grain filling period and maturity date), morphological data (plant height and panicle length), and yield and yield related traits (grain yield and thousand grain weight) were collected.

3.4.1. Data collected on plant basis

From the two rows five plants were selected randomly and tagged to collect the morphological data such as, plant height and panicle length. The detail of the data collection for each trait was carried out as follows:

1. **Plant height (PH):** was determined from the average height of five plants in cm from ground level to the tip of the panicle (at physiological maturity).
2. **Panicle length**: was measured (cm) from the base of the panicle to the tip from five randomly selected plants per plot at maturity.

3.4.2. Data collected on plot basis

3. **Days to 50% seedling emergence:** The number of days from the date of sowing to the date at which 50% of the seedlings in a plot were emerged.

4. **Days to 50% flowering**: The number of days from 50% seedling emergence to the date at which 50 % of the plants in a plot started flowering.
5. **Days to 90% maturity**: The number of days from emergence to the stage when 90% of the plants in a plot have reached physiological maturity.
6. **Grain filling period**: The numbers of days from flowering to maturity, *i.e*. the number of days to maturity minus the number of days to flowering and it includes watery ripe stage, milk stage, soft dough stage, hard dough stage and ripening stage.
7. **Grain yield (kg ha^{-1}):** The panicles from the two rows of each plot were threshed, cleaned and adjusted to standard moisture level at 12.5% and weighted to get the grain yield per plot in grams and converted to kg ha^{-1} for analysis.
8. **Thousand grain weight:** The weight of 1000 randomly sampled grains from each plot was measured in grams using sensitive balance and adjusted at 12.5% moisture content.

3.5. Data Analyses

Different statistical softwares were used to analyze the data. Homogeneity of residual variances was tested prior to analysis over locations using Bartlett's tests (Steel and Torrie, 1980). Analysis of variance for each environment, combined analysis of variance over environments, AMMI analysis, correlation coefficient among stability parameters and agronomic traits were computed using GenStat 18th edition (2016), where GGE biplot was determined using Gea-R 2.0 statistical software. Coefficient of regression (bi) and deviation from regression (S^2di) stability parameters were also analyzed using SPAR 2.0 software.

3.5.1. Individaual and combined ANOVA

As the error variance was homogenous for all traits continued to combined analysis of variance from the mean data of all environments to detect the presence of GEI and to partition the variation for grain yield due to genotype, environment and GEI. Genotypes were assumed to be fixed and environment effects were treated as random. Genotype by environment interaction was quantified using pooled analysis of variance, which partitions the total variance into its component parts (genotype, environment, genotype x environment interaction and pooled error). Mean separations for the treatment means having significant differences at 5% probability levels was done using Duncan's Multiple Range Test (DMRT) comparison

procedure. GenStat 18th edition (2016) statistical software was used for statistical analyses. The relative efficiency of the simple lattice design over randomized complete block design (RCBD) was low (Appendix Table 2) for most yield related traits and since the computation of variances employed for the estimation of other traits is easier for RCBD; analysis of variance for each location and combined analysis of variance over locations as suggested by Gomez and Gomez (1984) was used. The model employed in the analysis was;

Yijk = μ + Gi + Ej + Bk + GEij + εijk where:

Yijk is the observed mean of the ith genotype (Gi) in the jth environment (Ej), in the kth block (Bk); μ is the overall mean; Gi is effect of the ith genotype; Ej is effect of the jth environment; Bk is block effect of the ith genotype in the jth environment; GEij is the interaction effects of the ith genotype and the jth environment; and εijk is the error term.

3.5.2. Eberhart and Russell's Stability Analysis

Eberhart and Russell (1966) procedure involves the use of joint linear regression where the yield of each genotype is regressed on the environmental mean yield. Then, the behavior of the genotype was assessed by the model: $Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$ using Spar 2.0 statistical 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. As a result, in order to test the validity of the hypothesis that whether there is significant difference among the 49 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.

3.5.3. AMMI analysis

The grain yield data were subjected to AMMI analysis, which combines analysis of variance (ANOVA) with additive and multiplicative interactions in to a single model (Gauch, 1988). After removing the replicate effect when combining the data, the genotypes and environments observations are partitioned in to two sources: Additive main effects for genotypes and environments; and Non-additive effects due to genotype by environment interaction. A biplot showing the genotype and environmental means against IPCA1 was also performed *via* this model using GenStat (V18) statistical software following the model indicated below.

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

Where: Y_{ij} = the mean grain yield of i^{th} genotype in the j^{th} environment, 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 number n is judged on the basis of empirical consideration of F-test of significance. 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.

3.5.4. Correlation and Coefficient of determination

Spearman's correlation coefficient between different stability parameters and among agronomic traits and coefficient of determination (r^2) for grain yield of each genotype was estimated by using GenStat 18^{th} edition (2016) statistical software and Microsoft excel, respectively.

3.5.5. GGE biplot analysis

Yan *et al*. (2000) proposed a modification of the conventional AMMI analysis called GGE (Genotype main effects and Genotype x environment interaction effects) that has been used for

GxE analysis. GGE biplot is used to identify identical locations (mega environments) and "which-won-where" pattern of stable genotypes for the testing environments. GGE biplot was determined using Gea-R 2.0 software for grain yield. The GGE biplot was computed according to the formula given by Yan *et al*. (2000) as follows:

$$y_{ij} - \mu - \beta_j = \lambda_1 \xi_{1i} \eta_{1j} + \lambda_2 \xi_{2i} \eta_{2j} + \varepsilon_{ij}$$

Where**:** Yij = the mean grain yield of i^{th} genotype in the j^{th} environment, μ = is the overall mean, β = the effect for the j^{th} environment, λ1 and λ2= the singular values of the first and second principal components (PC1 and PC2), ξ1 and ξ2 = the eigenvectors of i^{th} genotype for PC1 and PC2, η1 and η2 are the eigenvectors of the j^{th} environment for PC1 and PC2.

3.5.6. AMMI Stability Value (ASV)

After the testing of the significance of the GEI mean square, mean over five environments for grain yield of genotypes i at location j was subjected to AMMI stability analysis. AMMI stability value (ASV) was calculated in the excel spread sheet using the formula suggested by Purchase *et al*. (1997):

$$\text{ASV} = \sqrt{\left[\frac{\text{SS}_{\text{IPCA1}}}{\text{SS}_{\text{IPCA2}}}(\text{IPCA1}_{\text{score}})\right]^2 + (\text{IPCA2}_{\text{score}})^2}$$

Where, ASV= AMMI's stability value, SS=sum of squares, IPCA1=interaction of principal component axis one, IPCA2 = interaction of principal component axis two. In effect the ASV is the distance from zero in a two dimensional scatter gragh of IPCA1 (Interaction Principal Component Analysis axis 1) scores against IPCA2 scores.

Similarly yield stability index (YSI) was also computed by summing up the ranks from ASV and mean grain yield (Farshadfar *et al*., 2011):

YSI= RASV+RGY;

Where: RASV is rank of AMMI stability value and RGY is rank of mean grain yield to statistically compare the stability analysis procedures used in the study.

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance

4.1.1. Analysis of variance for individual location for grain yield

The analysis of variance of an individual environment showed that grain yield was very highly significant ($P<0.001$) among sorghum genotypes at all testing environments (Appendix Table 1 or 5). This indicates that genotypes may not express the same phenotypic performance under different environmental conditions or different genotypes may respond differently to a specific environment. For example, at Kobo, genotype G29 ranked first with a grain yield of 1732 kg ha^{-1} while it ranked 10^{th} at fedis with mean grain yield of 1821 kg ha^{-1} and 25^{th} at Humera with mean grain yield of 515 kg ha^{-1} (Table 3).

Since yield is the final result of many plant characters, which are interacting with numerous external factors during the life span of the plants, ranking of genotypes based on grain yield may be considered as a reliable measure for genotypic performance. Thus, the highest and the lowest mean grain yield performance of genotypes across the testing environments were 6667 kg ha^{-1} at Mehoni and 165 kg ha^{-1} at Kobo, which were recorded by genotypes G49 (ESH-1) and G11 (5151), respectively (Table 3). Generally, at Humera and Kobo genotypes showed lower yielding performance than their performance on the other testing environments. This may be due to the very low rainfall distribution during flowering time. Stresses at any stage of crop growth can cause an irreversible loss in yield potential (Hamidi and Pirasteh-Anosheh, 2013).

At Fedis, genotype G4 (K7437) was the best genotype with average grain yield of 2887 kg ha^{-1} and followed by G16 (K7230) with mean grain yield of 2408 kg ha^{-1}. With regard to yielding performance, G19 (7252) ranked 1^{st} at Sheraro with mean yield of 6426 kg ha^{-1}, while, it ranked 43^{th} at fedis with mean grain yield of 830 kg ha^{-1}. Among the tested genotypes, the highest mean yield performance of genotypes for Humera, Kobo, Fedis, Mehoni and Sheraro were recorded by K7439, K7252, K7437, ESH-1 and K7233, whereas, the lowest mean yield were recorded by the genotypes 5136, 5153, 5160, 5136 and 5160 with mean grain yield of 1321, 1732, 2887, 6667, and 6426; 263, 165, 327, 866 and 1100 kg ha^{-1}, respectively.

Most of the genotypes at Mehoni and Sheraro were scored higher average grain yield than the grand mean of the tested environments. This indicated that genotypes performed well at Mehoni and Sheraro (Table 3). Unfortunately, there was no genotype that was found to have higher average grain yield than the grand mean of the tested environments at kobo, Humera and Fedis (except two genotypes). In line with the current study, significant effect of a multi environment yield trial growing environment for grain yield was reported by the previous works of Dawit (2008), Solomon et al. (2008), Ahmed et al. (2012), Fahri (2012), Abubakar and Bubuche (2013), Shrestha (2013), Mesfin et al. (2014), Tekle and Zemach (2014) Abiy (2015), Lalise (2015) and Gezahegn et al. (2017).

Table 3. Mean grain yield (kg ha^{-1}) of 49 sorghum genotypes evaluated at five environments in Ethiopia during 2016 cropping season

	Testing Environments					
Genotypes	Humera	Kobo	Fedis	Mehoni	Sheraro	GM
G1	670^{d-i}	1007^{d-m}	1548^{c-j}	5001^{b-e}	5233^{a-j}	2692^{b-f}
G10	693^{d-h}	384^{no}	651^{l-o}	1533^{q-t}	1740^{op}	1000^{pq}
G11	425^{h-l}	165^{o}	400^{no}	1400^{rst}	2266^{n-p}	932^{pq}
G12	797^{c-f}	615^{j-o}	1086^{g-n}	2684^{j-s}	2620^{m-o}	1561^{m-o}
G13	1069^{abc}	409^{no}	741^{k-o}	1667^{p-t}	1906^{op}	1159^{o-q}
G14	548^{e-l}	211^{o}	327^{o}	2001^{o-t}	1100^{p}	838^{q}
G15	780^{c-g}	1037^{c-l}	1841^{b-f}	2267^{l-t}	5320^{a-j}	2249^{e-j}
G16	671^{d-i}	824^{g-n}	2408^{ab}	4468b-i	4920^{b-k}	2658^{b-f}
G17	307^{jkl}	1178^{a-j}	998^{i-o}	3932^{c-l}	4840^{b-l}	2251^{e-i}
G18	1075^{abc}	1348^{a-g}	1273^{f-l}	4534^{b-h}	4886^{b-k}	2623^{b-f}
G19	510^{f-l}	1178^{a-j}	830^{j-o}	3335^{e-p}	6426^{a}	2456^{c-g}
G2	635^{e-j}	697^{h-o}	976^{i-o}	3733^{c-m}	3448^{l-n}	1898^{h-m}
G20	541^{e-l}	1435^{a-f}	1737^{b-g}	5468^{abc}	5286^{a-j}	2894^{abc}
G21	332^{jkl}	1361^{a-g}	2060^{bcd}	4467^{b-i}	5920^{a-d}	2828^{a-d}
G22	330^{jkl}	1108^{b-j}	1720^{b-h}	4268^{b-j}	5833^{a-e}	2652^{b-f}
G23	391^{h-l}	888^{f-n}	1225^{f-l}	3602^{d-o}	4766^{c-l}	2175^{e-l}
G24	343^{i-l}	1197^{a-j}	1825^{b-f}	4801^{b-g}	5227^{a-j}	2679^{b-f}
G25	668^{e-k}	842^{g-n}	1436^{c-k}	4933^{b-f}	4173^{h-l}	2410^{c-h}
G26	856^{b-e}	644^{i-o}	1427^{d-k}	4034^{c-k}	4407^{e-l}	2274^{e-h}
G27	1089^{abc}	1076^{c-k}	1274^{f-l}	3066^{g-r}	5007^{b-k}	2303^{d-h}
G28	871^{b-e}	1489^{a-e}	1821^{b-f}	2933^{h-r}	5720^{a-g}	2567^{b-g}
G29	515^{f-l}	1732^{a}	1821^{b-f}	5000^{b-e}	6187^{abc}	3051^{ab}
G3	441^{h-l}	866^{f-n}	1091^{g-n}	4000^{c-l}	4820^{b-l}	2244^{e-k}

Table 3. (continued)

Genotypes	Humera	Kobo	Fedis	Mehoni	Sheraro	GM
G31	316^{jkl}	1369^{a-g}	1102^{g-n}	3599^{d-o}	4600^{d-l}	2197^{e-k}
G32	643^{e-j}	1587^{a-d}	931^{i-o}	3334^{e-p}	5386^{a-i}	2377^{c-h}
G33	448^{g-l}	618^{j-o}	1128^{f-m}	3133^{g-q}	5533^{a-h}	2172^{e-l}
G34	283^{kl}	891^{f-n}	1290^{f-l}	4367^{b-j}	5720^{a-g}	2510^{c-g}
G35	469^{f-l}	1307^{a-g}	1795^{b-g}	2734^{i-s}	3893^{jkl}	2040^{g-m}
G36	296^{kl}	1362^{a-g}	1606^{c-i}	4101^{b-k}	4926^{b-k}	2458^{c-g}
G37	385^{h-l}	470^{l-o}	967^{i-o}	4000^{c-l}	5073^{a-k}	2179^{e-l}
G38	684^{d-h}	1678^{ab}	1017^{h-o}	3799^{c-l}	4347^{f-l}	2305^{d-h}
G39	617^{e-k}	1321^{a-g}	1431^{d-k}	3933^{c-l}	4566^{d-l}	2374^{c-h}
G4	444^{h-l}	831^{g-n}	2887^{a}	4467^{b-i}	4933^{b-k}	2713^{b-f}
G40	342^{ijkl}	1484^{a-e}	1189^{f-m}	5800^{ab}	4813^{b-l}	2726^{b-f}
G41	1030^{abc}	1157^{a-j}	1177^{f-m}	3733^{c-n}	4673^{d-l}	2354^{c-h}
G42	462^{g-l}	1214^{a-i}	979^{i-o}	3002^{h-r}	5633^{a-g}	2258^{e-h}
G43	980^{bcd}	1601^{abc}	1196^{f-m}	3667^{d-o}	4160^{h-l}	2321^{d-h}
G44	495^{f-l}	1135^{b-j}	1088^{g-n}	3266^{e-p}	5773^{a-f}	2352^{c-h}
G45	643^{e-j}	1180^{a-j}	1202^{f-m}	1665^{p-t}	3673^{k-m}	1673^{l-n}
G46	561^{e-l}	962^{e-n}	981^{i-o}	2001^{m-t}	4087^{i-l}	1718^{i-n}
G47	286^{kl}	910^{e-n}	1313^{e-l}	2466^{k-t}	4520^{d-l}	1899^{h-m}
G48	286^{kl}	493^{k-o}	504^{m-o}	1533^{q-t}	3947^{jkl}	1353^{n-p}
G49	437^{h-l}	1250^{a-h}	1834^{b-f}	6667^{a}	6200^{ab}	3278^{a}
G5	1146^{ab}	794^{g-n}	1381^{d-k}	3200^{f-q}	4326^{g-l}	2170^{f-l}
G6	1321^{a}	996^{e-m}	2137^{bc}	4467^{b-i}	4740^{d-l}	2732^{b-e}
G7	585^{e-l}	862^{f-n}	2003^{b-e}	5267^{a-d}	4533^{d-l}	2650^{b-f}
G8	263^{l}	430^{m-o}	399no	866^{t}	1713^{op}	735^{q}
G9	341^{i-l}	205^{o}	998^{i-o}	1067st	1680^{op}	858^{q}
EM	588	985	1319	3518	4508	2184
CV (%)	23.2	24.3	22	20.1	12.8	20.4

Where: GM=Genotypic means, EM=Environment means; CV (%) = Coefficient of variation in percent and values with the same letters in a column are not significantly different P≤ 0.05.

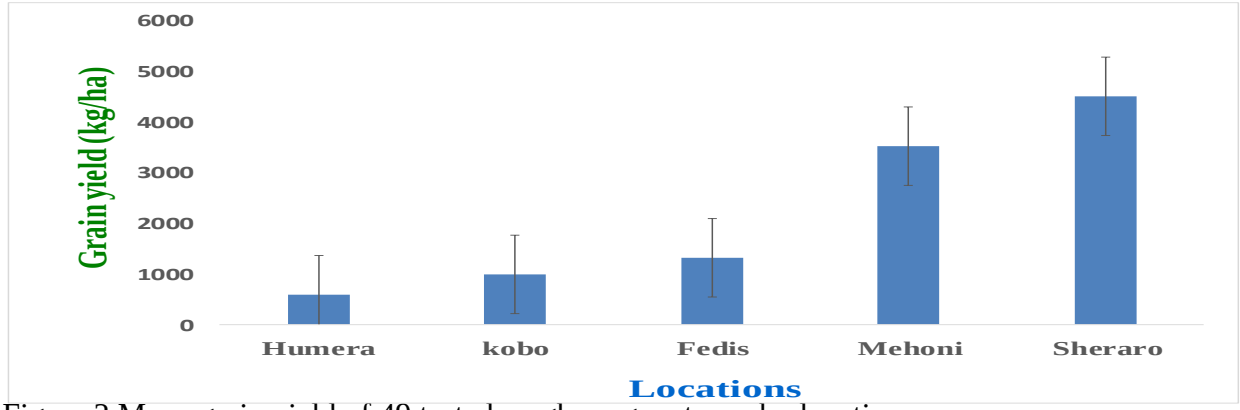

Figure 2.Mean grain yield of 49 tested sorghum genotypes by locations

4.1.2. Combined ANOVA across locations for grain yield

The homogeneity of error variance from result of the Bartlett's test revealed that the mean squares of individual environments were homogenous for grain yield and so a combined ANOVA was done. The combined analysis of variance revealed that the genotype, environment and genotype × environment interaction were highly significant ($P \leq 0.001$). The total sum of square explained by the environment was 76.13% followed by genotype by environment interaction (12.66%) while the genotype explained least (11.21%) (Table 4). The magnitude of the environment was 6.8 times greater than the genotype, implying that most of the variation in grain yield was due to the environment. In comparison from the overall grand mean three of the testing environments, E1 (Humera), E2 (Kobo) and E3 (Fedis) had the lower mean grain yield, while two of the testing environments, E4 (Mehoni) and E5 (Sheraro) scored the higher mean grain yield (Figure 2). The mean grain yield of the tested genotypes showed ranking difference across the testing environments (Table 3). Thirty two genotypes scored above the genotypic grand mean yield (2184 kg ha-1); however seventeen out of 49 genotypes had scored below genotypic mean yield, ranging from 735 kg ha-1 to 2179 kg ha-1. In comparison to the standard hybrid check (ESH-1) the newly evaluated hybrids had the low mean grain yield across all locations except at Sheraro; one hybrid (G19) gave the highest mean grain yield than the standard hybrid check. The large variation of locations on grain yield might be due to the difference in total amount of rain fall at different growing stages, temperature, and soil conditions.

Many researchers (Asfaw, 2007; Abiy, 2015; Habte *et al*, 2016; Kinde *et al*., 2016) have conducted experiment in a multi environment on sorghum genotypes and reported the highest contribution of environmental sum square to the total variation. Similar results were also reported by Asfaw *et al*. (2011) and Molla *et al*. (2013) on finger millet; Solomon *et al*. (2008),Workie *et al*. (2013) and Lalise (2015) on maize. The significant genotype by environment interaction effects showed that genotypes responded differently to the variation in environmental conditions of location which indicated the need for testing sorghum hybrids at multiple locations. Thus, sorghum genotypes responded differently for grain yield across the test environments due to differential responses of the genotypes to various edaphic, climatic and biotic factors.

Table 4. Combined analysis of variance for grain yield of 49 sorghum genotypes evaluated at five environments in Ethiopia during 2016 cropping season

Source	DF	SS	MS	% explained
Reps. within Env.	5	2942779	588556	
Environment (E)	4	1167796816	291949204***	76.13
Genotype (G)	48	171888246	3581005***	11.21
GxE Interaction	192	194226843	1011598***	12.66
Error	240	58359242	243164	

***= significant at P≤ 0.001, DF = degree of freedom, SS = sum of square, MS = mean square

4.2. Mean Performance of Genotypes

The overall performance of 49 sorghum genotypes tested based on mean grain yield and other agronomic traits across locations is presented in Appendix Table 6. In this study days to flowering, maturity, plant height, panicle length, grain yield and thousand grain weight were highly significantly (P≤ 0.001) affected by the combined effect of both genotype and growing conditions of locations, whereas days to emergence and grain filling period were non-significant (Table 5). Thus, for significant traits, genotypes are compared based on mean values of single location (Appendix Table 4).

Grain yield

The mean grain yield obtained by the genotypes at the five locations was 2184 kg ha^{-1} as shown in Table 3. The standard hybrid check ESH-1(G49) and K7252 (G29) produced higher mean grain yield with yield of 3278 and 3051 kg ha^{-1} respectively, whereas, G8 (5136) had the lowest mean grain yield with 735 kg ha^{-1}. However, the newly evaluated hybrids had not shown yield advantage over the standard hybrid check. In disagreement with this study, many researchers (Abiy, 2015; Kassahun *et al*., 2015; Habte *et al*., 2016; Kinde *et al*., 2016; Taye *et al*, 2016; Fantaye and Hintsa, 2017) reported that tested varieties/ hybrids showed better performance than the best check for most of yield and other traits in sorghum.

Days to flowering and maturity

Days to flowering of the genotypes ranged between 58 to 69 days and the mean days to flowering obtained was 63 days as shown in Appendix Table 6. The smallest days to flowering was recorded by genotype 7270 (G39) while G14 (5160) had recorded shorter days to

flowering. The genotype K7445 (G7) had shorter days (95) to 90% maturity, whereas, the longest days to maturity (106) was recorded for genotype 5152 (G10).

Plant height and panicle length

The genotype with the tallest plant height was K7438 (G5) followed by K7235 (G21) with 163.28 and 162.3 cm, whereas, the standard hybrid check ESH-4 (G48) recorded the shortest plant height (117.22 cm). The genotype with tallest panicle length was K7276 (G42) with 32.81 cm, whereas, the shortest was G9 (5151) with 26.79 cm and the difference with the other hybrids was significant at P≤ 0.05 (Table 5).

Thousand grain weight

The average thousand grain weight (TGW) of the genotypes was 26.25g. The genotype with the maximum (28.3g) TGW was G19 (K7233) while genotype G4 (K7437) recoreded minimum (23.7g).

Table 5. Mean squares of yield and other traits from combined analysis of variance of 49 sorghum genotypes grown at five locations in 2016 cropping season.

Source	DF	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
Rep/en	5	1.218	48.09	172.2	107.66	759	190.5	588556	89.1
E	4	33.814	106.17	978.3	491.14	34491	908.6	291949204	3648.9
G	48	1.314	52.79	46	18.57	1064	19.7	3581005	12.7
GEI	192	0.385^{ns}	17.12**	21.6**	19.20^{ns}	268***	8.9*	1011598***	11.5*
Error	240	0.502	11.08	15.5	15.87	127	6.7	243164	7.8
Mean		6.34	62.71	100	37.29	147	29.70	2184	26.25
CV (%)		11.2	5.9	4.4	10	7.8	10.9	20.4	11.6

*, **,*** = significant at P≤ 0.05, P≤ 0.01 and P≤ 0.001, respectively, Rep/en= replication within environment, E= environment, G= genotype, GEI= genotype by environment interaction, DF = degree of freedom, DTE = Days to emergence (days), DTF = Days to flowering (days), DTM = Days to maturity (days), PTH = plant height (cm), PL= panicle length (cm), GY = grain yield (kg ha-1), TGW= thousand grain weight (g), CV (%) = coefficient of variation in percent.

4.3. Spearman's Correlation Coefficient Among Traits

Grain yield is the most complex trait and it is influenced by genetic and environmental factors that determine productivity of the genotypes. Therefore, understanding of interrelationships of grain yield and other traits are highly important for formulating selection.

The Pearson Correlation coefficient between grain yield and other agronomic traits revealed that grain yield had very highly significant (P≤ 0.001) positive correlation with plant height (r = 0.723), panicle length (r = 0.631) and thousand grain weight (r = 0.762) (Table 6). The result agreed with findings of Abdel *et al.* (2013) and Nada *et al*. (2016) who found highly significant and positive correlation of grain yield with panicle length and thousand grain weight.

Similarly, thousand grain weight had highly significant (P≤ 0.001) positive correlation with plant height (r = 0.634) and panicle length (r = 0.525). This confirmed the fact that better plant biomass can contribute for increased grain size due the advantage of having better assimilate to store in the sink. This result was in line with previous work reported by Yang *et al*. (2010). Conversely, days to maturity had not correlated with grain yield; this could be related to the low variability of the test hybrids for the trait.

Earliness is a very important trait under low- rainfall conditions. The trait having the most dominant effect on fitting a plant to its environment for maximum productivity is the appropriate phenological development (Muchow *et al*, 1994). Conforming to the association among grain yield and other measured traits, the association between grain yield and days to flowering was strongly negative (r = -0.580) and highly significant (P≤ 0.001) while days to maturity was weakly negativly correlated with grain yield; r = -0.095 and non-significant. But, the association between days to maturity and days to flowering was positive (r = 0.773) and highly significant (P≤ 0.001).

The negative association between grain yield with days to flowering and maturity indicated that moisture stress after flowering might have caused a yield reduction in the late maturing genotypes, whereas, the early flowering and early maturing genotypes had the advantage to filled grain early and escaped the moisture stress conditions. Similar results were reported by Kassahun *et al*. (2015), Taye *et al*. (2016) on sorghum; Assefa *et al*. (2014) in wheat and Yirga (2017) in sesame.

Table 6. Correlation coefficients among some agronomic traits of 49 sorghum genotypes evaluated at five locations in Ethiopia in 2016 growing season.

	DTF	DTM	GY	PHT	PL	TGW
DTF	**1**					
DTM	0.773***	**1**				
GY	-0.580***	-0.095^{ns}	**1**			
PHT	-0.369^{ns}	-0.068^{ns}	0.723***	**1**		
PL	-0.049^{ns}	0.054^{ns}	0.631***	0.461***	**1**	
TGW	-0.061^{ns}	0.034^{ns}	0.762***	0.634***	0.525***	**1**

*, **,*** = significant at P≤ 0.05, P≤ 0.01 and P≤ 0.001, respectively, ns = non-significant, DTF = Days to flowering (days), DTM = Days to maturity (days), PTH = plant height (cm), PL=panicle length (cm), GY = grain yield (kg ha-1), TGW= thousand grain weight (g)

4.4. Grain Yield Stability Analysis

4.4.1. AMMI Analysis

The result for the additive main effects and multiplicative interaction (AMMI) model across the five test environments is presented in Table 7. The AMMI analysis of variance for grain yield (kg ha^{-1}) showed that the mean squares for genotypes, environments and GEI were highly significant (P≤ 0.001). The larger sum of square and highly significant mean squares of environments indicated that the environments were diverse, which is in agreement with the previous findings of Alberts (2004), Solomon *et al*. (2008), Abdurahman (2009) and Gezahegn *et al.* (2017).

The significant genotype by environment interaction effect was further partitioned in to two interaction principal component axis (IPCA).The results of AMMI analysis showed highly significant (P≤ 0.001) differences for the first two interaction principal component axis (IPCA). The first interaction principal component (IPCA1) captured 62.46% and the second (IPCA2) further explained 27.71% and the two interaction principal components cumulatively explained 90.20% of the genotype by environment interaction sum of square and the rest 9.80% was contributed due to noise.

Based on Gollob (1968) F-test the two interaction principal components were significant (P≤ 0.001) while the IPCA3 was non-significant. Therefore, the AMMI-1 with only the two interaction principal component axis was the best predicative model for grain yield. This is in harmony with Zobel *et al*. (1988) and Annicciarico (2002). The third interaction principal component axis captured mostly noise and did not help to predict valid observations. Hence, the interaction of the 49 genotypes with five environments was best predicted by the two interaction principal components. In general, factors like type of crop, diversity of the genotype and range of environmental conditions affect the degree of complexity of the best predictive model (Crossa, 1990).

Table 7. Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield (kg ha^{-1}) of 49 sorghum genotypes evaluated at five environments in Ethiopia during 2016 cropping season.

Source	DF	SS	MS	Sum of squares % explained		
				Total	GEI	GEI Cmu.
Reps. within env.	5	2942779	588556^{ns}			
Environment (E)	4	1167796816	291949204***	76.13		
Genotype (G)	48	171888246	3581005***	11.21		
GxE Interaction	192	194226843	1011598***	12.66		
IPCA 1	51	121313805	2378702***		62.46	62.46
IPCA 2	49	53825505	1098480***		27.71	90.20
IPCA 3	47	13061480	277904^{ns}		0.27	
Residuals	45	6026054	133912^{ns}			
Pooled error	240	58359242	243164			
Total	489	1595213927				

***= significant at P-value≤ 0.001 and ns = non-significant, IPCA=interaction principal component axis, GEI = Genotype by Environment Interaction explained and GEI cum. = GEI cumulative, SS=Sum of Squares, MS= Mean Square.

AMMI-1 biplot of forty nine sorghum genotypes evaluated at five environments was generated using genotypic and environmental mean grain yield plotted against their first IPCA scores (Figure 3). Stable genotypes were adaptive to wider areas and gave consistet mean yield across the test locations. G6, G28, G41, G39, G38, G27 and G32 were found nearly closer to the origin are the most stable and little responsive to the environment. In contrast, genotypes far from the origin are sensitive to environmental changes. Hence, G49, G29, G20, G21, G40, G4, G1, G24, G16, G22, G7, G18, G28, G34, G36, G19, G25 and G32 were unstable.

The AMMI analysis provided a biplot of main effects and the first principal component scores of interaction (IPCA 1) of both genotypes and environments. This biplot helped in the interpretation of the interaction effects among genotypes and environments and for assessment of the stability of genotypes across environments. The differences among the genotypes in terms of direction and magnitude along the x-axis (yield) and y-axis (IPCA 1 scores) are important. Genotypes or environments on the right side of the midpoint of the perpendicular line have higher yields than those on the left side. Based on the biplot analysis, environments and genotypes show high variability in both main effects and interaction effects (IPCA-1) for mean grain yield.

Accordingly, Mehoni and Sheraro were considered as favorable environments, which had a positive IPCA-1 score and high mean grain yield. On the contrary, Humera, Kobo and Fedis were unfavorable environments for all genotypes with negative IPCA-1 score and different yield response of 588, 985 and 1319 kg ha^{-1}, respectively, which is below average grain yield. The unfavorable genotypes with poorly adapted to three of the testing locations were G2, G5, G8, G9, G10, G11,G12, G13, G14, G23, G33, G35, G37, G45, G46, G47 and G48. In the biplot display, genotypes or environments that appear almost on a perpendicular line of a graph had similar mean yields and those that fell almost on a horizontal line had similar interactions (Crossa, 1990). Thus, the relative variability due to environments was greater than that due to genotypic differences.

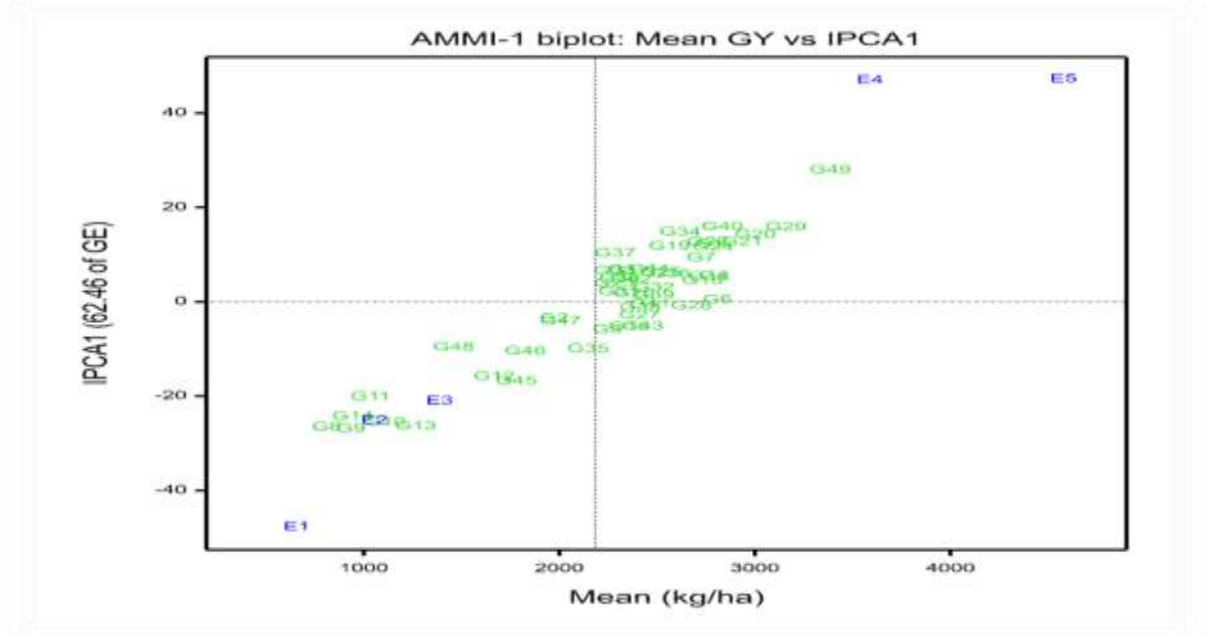

Figure 3. AMMI-1 biplot of main effects and interactions for grain yield of 49 sorghum genotypes at five environments. Where: E1= Humera, E2= Kobo, E3= Fedis, E4= Mehoni and E5= Sheraro.

4.4.2. GGE Biplot Analysis

In the AMMI model, only the GEI term is absorbed, whereas in the GGE model, the main effects of genotypes (G) plus the GEI, are the two sources of variation of GGE biplot. In GGE biplot, the best genotype is the one with large PC1 scores (high mean yield) and near zero PC2 scores (high stability). In this study PC1 and PC2 accounted for 77.12% and 14.71% of the total G+GE (genotype and genotype by environment interaction), respectively, and a total of 91.83% of G+GE. GGE biplot was used to identify mega environments, genotype and environment evaluation, stability of genotypes and identification of ideal genotype and environments.

4.2.2.1. The Mean Performance and Stability of Genotypes

The graphical method for mean performance and stability analysis of genotypes is presented in Figure 4. It was based on row metric preserving where the singular values were entirely partitioned into genotype scores. For this procedure, single arrowed line that passes through the biplot origin and points to higher mean yield across environments was drawn. This line is called the average environment coordination (AEC) abscissa and labeled as AEA. The arrow directs towards higher average yield and hence genotypes on the right side most of this line have highest average yield. Single arrowed line that is perpendicular to AEC abscissa was also drown and this line is called the AEC ordinate and is labeled as Perpendicular Line (PL). This line points towards greater variability in either direction and hence genotype that has longer vector along this line is highly unstable (Ilker *et al*., 2011).

The shorter the genotype vector is the more stable than others. Thus, among the tested genotypes G29, G21, G22, G24 and G34 were identified as high yielder and stable genotypes while G14, G12, G2, G15, G48, G28, G42 and G19 were found to have lower mean grain yield with longer vector length and identified as the most unstable genotypes across the test environments, which is in agreement with the previous findings of Habte *et al.* (2016) in sorghum, Demissew *et al*. (2016) in quality protein maize hybrids and Dejene (2016) in bread wheat.

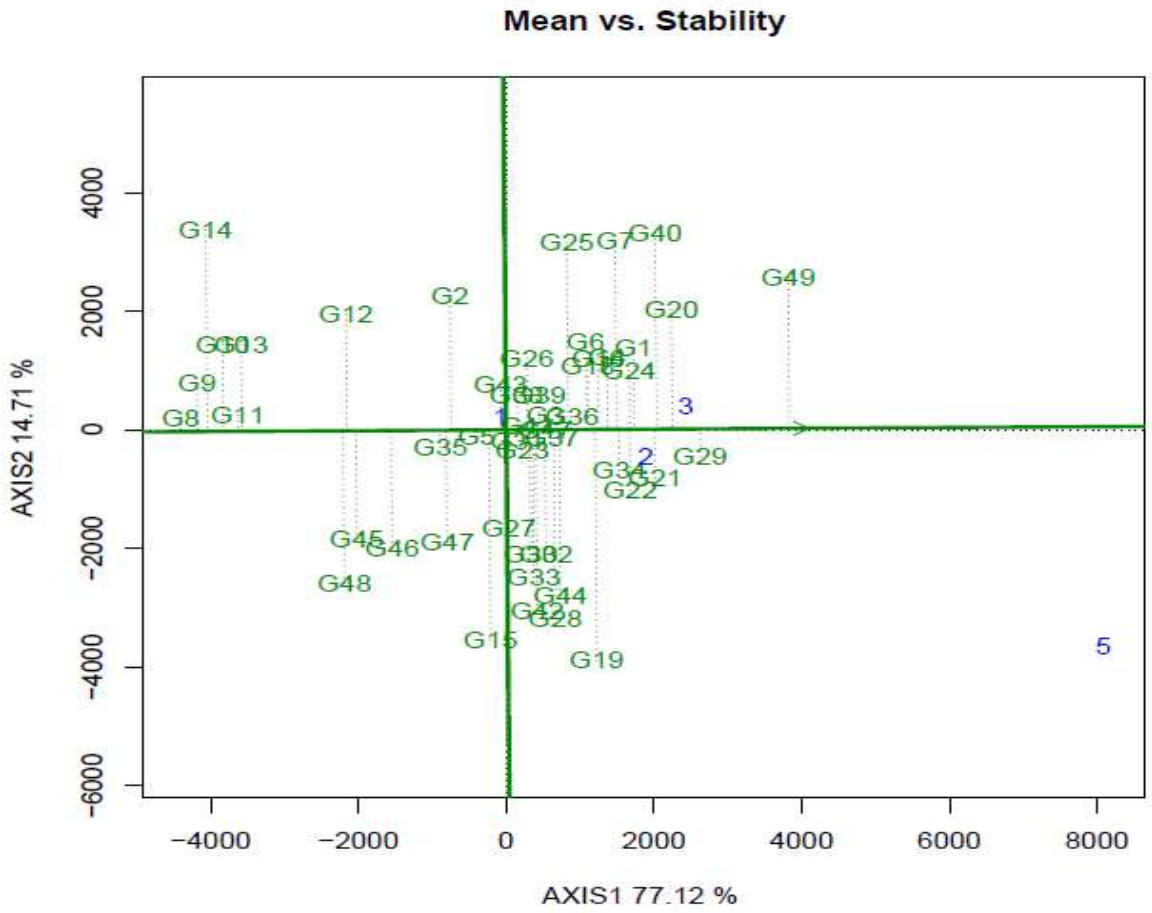

Figure 4. The mean performance and stability view of the GGE biplot of 49 sorghum genotypes at five environments

4.4.2.2. Ranking Genotypes Relative to the Ideal Genotype

GGE biplot based on ranking of genotypes relative to the ideal genotype for grain yield is presented (center of the concentric circle) in Figure 5. According to this ranking procedure, the genotypes closer to the ideal genotype were the stable ones, while genotypes far from the ideal genotypes were the unstable. G29 was the "ideal" genotype with high mean grain yield and closer to the small circle being located on the AEC abscissa and with an arrow pointing to it (Fig. 5). Genotype is more desirable if it is located closer to the ideal genotype. Therefore, G29 followed by G21, G22, G34 and G24 were plotted closer or near to the ideal genotype and considered as the most desirable and stable genotypes, while G49, G40 and G20 were high yielding genotypes associated with genotypic instability. Similar result was reported by

various authors, Habte *et al*. (2016) on sorghum; Farshadfar *et al*. (2012); Mitrovic *et al*. (2012) and Yirga, (2016) on sesame.

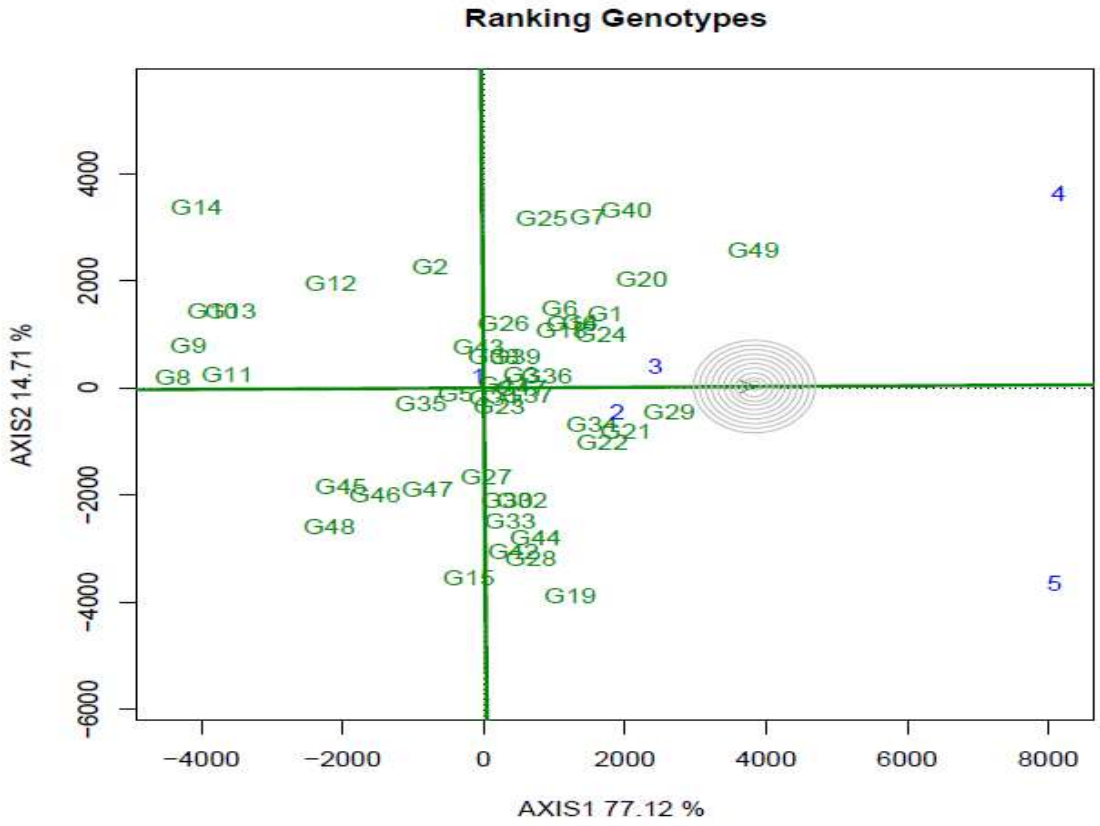

Figure 5. GGE-biplot showing the "ideal" sorghum genotype

4.4.2.3. 'Which-Won-Where' Pattern and Mega-environment Identification

The polygon in Figure 6 is formed by connecting the markers of the genotypes that are further away from the biplot origin such that all other genotypes are contained in the polygon. One of the most important properties of GGE biplot is its ability to show the which-won-where pattern and mega environment differentiation from the genotype by environment interaction and hence is a concise summary of the G × E pattern of a multi environment trials data set (Yan, 2002). Mega environment is a group (cluster) of locations or environments that constantly share the same best/winning genotype. Genotype evaluation within a mega-environment should, therefore, be based on both mean performance and stability to avoid the random GEI. This could be done by identifying the ideal genotype. The testing environments (Figure 6) fell into seven sectors with different winner genotypes and the biplot showed that

six vertex genotypes, G8, G14, G19, G40, G48 and G49. According to Yan and Kang (2003) genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments.

Therefore, the GGE biplot graph identified two different sorghum growing mega-environments for grain yield. The first environment includes higher yielding E4 (Mehoni) to lower yielding E1 (Humera), E2 (Kobo) and E3 (Fedis) environments, respectively with the winner genotype G49; the second environment containing the highest yielding environment (E5) in Sheraro area with winner genotype G19 presented in Figure 6. On the contrary, the result also showed some genotypes which fell in sectors where there were no locations at all; these genotypes are poorly adapted to five of the testing locations (G2, G3, G5, G9, G10, G12, G35, G45, G46 and G47). Gasura *et al.* (2015) and Habte *et al.* (2016) are among the many authors who used GGE bi-plot to identify mega environments, to evaluate the genotypes and to test the environments in sorghum.

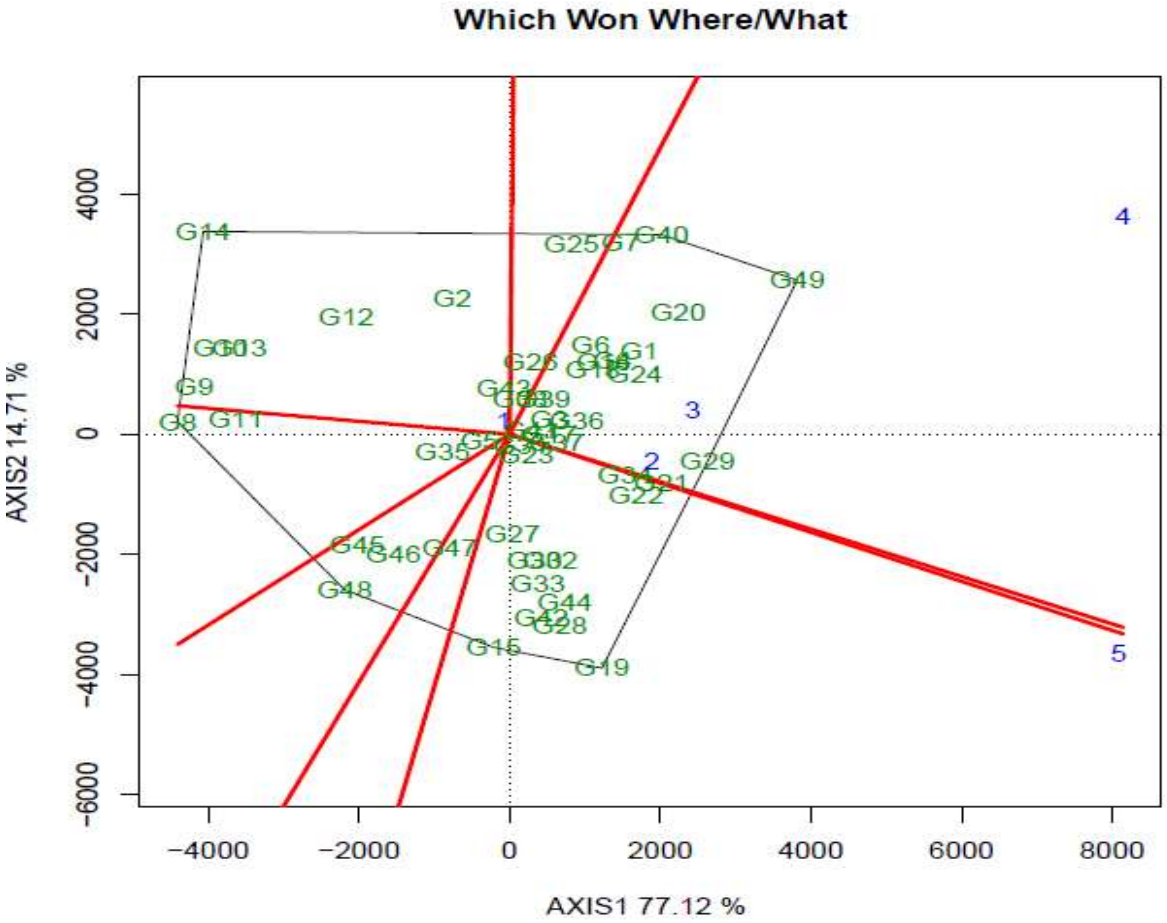

Figure 6. Polygon view of GGE biplot graph for which-won-where pattern of GEI for grain yield.

4.4.3. Eberhart and Russell's Linear Regression Model

The analysis of variance by Eberhart and Russel's Model of *striga* resistant sorghum hybrids on mean grain yield (kg ha^{-1}) tested at five locations is presented in Table 8. Genotype x environment interaction ANOVA of joint linear regression model is used for estimation and partitioning of genotype by environment interaction in to components. Hence, it permitted the partitioning of the sources of variation in to environment (linear), G x L (linear) interaction effects (sum of squares due to regression, bi) and unexplained deviation from linear regression (pooled deviation mean squares (S^2di). 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 GEI in the ANOVA. The result of Eberhart and Russell's ANOVA revealed highly significant ($P \leq 0.01$) difference among the genotypes for grain yield indicating the yield performance of genotypes was significantly different. The GE (linear) interaction was significant. Thus, the GE interaction was linear type and shows the existence of genetic differences among genotypes for their response to varying locations.

Table 8. Analysis of variance by Eberhart and Russel's Model of striga resistant sorghum hybrids on mean grain yield (kg ha^{-1}) tested at five locations.

Source of Variation	Df	Sum squares	Mean squares
Total	244	767110004.9	
Genotype	48	85921925.17	1790040.11**
Loc. + (Gen. x Loc.)	196	681188079.7	4633932.52**
Location (Linear)	1	584058035.5	3973183.92**
Genotype x Location (Linear)	48	58690982.96	1222728.81*
Pooled Deviation	147	38439061.23	261490.21**
Genotype 1	3	574234.85	3906.36^{ns}
Genotype 2	3	745988.28	248662.76*
Genotype 3	3	82574.58	27524.86^{ns}
Genotype 4	3	2039112.33	679704.11**
Genotype 5	3	280858.64	93619.55^{ns}
Genotype 6	3	655330.16	218443.39^{ns}
Genotype 7	3	2132838.04	710946.01**

Table 8. (continued)

Source of Variation	Df	Sum squares	Mean squares
Genotype 8	3	153588.24	51196.08^{ns}
Genotype 9	3	298582.15	99527.38^{ns}
Genotype 10	3	110057.4	36685.8^{ns}
Genotype 11	3	192264.15	64088.05^{ns}
Genotype 12	3	292077.43	97359.14^{ns}
Genotype 13	3	338435.85	112811.95^{ns}
Genotype 14	3	936612.6	312204.2*
Genotype 15	3	2484781.66	828260.55**
Genotype 16	3	1011722.76	337240.92*
Genotype 17	3	199982.32	66660.77^{ns}
Genotype 18	3	485531.3	161843.77^{ns}
Genotype 19	3	1904662.13	634887.38**
Genotype 20	3	1187239.31	395746.44*
Genotype 21	3	318954.6	106318.2^{ns}
Genotype 22	3	122671.89	40890.63^{ns}
Genotype 23	3	4589.43	1529.81^{ns}
Genotype 24	3	500019.4	166673.13^{ns}
Genotype 25	3	1805630.09	601876.7**
Genotype 26	3	426170.18	142056.73^{ns}
Genotype 27	3	636304.8	212101.6^{ns}
Genotype 28	3	1637767.97	545922.66**
Genotype 29	3	238823.6	79607.87^{ns}
Genotype 30	3	894564.386	298188.13*
Genotype 31	3	262716.58	87572.19^{ns}
Genotype 32	3	989206.13	329735.38*
Genotype 33	3	780329.85	260109.95*
Genotype 34	3	2598.09	866.03^{ns}
Genotype 35	3	435852.6	145284.2^{ns}
Genotype 36	3	253606.44	84535.48^{ns}
Genotype 37	3	121610.96	40536.99^{ns}
Genotype 38	3	568151.998	189383.999^{ns}
Genotype 39	3	119152.27	39717.424^{ns}
Genotype 40	3	3030245.77	1010081.925**
Genotype 41	3	172749.24	57583.08^{ns}
Genotype 42	3	1303019.87	434339.96*
Genotype 43	3	304362.1	101454.034^{ns}
Genotype 44	3	963541.65	321180.55*
Genotype 45	3	1078479.7	359493.23*

Table 8. (continued)

Source of Variation	Df	Sum squares	Mean squares
Genotype 46	3	927793.17	309264.39*
Genotype 47	3	745636.08	248545.36*
Genotype 48	3	1402267.99	467422.66**
Genotype 49	3	2285770.2	761923.42**
Pooled Error	245	24270710.75	99064.13

*, ** = significant at P≤ 0.05 and P≤ 0.01, respectively, ns = non-significant.

The stability parameters of Eberhart and Russell (1966) model for grain yield of *striga* resistant sorghum genotypes tested at five locations is presented in Table 9. According to this model, the genotype's performance is expressed in terms of three parameters, mean yield, regression coefficient and the deviation from the regression. Therefore, a stable genotype is one with high mean yield, bi=1, and S^2di not significantly different from zero. Based on these three preconditions, G6, G38, G27, G41 and G43 had relatively high yield, near to unity regression coefficient (bi) and deviation from regression (S^2di) not significantly different from zero and considered as stable genotypes, while G49, G29, G20, G21, G40, G4, G1, G24, G16, G22, G7, G18, G28, G34, G36, G19, G25 and G32 had greater than unity estimated value (bi >1); suitable for high potential environments and considered as unstable genotypes for grain yield.

Table 9. Estimates of stability parameters and their ranking order for mean yield (kg ha-1), regression coefficient (bi), deviation from regression (S^2di) and coefficient of determination of 49 sorghum genotypes evaluated at five locations.

Genotypes	bi	Rank	S^2di	Rank	r^2	Gy	Rank
G1	1.278**	41	69814.4ns	18	0.9713	2692	8
G10	0.3324**	5	-62378ns	23	0.923	1000	45
G11	0.4962**	6	-34976ns	15	0.9386	932	46
G12	0.5642**	7	-1705ns	7	0.9285	1561	42
G13	0.3205**	3	-8861.9ns	1	0.7835	1159	44
G14	0.3203*	2	190574*	34	0.5662	838	48
G15	0.9493**	17	706649*	48	0.8121	2249	29
G16	1.1127**	30	215819*	37	0.9358	2658	10
G17	1.1526**	32	-32403ns	14	0.9875	2251	28
G18	1.0892**	26	40121.2ns	11	0.9668	2623	13
G19	1.380**	46	513064**	44	0.9226	2456	17

Table 9. (continued)

Genotypes	bi	Rank	S^2di	Rank	r^2	Gy	Rank
G2	0.8648**	13	127012ns	29	0.9228	1898	39
G20	1.3008**	42	274409*	39	0.9444	2894	3
G21	1.3243**	44	7254.07ns	2	0.9849	2828	4
G22	1.3354**	45	-58174ns	20	0.9942	2652	11
G23	1.1026**	27	-97534ns	27	0.9997	2175	34
G24	1.2586**	39	45370.8ns	13	0.9742	2679	9
G25	1.0882**	25	479635**	43	0.8867	2410	18
G26	1.0285**	22	20318.4ns	4	0.9673	2274	26
G27	0.9736**	18	90294.4ns	24	0.9467	2303	25
G28	1.0458**	24	424360*	42	0.8884	2567	14
G29	1.3915**	48	-19456ns	12	0.9897	3051	2
G3	1.1629**	33	-71539ns	25	0.9949	2244	30
G30	1.1801**	35	176483*	32	0.9489	2200	31
G31	1.0404**	23	-11492ns	9	0.98	2197	32
G32	1.1108**	29	208124*	36	0.937	2377	19
G33	1.2262**	37	138334ns	31	0.9583	2172	35
G34	1.3838**	47	-98198ns	28	0.9999	2510	15
G35	0.7411**	9	23898ns	6	0.9375	2040	37
G36	1.1271**	31	-14529ns	10	0.9835	2458	16
G37	1.2686**	40	-58527ns	21	0.9937	2179	33
G38	0.9393**	16	67880.1ns	17	0.9487	2305	24
G39	1.0119**	21	-59347ns	22	0.9903	2374	20
G4	1.1101**	28	558497*	45	0.878	2713	7
G40	1.3072**	43	888764**	49	0.8704	2726	6
G41	0.990**	19	-41481ns	16	0.9855	2354	21
G42	1.1801**	36	312688*	40	0.9272	2258	27
G43	0.8432**	12	-20131ns	3	0.9653	2321	23
G44	1.2326**	38	199506*	35	0.9495	2352	22
G45	0.6110**	8	237934*	38	0.8049	1673	41
G46	0.7782**	10	187638*	33	0.8861	1718	40
G47	0.9327**	15	127042ns	30	0.9329	1899	38
G48	0.8172**	11	345709*	41	0.8502	1353	43
G49	1.6388**	49	640592**	47	0.9333	3278	1
G5	0.8689**	14	-5444.6ns	8	0.9698	2170	36
G6	0.9927**	20	96744.7ns	26	0.9472	2732	5
G7	1.1639**	34	589528*	46	0.8833	2650	12
G8	0.3237**	4	-47868ns	19	0.8905	735	49
G9	0.3085**	1	463.27ns	5	0.7916	858	47

*, ** = significant at P≤ 0.05 and P≤ 0.01, respectively, ns = non-significant, bi= regression coefficient and S^2di= deviation from regression, r^2= coefficient of determination

The stability analysis of variance revealed highly significant (P≤ 0.01) difference between genotypes, suggesting that there was considerable differential performance of the genotypes; this result was in line with Mekonen *et al.* (2015) on sesame and Lalise (2015) on maize. The GEI (linear) interaction of grain yield (kg ha^{-1}) was highly significant (P≤ 0.01), indicating that the stability parameter (bi) estimated by linear response to change in environment was different for all genotypes or genotypes had different slopes (Table 9). This confirms that GEI was in a linear function of environment indices as the mean of all the genotypes tested.

Coefficient of determination (r^2) represents the predictability of estimated response of the genotypes. The values of coefficient of determination ranged between 0.5662 for G14 and 0.9999 for G34, suggesting that linear regression accounted from 56.62% to 99.99%. This result showed that the variation in sorghum mean grain yield was explained by genotype response across the testing environments, which is in agreement with the previous findings of Showemimo (2007) in sorghum. Except one genotype (G14), all genotypes showed high coefficient of determination. However, seventeen out of 49 genotypes had yielded below average. Hence the interest of plant breeder is to develop genotypes with highest mean yield and which can be overcome by both predictable and unpredictable environment fluctuations.

4.4.4. AMMI Stability Value

The result for stability analysis of genotypes using AMMI stability value (ASV) was given in Table 10. This stability analysis was based on the value of the first two IPCA scores of genotypes. According to this stability measure, the highest rank is given to the genotype that is close to the biplot origin, *i.e*, genotype that has the smallest ASV (ASV value closest to zero). Accordingly, G6 (K7439) was found to be the most stable genotype, followed by G28 (K7251), G39 (K7270), G41 (K7274), G26 (K7245), G38 (K7268), G32 (K7259), G27 (K7249), G2 (K7417), G42 (K7276), G47(P9403) and G15 (K7229) using this method. The procedure also identified G8 (5136), G11 (5153), G9 (5151), G13 (5156), G37 (K7267) and G10 (5152) as the most unstable genotypes (genotypes with inconsistent performance) across the test environments.

Stability studies have allowed researchers to identify broadly adapted cultivar for use in breeding programs and have assisted to advance suggestions to farmers (Yayeh and Bosland, 2000). The most stable and adapted genotypes can be identified using ASV as that of Lins and Binns method. Almeida *et al*. (2014), Vange *et al*. (2014), Abiy (2015) and Lalise (2015) used also this stability parameter to characterize the stability of sorghum and maize. Moreover, the model was used in Sesame by Zenebe and Hussein (2009), Fiseha *et al*. (2015) and Yirga (2016), in triticale by Dagnachew *et al*. (2014), and in malt barely by Muez *et al*. (2014).

4.4.5. Yield Stability Index

Genotypes with lowest estimated values of yield stability index (YSI) are desirable and considered as the most stable. Based on YSI, G6, G38, G27, G41 and G43 were the most stable. Conversely, G8, G9, G10, G11 and G14 were the most unstable genotpes (Table 10). Harmoniously, Showemimo (2007) in sorghum; Olayiwola and Ariyo (2013) in okra, Mohammed (2015) and Yirga (2016) in sesame used this model to identify stable genotypes.

Table 10. Mean yield (kg ha^{-1}), rank, IPCA1 and IPCA2 scores and AMMI stability values (ASV) of 49 sorghum genotypes tested at five environments of Ethiopia during 2016.

Gen	Yield	R^y	IPCA1	IPCA2	ASV	R^a	YSI (R^y+ R^a)	R
G1	2692	8	-0.43486	-0.27657	0.545	30	38	17
G10	1000	45	0.918905	-0.27442	1.682	44	89	45
G11	932	46	0.724628	-0.0436	2.954	48	94	47
G12	1561	42	0.571187	-0.37671	0.703	35	77	41
G13	1159	44	0.948248	-0.27019	1.776	46	90	46
G14	838	48	0.873606	-0.6576	1.007	39	87	44
G15	2249	29	0.192897	0.705534	0.1007	12	41	20
G16	2658	10	-0.18914	-0.23394	0.17	19	29	7
G17	2251	28	-0.23203	-0.00678	1.358	41	69	39
G18	2623	13	-0.15679	-0.21299	0.135	16	29	8
G19	2456	17	-0.41929	0.757454	0.32	25	42	21
G2	1898	39	0.127688	-0.44776	0.068	9	48	30
G20	2894	3	-0.50753	-0.40521	0.568	31	34	13
G21	2828	4	-0.45226	0.15598	0.77	36	40	18
G22	2652	11	-0.45319	0.194041	0.693	34	45	25
G23	2175	34	-0.13771	0.061383	0.206	21	55	33
G24	2679	9	-0.4133	-0.20336	0.589	33	42	22
G25	2410	18	-0.22022	-0.62553	0.131	15	33	11
G26	2274	26	-0.05949	-0.24029	0.03	5	31	10

Table 10. (continued)

Gen	Yield	R^y	IPCA1	IPCA2	ASV	R^a	YSI (R^y+ R^a)	R
G27	2303	25	0.105713	0.331416	0.06	8	33	12
G28	2567	14	0.0326	0.632006	0.007	2	16	2
G29	3051	2	-0.56516	0.084624	1.461	43	45	26
G3	2244	30	-0.24005	-0.05747	0.491	28	58	35
G30	2200	31	-0.1721	0.40828	0.112	14	45	27
G31	2197	32	-0.0736	0.032812	0.11	13	45	28
G32	2377	19	-0.10665	0.41107	0.054	7	26	5
G33	2172	35	-0.23138	0.482005	0.16	17	52	32
G34	2510	15	-0.52739	0.123366	1.09	40	55	34
G35	2040	37	0.360673	0.064443	0.853	38	75	40
G36	2458	16	-0.20918	-0.04593	0.446	27	43	23
G37	2179	33	-0.36537	0.015762	1.759	45	78	42
G38	2305	24	0.046851	-0.11245	0.03	6	30	9
G39	2374	20	-0.04575	-0.11307	0.029	3	23	3
G4	2713	7	-0.1944	-0.24062	0.175	20	27	6
G40	2726	6	-0.5678	-0.66397	0.525	29	35	14
G41	2354	21	0.02126	-0.01097	0.029	4	25	4
G42	2258	27	-0.16702	0.596513	0.088	10	37	16
G43	2321	23	0.189446	-0.14471	0.217	22	45	29
G44	2352	22	-0.24585	0.544461	0.165	18	40	19
G45	1673	41	0.605294	0.373869	0.77	37	78	43
G46	1718	40	0.377955	0.396967	0.369	26	66	36
G47	1899	38	0.149284	0.374734	0.094	11	49	31
G48	1353	43	0.348024	0.508453	0.288	24	67	37
G49	3278	1	-1	-0.5198	1.387	42	43	24
G5	2170	36	0.214792	0.029762	0.577	32	68	38
G6	2732	5	-0.01311	-0.28803	0.003	1	6	1
G7	2650	12	-0.33157	-0.63343	0.24	23	35	15
G8	735	49	0.95511	-0.03313	5.128	49	98	49
G9	858	47	0.968017	-0.14643	2.489	47	94	48

R^a = Rank by ASV, R^y = Rank by grain yield, YSI = yield stability index

4.4.6. Relationship of Stability Parameters

The result of spearman's rank correlation coefficient presented in Table 11 showed that mean grain yield was positively and highly significantly ($P \leq 0.01$) correlated with bi (r= 0.91), r^2 (r= 0.55) and negatively and highly significantly ($P \leq 0.01$) correlated with IPCA1 (r= -0.91) and ASV (r= -0.56). This result is in line with the findings of Solomon *et al*. (2008) and Lalise (2015) on maize. However, there was no significant correlation between mean grain yield with

Eberhart and Rusell's deviation from regression (S^2di) (r=0.269) stability parameter and IPCA2 (r= -0.10).

The non-significant correlation among yield and stability statistics indicated that, stability statistics provide information that cannot be collected from average yield alone (Duarte & Zimmerman, 1995). The high correlation among mean grain yield, bi, and r^2 is expected as the values of these statistics were higher for high yielding genotypes. The positive and significant correlations between mean grain yield and r^2, and bi and r^2 suggest that the parameter, r^2 should be considered only in measuring dimensions of grain yield, but could not adequately detect stability and, hence, its efficiency in selecting desirable genotypes is limited when used alone. The same suggestion was given by Setegn and Habtu (2003), Nigussie (2012). The negative correlation between grain yield and S^2di indicated that high yielding genotypes may be associated with low S^2di.

Table 11. The Spearman's rank correlation for all estimates of stability parameter

	Gy	bi	S^2di	r^2	IPCA1	IPCA2	ASV
Gy	1						
Bi	0.91**	1					
S^2di	0.269^{ns}	0.132^{ns}	1				
r^2	0.55**	0.495**	-0.40*	1			
IPCA1	-0.92**	-0.99**	-0.126^{ns}	-0.57**	1		
IPCA2	-0.160^{ns}	0.117^{ns}	-0.011^{ns}	0.138^{ns}	-0.035^{ns}	1	
ASV	-0.56**	-0.46**	-0.29^{ns}	-0.05^{ns}	0.44**	-0.192^{ns}	1

*, ** = significant at P≤ 0.05 and P≤ 0.01, respectively, ns= non-significant; bi = Eberhart and Russell's regression coefficient; S^2di = Eberhart and Russell (1966) deviation from regression coefficient, ASV=AMMI stability value, r^2 = Coefficient of determination.

4.5. Genotypes Selection by AMMI model

Multi-location trials are very important for selecting the best genotype for wide or specific environments before any recommendation of genotypes for future commercial production. The four best hybrids selected by AMMI model for each environment are presented in Table 12. Genotypes selected in all environments are an indication of the best adapted genotype for each testing environment were obtained from the AMMI model. In this study, genotypes were

reacted differently to environmental fluctuation (have high GEI), as the result the best AMMI model allows as to select relatively better genotypes that suit to a specific environment.

Accordingly, genotype G49 was best for high yielding environments of Mehoni and Sheraro and genotypes G19 and G4 were the best genotypes which specifically adapted to Sheraro and Fedis (Table 12). G29, G20 and G21 better performed in the high yielding to low yielding environments and stable across environments, whereas G6 was the best genotype for low to medium yielding environments of Humera and Fedis. The other hybrids that were selected did not show a distinct pattern of adaptation and more specific adapted either lower or higher yielding environments.

Table 12. The AMMI model's best four sorghum hybrids selection for grain yield per environment

			IPCA 1	The first four AMMI selected hybrids			
Environment	Sites	Mean	Score	1	2	3	4
E5	Sheraro	4508	47.19	G19	G49	G29	G21
E4	Mehoni	3518	46.89	G49	G40	G20	G7
E3	Fedis	1319	-21.09	G4	G16	G6	G21
E2	Kobo	985	-25.23	G29	G38	G43	G32
E1	Humera	588	-47.76	G6	G5	G27	G18

5. SUMMARY AND CONCLUSION

Sorghum, known as a Camel crop of cereals, is among the dominant staple food grains for the majority of Ethiopians. In spite of biotic and abiotic stress tolerance, the procedures in the selection of good performing and stable genotypes are complicated by the phenomenon of genotype by environment interaction to recommend new sorghum genotypes for different environments. The large variation in environmental factor causes the relative ranking of the genotype to change from location to location and from year to year. Therefore, 49 genotypes (hybrids + varieties) were tested at five locations in a simple lattice design with two replications during the 2016 main cropping season. The experiment was carried out to estimate the magnitude and nature of GEI for yield and yield related traits and to determine yield stability of striga resistant sorghum genotypes.

The results of the study indicated that there were significant differences among genotypes, environments and GEI. The significant effect of GEI on grain yield suggested the need to assess the stability of genotypes overall environments. Based on the combined analysis of variance over locations the mean grain yield of environments ranged from 588 kg ha^{-1} in E1 (Humera) to 4508 kg ha^{-1} in E5 (Sheraro).The highest yield was obtained from G49 (3278 kg ha^{-1}), while the lowest was from G8 (735 kg ha^{-1}). However, the newly evaluated hybrids had not shown yield advantage over the standard hybrid check.

Combined analysis of variance revealed significant ($P \leq 0.001$) variations of genotypes, environments and GEI, suggesting the high environmental variations and differential response of genotypes to the variable environments thus leading to inconsistet in ranking of genotypes. The large sum of square and highly significant environment effect indicated that the environments were diverse and caused most of the variation in grain yield. The environment, genotype and their interaction (GEI) contributed by 76.13%, 11.21% and 12.66% to the total variation, respectively. Therefore the largest proportion of the total variation in grain yield was attributed to environments. This indicates the existence of a considerable amount of differential response among the genotypes to the changes of growing environments and the differential discriminating ability of the test environments.

Different stability models were used in measuring of genotype stability such as AMMI model, AMMI Stability Value (ASV), Yield Stability Index (YSI), GGE biplot, coefficient of regression (bi) and deviation from regression (S^2di). Yield was significantly correlated with bi (0.91), r^2 (0.55) and ASV (-0.56), while it was not correlated with S^2di (-0.26). The non-significant correlation among yield and stability statistics indicated that, stability statistics provide information that cannot be collected from average yield. The high positive correlation among mean grain yield and stability parameters is expected as the values of these parameters were higher for high yielding genotypes and the vice versa. Highly correlated stability parameter indicate that they can measure stability similarly.

There were inconsistencies with the univariate stability parameters used, which created uncertainty to select or recommend the stable genotypes. However, the multivariate models, AMMI model and GGE biplot were better for partitioning the GEI into the causes of variation and the best multivariate models to analyse data collected in this study. AMMI model was used to identify superior genotypes for specific and wide adaptation. Therefore, the following genotypes had good specific adaptation: K7437 (G4) and K7439 (G6) were specifically adapted to low yielding environments of Fedis and Humera. Whereas, the standard hybrid check, ESH-1 (G49) and K7233 (G19) were best genotypes for favorable environments of Mehoni and Sheraro, respectively. Whereas G29, G20 and G21 were best genotypes for low (Kobo) to high (Sheraro) yielding environments and stable across environments. Based on the GGE biplot analysis different sorghum growing environments were grouped in to two: The first environment includes higher E4 (Mehoni) to low yielding E1 (Humera), E2 (Kobo) and E3 (Fedis) environments, respectively with the winner genotype ESH-1. The second environment contained the highest yielding environment (E5) in Sheraro area with winner genotype K7233. Sheraro and Mehoni were considered as favorable dry lowland environments for selecting widely adaptable and high yielding sorghum genotypes.

Generally, the main problem of selection of superior genotypes in Ethiopia is the unpredictable weather changes from year to year and the variations of agro-ecologies leading to high contributor to genotype x environment interactions. Therefore, as the data is from one year, it is necessary to repeat the experiment across locations at least for one year to identify locations where the genotypes to be tested.

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7. APPENDICES

Appendix Table 1. Mean squares from analysis of variance and percentage of variance components for grain yield of 49 sorghum genotypes evaluated at each location

Humera

Source of variation	Degrees of freedom	Sum of square	Mean square	% Explained
Rep	1	290540	290540	3.66
Gen	48	6769666	141035***	85.16
Error	48	889197	18525	11.19
Total	97	7949403		

Kobo

Source of variation	Degrees of freedom	Sum of square	Mean square	% Explained
Rep	1	400512	400512	2.11
Gen	48	15866253	330547***	83.45
Error	48	2745281	57193	14.44
Total	97	19012046		

Fedis

Source of variation	Degrees of freedom	Sum of square	Mean square	% Explained
Rep	1	171029	171029	0.57
Gen	48	26052685	542764***	86.12
Error	48	4029891	83956	13.32
Total	97	30253605		

Mehoni

Source of variation	Degrees of freedom	Sum of square	Mean square	% Explained
Rep	1	17139	17139	0.01
Gen	48	159513498	3323198***	86.93
Error	48	23974477	499468	13.07
Total	97	183505114		

Sheraro

Source of variation	Degrees of freedom	Sum of square	Mean square	% Explained
Rep	1	6498	6498	0.01
Gen	48	157901836	3289622***	90.79
Error	48	16016857	333685	9.21
Total	97	173925191		

Appendix Table 2. Relative efficiency of lattice design to RCBD

Traits	Mean square			Efficiency (%)
	Rep/ evn.	Trt (GxE)	Error	
DTF	48.09	17.12	11.08	108.58
DTM	172.20	21.6	15.5	92.55
PHT	759.00	268	127	133.89
PL	190.5	8.9	6.7	107.94
TGW	89.1	11.5	7.8	85.2814
GY	588556	1011598	243164	104.22

Rep/en= replication within environment, Trt= treatment, GxE = genotype by environment interaction, DTE = Days to emergence , DTF = Days to flowering, DTM = Days to maturity, PTH = plant height, PL= panicle length, GY = grain yield, TGW= thousand grain weight.

Appendix Table 3. IPCA1, IPCA2 scores and environmental index for five locations

Environment	Graph ID	En. Mean	En. Index	IPCA1	IPCA2
Humera	E1	588	-1596.00	-47.76	1.96
Kobo	E2	985	-1198.80	-25.23	-7.08
Fedis	E3	1319	-864.71	-21.09	4.56
Mehoni	E4	3518	1334.86	46.89	50.84
Sheraro	E5	4508	2324.47	47.19	-50.28

En. Mean = environmental mean and En. Index = environmental index.

Appendix Table 4. Response of 49 sorghum genotypes for agronomic traits in respective environments

Humera

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G1	5.00 j	62.50 a-e	97.50 a-e	35.00 a-f	111.m-q	26.00 abc	670.00 d-i	20.00 abc
G10	6.00 a-i	68.00 abc	101.00 ab	33.00 a-f	150.50 b-g	28.40 abc	693.00 d-h	21.50 abc
G11	6.00 a-i	67.00 a-e	97.00 a-e	30.00 d-f	123.10 i-p	29.70 abc	425.00 h-l	17.00 bc
G12	5.50 ij	54.00 e	91.50 a-e	37.50 a-d	159.20 a-d	29.40 abc	797.00 c-f	18.00 bc
G13	6.50 a-h	66.00 a-e	95.50 a-e	29.50 e-f	151.00 b-g	31.50 a	1069.00 abc	21.50 abc
G14	6.00 a-i	67.00 a-e	97.50 a-e	30.50 c-f	163.00 ab	29.40 abc	548.00 e-l	20.00 abc
G15	5.50 ij	56.50 a-e	94.00 a-e	37.50 a-d	129.20 f-o	30.60 ab	780.00 c-g	19.00 abc
G16	5.00 j	57.00 a-e	96.00 a-e	39.00 ab	155.00 b-e	27.10 abc	671.00 d-i	17.00 bc
G17	5.00 j	60.00 a-e	94.00 a-e	34.00 a-f	160.00 abc	27.00 abc	307.00 kjl	17.50 bc
G18	6.00 a-i	66.00 a-e	100.00 a-e	34.00 a-f	140.00 b-j	28.10 abc	1075.00 abc	27.00 a
G19	5.00 j	64.50 a-e	97.50 a-e	33.00 a-f	152.00 b-f	27.30 abc	510.00 f-l	22.50 abc
G2	5.00 j	63.00 a-e	96.00 a-e	33.00 a-f	119.10 j-p	22.80 c	635.00 e-j	18.00 bc
G20	5.00 j	62.50 a-e	97.00 a-e	34.50 a-f	123.10 i-p	28.50 abc	541.00 e-l	19.50 abc
G21	5.00 j	60.00 a-e	97.00 a-e	37.00 a-e	152.00 b-f	29.20 abc	332.00 j-l	18.00 bc
G22	5.00 j	56.00 b-e	93.00 a-e	37.00 a-e	111.80 l-q	28.10 abc	330.00 j-i	22.00 abc
G23	5.00 j	67.50 a-d	99.00 a-e	31.50 b-f	104.50 pq	28.30 abc	391.00 h-l	16.00 c
G24	5.00 j	69.00 ab	101.50 a	32.50 a-f	114.10 k-q	27.30 abc	343.00 i-l	17.00 bc
G25	5.00 j	61.50 a-e	96.00 a-e	34.50 a-f	130.10 f-n	24.20 bc	668.00 e-k	21.00 abc

Appendix Table 4. (continued) Humera

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G26	5.50 ij	54.50 de	92.50 a-e	38.00 abc	136.80 c-k	30.10 ab	856.00 b-e	20.00 abc
G27	5.00 j	62.50 a-e	93.00 a-e	30.50 c-f	131.00 f-m	28.10 abc	1089.00 abc	20.50 abc
G28	5.00 j	55.50 c-e	91.50 c-e	36.00 a-e	141.90 b-j	26.80 abc	871.00 b-e	19.50 abc
G29	5.00 j	55.50 c-e	92.00 b-e	36.50 a-f	128.30 g-o	29.90 abc	515.00 f-l	19.00 abc
G3	5.00 j	62.50 a-e	95.00 a-e	32.50 a-f	106.40 o-q	25.30 abc	441.00 h-l	20.50 abc
G30	5.00 j	62.50 a-e	95.50 a-e	33.00 a-f	131.50 f-m	31.00 ab	471.00 f-l	19.00 abc
G31	5.00 j	62.50 a-e	95.50 a-e	33.00 a-f	123.70 i-p	31.30 ab	316.00 j-i	17.50 bc
G32	5.00 j	55.00 c-e	91.00 de	36.00 a-e	177.50 a	29.40 abc	643.00 e-j	17.00 bc
G33	5.00 j	69.50 a	101.00 ab	31.50 b-e	113.80 k-p	28.80 abc	448.00 g-l	19.00 abc
G34	5.00 j	68.00 abc	99.00 a-e	31.00 c-f	124.00 i-p	28.00 abc	283.00 kl	18.50 bc
G35	5.00 j	63.00 a-e	96.50 a-e	33.50 a-f	129.30 f-o	24.80 abc	469.00 f-l	23.00 abc
G36	5.00 j	67.50 a-d	99.00 a-e	31.50 b-f	124.50 h-p	30.90 ab	296.00 kl	18.50 bc
G37	5.00 j	67.00 a-e	97.00 a-e	30.00 d-f	112.75 i-q	29.80 abc	385.00 h-l	17.50 bc
G38	5.00 j	62.00 a-e	97.00 a-e	35.00 a-f	123.40 i-p	30.30 ab	684.00 d-h	19.00 abc
G39	5.00 j	55.50 c-e	93.50 a-e	38.00 abc	124.80 h-p	28.30 abc	617.00 e-k	20.00 abc
G4	5.00 j	57.00 a-e	93.00 a-e	36.00 a-e	147.60 b-h	27.80 abc	444.00 h-l	17.50 bc
G40	5.00 j	63.00 a-e	96.50 a-e	33.50 a-f	92.40 q	26.70 abc	342.00 i-l	22.50 abc
G41	5.00 j	56.00 bc	93.00 a-e	37.00 a-e	136.40 d-k	27.80 abc	1030.00 abc	18.00 bc
G42	5.00 j	68.00 abc	95.50 a-e	27.50 f	142.50 b-j	30.10 abc	462.00 g-l	24.50 ab
G43	5.00 j	68.00 abc	100.50 abc	32.50 a-f	121.80 i--p	26.80 abc	980.00 b-d	17.50 bc

Appendix Table 4. (continued) Humera

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G44	5.00 j	62.00 a-e	96.00 a-e	34.00 a-f	135.10 c-l	30.80 ab	495.00 f-l	20.50 abc
G45	5.50 ij	55.00 a-e	91.50 a-e	36.50 a-e	124.20 h-p	28.10 abc	643.00 e-j	17.00 bc
G46	6.50 a-h	68.00 abc	99.00 a-e	31.00 c-f	144.70 b-i	25.10 abc	561.00 e-l	18.00 bc
G47	5.00 j	56.00 b-e	90.50 e	34.50 a-f	110.00 m-q	31.10 ab	286.00 kl	20.50 abc
G48	7.00 a	54.00 c	91.00 de	37.00 a-e	106.50 n-q	31.80 a	286.00 kl	17.50 bc
G49	6.00 a-i	65.00 a-e	97.00 a-e	32.00 b-f	119.00 j-p	31.60 a	437.00 h-l	21.50 abc
G5	5.00 j	64.50 a-e	97.50 a-e	33.00 a-f	141.60 b-j	28.10 abc	1146.00 ab	18.00 bc
G6	5.00 j	55.00 c-e	91.00 de	36.00 a-c	148.70 b-g	26.10 abc	1321.00 a	19.50 abc
G7	5.50 ij	55.00 c-e	91.50 a-e	36.50 a-e	123.00 i-p	26.10 abc	585.00 e-l	15.50 bc
G8	6.00 a-i	54.00 c	94.00 a-e	40.00 a	143.60 b-i	28.30 abc	263.00 l	18.00 bc
G9	5.50 ij	56.00 b-e	95.00 a-e	39.00 ab	138.90 c-j	28.10 abc	341.00 k-l	20.00 abc
Mean	5.29	61.38	95.56	34.18	131.73	28.37	587.57	19.33
CV (%)	7.70	8.70	3.90	9.10	7.30	10.30	23.20	17.60

Kobo

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G1	6.00 bc	61.00 c-i	101.00 ab	40.00 a-d	126.00 b-j	25.90 a-f	1007.00 d-m	21.00 b-k
G10	8.00 a	65.00 a-e	101.50 ab	36.50 a-h	137.00 a-j	25.70 b-f	384.00 no	19.00 e-m
G11	8.00 a	64.50 a-f	100.00 ab	35.50 b-h	121.50 b-j	23.50 d-f	165.00 o	22.50 a-h
G12	7.00 abc	66.00 abc	98.00 ab	32.00 e-h	122.00 b-j	25.70 b-f	615.00 j-o	20.00 c-k
G13	6.50 abc	66.00 abc	96.00 b	30.00 h	121.00 c-j	23.90 c-f	409.00 no	20.00 c-k

Appendix Table 4. (continued) kobo

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G14	6.00 bc	66.00 abc	101.50 ab	35.50 b-h	109.00 j	22.60 f	211.00 c	21.50 a-j
G15	7.00 abc	61.00 c-i	98.50 ab	37.50 a-h	143.50 a-g	28.50 a-f	1037.00 c-l	22.50 a-h
G16	7.00 abc	63.50 a-h	97.50 ab	34.00 c-h	130.50 a-j	27.00 a-f	824.00 g-n	20.50 b-k
G17	6.00 bc	62.50 a-i	97.00 b	34.50 b-h	144.50 a-g	27.60 a-f	1178.00 a-j	23.50 a-f
G18	6.50 abc	62.50 a-i	100.50 ab	38.00 a-h	149.50 a-d	29.80 abc	1348.00 a-g	26.00 abc
G19	7.00 abc	62.00 a-i	98.00 ab	36.00 b-h	137.00 a-j	28.10 a-f	1178.00 h-j	23.50 a-f
G2	6.50 abc	61.50 b-i	98.00 ab	36.50 a-h	119.50 d-j	26.20 a-f	697.00 h-o	21.50 a-j
G20	5.50 c	62.00 a-i	101.50 ab	39.50 a-e	158.50 a	27.60 a-f	1435.00 a-f	18.00 f-m
G21	6.50 abc	63.00 a-i	97.50 ab	34.50 b-h	152.50 abc	27.90 a-f	1361.00 a-g	24.50 a-e
G22	6.00 bc	64.00 a-g	98.50 ab	34.50 b-h	132.00 a-j	25.50 b-f	1108.00 b-j	26.50 ab
G23	6.00 bc	58.50 hi	102.50 ab	44.00 a	147.00 a-c	26.70 a-f	888.00 f-n	20.00 c-k
G24	6.00 bc	62.50 a-i	102.50 ab	40.00 a-d	133.50 a-j	26.60 a-f	1197.00 a-j	16.50 h-m
G25	5.50 c	64.00 a-g	97.00 b	33.00 d-h	127.00 a-j	24.30 b-f	842.00 g-n	19.00 e-m
G26	6.00 bc	59.00 g-i	97.50 ab	38.50 a-f	131.00 a-j	25.90 b-f	644.00 i-o	18.00 f-m
G27	6.00 bc	58.50 hi	96.50 b	38.00 a-g	141.00 a-j	30.10 abc	1076.00 c-k	21.50 a-j
G28	6.50 abc	61.00 c-i	96.50 b	35.50 b-h	142.50 a-j	31.10 ab	1489.00 a-e	23.50 a-f
G29	7.00 abc	60.00 e-i	95.50 b	35.50 b-h	153.00 ab	29.90 abc	1732.00 a	16.00 i-m
G3	6.50 abc	63.00 a-i	95.50 b	32.50 d-h	117.00 e-j	25.50 b-f	866.00 f-n	21.50 a-j
G30	7.50 ab	62.50 a-i	97.50 ab	35.00 b-h	135.50 a-j	24.10 c-f	447.00 m-o	22.00 a-i
G31	6.00 bc	58.50 hi	96.50 b	38.00 a-g	146.00 a-e	27.50 a-f	1369.00 a-g	19.00 k-m
G32	6.50 a-e	60.50 d-i	95.50 b	35.00 b-h	146.00 a-e	29.10 a-d	1587.00 a-d	20.00 c-k

Appendix Table 4. (continued) kobo

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G33	7.00 abc	62.00 a-i	98.50 ab	36.50 a-h	124.50 b-j	24.60 c-f	618.00 j-o	20.50 b-k
G34	7.00 abc	64.00 a-g	97.50 ab	33.50 d-h	129.50 a-j	27.90 a-f	891.00 f-n	24.00 a-f
G35	6.50 abc	64.50 a-f	97.50 ab	33.00 d-h	140.50 a-j	28.60 a-f	1307.00 a-g	26.50 ab
G36	6.50 abc	63.50 a-h	96.50 b	33.00 d-h	125.50 b-j	27.10 a-f	1362.00 a-g	20.50 b-k
G37	7.00 abc	65.50 a-d	97.50 ab	32.00 e-h	114.00 f-j	24.70 c-f	470.00 l-o	22.50 a-h
G38	6.50 abc	62.50 a-i	96.00 b	33.50 d-h	147.50 a-j	27.10 a-f	1678.00 ab	27.50 a
G39	7.00 abc	58.00 i	96.00 b	38.00 a-g	130.50 a-j	28.90 a-e	1321.00 a-g	15.00 k-m
G4	6.50 abc	64.00 a-g	95.50 b	31.50 f-h	129.50 a-j	22.80 ef	831.00 g-n	15.50 j-m
G40	6.50 abc	60.50 d-i	98.00 b	37.50 a-h	132.50 a-j	26.80 a-f	1484.00 a-e	17.00 g-m
G41	6.00 abc	60.00 e-i	97.00 b	37.00 a-h	117.00 e-j	26.80 a-f	1157.00 a-j	19.50 d-l
G42	6.50 abc	63.00 a-i	104.50 a	41.50 abc	139.50 a-j	28.20 a-f	1214.00 a-i	20.50 b-k
G43	6.50 abc	59.00 g-i	101.00 ab	42.00 ab	134.00 a-j	29.90 abc	1601.00 abc	19.00 c-m
G44	7.50 ab	59.50 f-i	97.50 ab	38.00 a-g	145.00 a-g	32.00 a	1135.00 b-j	13.00 m
G45	6.50 abc	63.50 a-h	99.50 ab	36.00 b-h	111.00 h-j	23.40 d-f	1180.00 b-j	15.50 j-m
G46	6.50 abc	65.00 a-e	101.00 ab	36.00 b-h	113.50 g-i	22.70 ef	962.00 a-j	23.00 a-g
G47	7.50 abc	63.50 a-h	96.50 b	33.00 b-h	127.50 a-j	26.80 a-f	910.00 e-n	20.00 c-k
G48	7.00 abc	65.50 a-d	97.50 ab	32.00 e-h	109.50 ij	26.60 a-f	493.00 k-o	16.00 i-m
G49	6.50 abc	63.50 a-h	98.00 ab	34.50 b-h	127.00 a-j	24.80 c-f	1250.00 a-h	13.50 lm
G5	7.50 ab	65.00 a-e	97.00 ab	32.00 e-h	145.50 a-f	23.90 c-f	794.00 g-n	22.00 a-i
G6	7.00 abc	64.00 a-g	96.50 ab	32.50 d-h	139.00 a-j	24.50 c-f	996.00 e-m	17.00 g-m

Appendix Table 4. (continued) kobo

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G7	6.50 abc	63.50 a-h	95.50 c-h	32.00 d-j	120.00 d-j	24.10 c-f	862.00 fn	16.00 g-m
G8	6.50 abc	66.50 ab	101.50 b-h	35.00 b-j	124.50 b-j	25.10 b-f	430.00 m-o	20.50 b-k
G9	7.50 ab	67.00 a	97.50 gh	30.50 e-j	117.00 e-j	22.50 f	205.00 o	25.50 a-d
Mean	6.63	62.68	98.19	35.51	131.99	26.45	984.59	20.36
CV (%)	10.40	3.30	3.00	8.70	9.60	9.50	24.30	12.50

Fedis

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G1	6.00 ab	60.00 bc	98.50 ab	38.50 abc	124.00 g-k	27.20 a-d	1548.00 c-j	30.00 a-d
G10	7.50 a	66.50 abc	110.50 a	44.00 ab	153.00 a-e	26.40 a-d	651.00 l-o	27.00 a-d
G11	7.50 a	67.50 abc	107.50 ab	40.00 abc	147.83 a-i	25.40 a-d	400.00 no	26.50 a-d
G12	6.50 ab	62.50 bc	108.50 ab	46.00 ab	151.17 a-f	27.40 a-d	1086.00 g-n	25.50 bcd
G13	7.50 a	66.00 abc	100.00 ab	34.00 bc	142.17 b-k	23.00 d	741.00 k-o	32.00 abc
G14	6.50 ab	73.00 a	98.50 ab	25.50 c	143.83 a-j	27.30 a-d	327.00 o	28.00 a-d
G15	7.00 ab	60.00 bc	102.50 ab	42.50 ab	150.00 a-g	26.50 a-d	1841.00 b-f	30.00 a-d
G16	7.00 ab	64.50 abc	103.50 ab	39.00 abc	156.50 a-d	27.10 a-d	2408.00 ab	31.00 a-d
G17	6.00 ab	65.00 abc	103.00 ab	38.00 abc	142.50 b-k	26.90 a-d	998.00 i-o	32.00 abc
G18	6.50 ab	62.50 bc	101.00 ab	38.50 abc	149.67 a-h	29.80 a-d	1273.00 f-l	26.50 a-d
G19	6.50 ab	60.50 bc	99.00 ab	38.50 abc	160.67 abc	25.90 a-d	830.00 j-o	32.00 abc
G2	7.00 ab	63.00 bc	100.00 ab	37.00 abc	123.50 h-k	25.50 a-d	976.00 i-o	22.50 d
G20	7.00 ab	62.50 bc	100.00 ab	37.50 abc	169.67 a	25.10 bcd	1737.00 b-g	28.50 a-d

Appendix Table 4. (continued) Fedis

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G21	7.00 ab	62.00 bc	101.50 ab	39.50 abc	148.50 a-i	26.00 a-d	2060.00 b-d	26.00 a-d
G22	6.00 ab	62.00 bc	108.50 ab	46.50 abc	137.33 c-k	24.40 cd	1720.00 b-h	25.50 a-d
G23	6.00 ab	63.00 bc	108.50 ab	45.50 abc	134.67 c-k	26.20 a-d	1225.00 f-l	30.00 a-d
G24	6.50 ab	64.00 bc	103.00 ab	39.00 abc	141.50 b-k	29.50 a-d	1825.00 b-f	30.00 a-d
G25	6.00 ab	66.00 abc	107.00 ab	41.00 abc	156.67 a-d	26.60 a-d	1436.00 c-k	29.00 a-d
G26	6.50 ab	64.50 abc	104.50 ab	40.00 abc	132.67 c-k	25.00 bcd	1427.00 d-k	27.50 a-d
G27	7.00 ab	61.00 bc	102.00 ab	41.00 abc	148.17 a-i	29.50 a-d	1274.00 f-l	34.50 a
G28	6.50 ab	58.50 bc	109.50 ab	51.00 abc	153.50 a-e	27.50 a-d	1821.00 b-f	27.50 a-d
G29	7.00 ab	63.50 bc	101.50 ab	38.00 abc	150.50 a-g	28.10 a-d	1821.00 b-f	25.00 b-d
G3	6.00 ab	63.50 bc	100.00 ab	36.50 abc	132.83 c-k	26.90 a-d	1091.00 g-n	29.50 a-d
G30	6.50 ab	60.50 bc	100.50 ab	40.00 abc	156.33 a-d	29.00 a-d	1564.00 c-i	28.00 a-d
G31	6.00 ab	60.50 bc	105.00 ab	44.50 abc	150.50 a-g	29.50 a-d	1102.00 g-n	32.50 abc
G32	5.50 b	60.00 bc	98.00 ab	38.00 abc	141.33 b-k	28.00 a-d	931.00 i-o	29.50 a-d
G33	6.50 ab	62.50 bc	105.00 ab	42.50 abc	150.50 a-g	29.50 a-d	1128.00 f-m	26.00 a-d
G34	7.00 ab	64.00 bc	97.50 ab	33.50 abc	150.00 a-g	28.70 a-d	1290.00 f-l	26.50 a-d
G35	7.00 ab	63.50 bc	103.00 ab	39.50 abc	166.83 ab	28.10 a-d	1795.00 b-g	31.00 a-d
G36	6.50 ab	62.00 bc	102.00 ab	40.00 abc	150.50 a-g	28.40 a-d	1606.00 c-i	27.00 a-d
G37	7.00 ab	63.50 bc	108.50 ab	45.00 abc	130.33 d-k	29.20 a-d	967.00 i-o	29.00 a-d
G38	6.50 ab	61.50 bc	97.50 ab	36.00 abc	151.33 a-f	31.90 ab	1017.00 h-o	26.50 a-d
G39	7.00 ab	61.00 bc	101.50 ab	40.50 abc	155.67 a-e	28.80 a-d	1431.00 d-k	26.00 a-d
G4	7.00 ab	62.50 bc	102.50 ab	40.00 abc	147.00 a-i	25.00 bcd	2887.00 a	26.00 a-d

Appendix Table 4. (continued) Fedis

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G40	7.00 ab	61.50 bc	99.50 ab	38.00 ab	146.00 a-i	29.00 a-d	1189.00 f-m	28.50 a-d
G41	5.50 b	64.50 abc	100.00 ab	35.50 ab	151.00 a-f	28.20 a-d	1177.00 f-m	29.00 a-d
G42	6.00 ab	64.50 abc	100.50 ab	36.00 ab	150.33 a-g	32.50 a	979.00 i-o	28.00 a-d
G43	5.50 b	61.50 bc	97.00 b	35.50 ab	148.67 a-i	30.80 abc	1196.00 f-m	28.50 a-d
G44	7.00 ab	60.00 bc	98.50 ab	38.50 ab	152.50 a-e	28.90 a-d	1088.00 g-n	33.00 ab
G45	7.00 ab	64.00 bc	108.50 ab	44.50 ab	117.50 k	29.00 a-d	1202.00 f-m	27.50 a-d
G46	7.00 ab	64.50 bc	104.00 ab	39.50 ab	122.33 i-k	32.10 ab	981.00 i-o	30.00 a-d
G47	7.00 ab	63.00 bc	104.50 ab	41.50 ab	118.33 j-k	31.60 ab	1313.00 e-l	28.00 a-d
G48	7.00 ab	63.50 bc	103.50 ab	40.00 ab	125.00 f-k	28.20 a-d	504.00 m-o	24.00 cd
G49	6.50 ab	68.50 ab	108.00 ab	39.50 ab	137.67 c-k	27.70 a-d	1834.00 b-f	32.50 abc
G5	7.00 ab	62.50 bc	107.50 ab	45.00 ab	145.50 a-i	24.20 cd	1381.00 d-k	30.50 a-d
G6	7.00 ab	62.50 bc	98.00 ab	35.50 ab	129.17 e-k	29.90 a-d	2137.00 bc	31.00 a-d
G7	6.00 ab	59.50 bc	101.50 ab	42.00 ab	147.00 a-i	27.80 a-d	2003.00 b-e	28.00 a-d
G8	7.00 ab	68.50 ab	102.00 ab	33.50 ab	147.00 a-i	26.40 a-d	399.00 no	26.00 a-d
G9	7.00 ab	63.50 bc	101.00 ab	37.50 ab	149.17 a-h	23.30 d	998.00 i-o	27.00 a-d
Mean	6.63	63.16	102.72	39.56	144.66	27.73	1318.67	28.48
CV (%)	11.50	5.70	5.30	16.20	7.40	10.30	22.00	12.20

Mehoni

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G1	6.00 a	60.50 f-i	95.50 i-l	40.00 bc	140.00 b-g	34.90 a-k	5001.00 b-e	28.50 b-f
G10	7.00 a	71.50 a	113.50 ab	47.00 abc	145.50 a-g	33.00 d-m	1533.00 q-t	29.50 a-f
G11	7.00 a	71.00 ab	113.00 abc	47.00 abc	143.50 a-g	32.10 g-n	1400.00 r-t	27.50 d-f
G12	7.00 a	67.00 a-d	108.00 a-h	46.00 bc	140.50 b-g	34.20 a-k	2684.00 j-s	31.00 a-f
G13	7.00 a	68.00 abc	111.50 a-d	48.50 abc	147.90 a-f	31.60 h-n	1667.00 p-t	29.50 a-f
G14	6.50 a	66.50 a-e	108.00 a-h	46.50 abc	148.80 a-f	33.30 c-m	2001.00 o-t	29.00 b-f
G15	7.50 a	66.50 a-e	106.50 a-j	45.00 abc	159.70 abc	31.20 i-n	2267.00 r-t	29.00 b-f
G16	6.50 a	64.50 c-h	98.50 f-l	39.00 c	159.00 a-d	33.40 c-m	4468.00 b-i	29.00 b-f
G17	7.00 a	64.00 c-h	99.00 f-l	40.00 bc	160.00 a-f	32.40 f-n	3932.00 c-l	32.50 abc
G18	6.50 a	62.00 d-i	97.00 h-l	40.00 bc	163.90 a-f	33.10 c-m	4534.00 b-h	29.50 a-f
G19	6.50 a	64.50 c-h	103.00 b-l	43.50 abc	149.30 a-e	33.10 c-m	3335.00 e-p	30.00 a-f
G2	6.00 a	68.00 abc	107.00 a-i	44.00 abc	144.60 a-g	35.30 a-j	3733.00 c-m	26.50 f
G20	6.50 a	63.50 c-h	98.00 f-l	39.50bc	165.20 ab	31.80 h-n	5468.00 abc	30.00 a-f
G21	6.50 a	63.00 c-h	99.50 f-l	41.50 abc	158.20 a-d	33.60 c-m	4467.00 b-i	33.00 ab
G22	6.50 a	63.50 c-h	101.50 d-l	43.00 abc	145.80 a-f	33.20 c-m	4268.00 b-j	28.50 b-f
G23	6.50 a	61.50 d-i	95.50 j-l	39.00 c	153.20 a-d	31.90 g-n	3602.00 d-o	30.00 a-f
G24	6.50 a	63.50 c-h	101.00 d-l	42.50 abc	149.70 a-e	30.60 -n	4801.00 b-g	29.00 b-f
G25	6.00 a	62.00 d-i	99.50 e-l	42.50 abc	165.70 ab	33.30 c-m	4933.00 b-f	29.00 b-f
G26	7.00 a	57.00 i	97.50 g-l	45.50 abc	165.80 ab	34.00 a-l	4034.00 c-k	31.00 a-f

Appendix Table 4. (continued) Mehoni

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G27	6.50 a	63.00 c-h	102.00 c-l	44.00 abc	156.00 a-d	30.80 j-n	3066.00 g-r	30.00 a-f
G28	6.00 a	63.50 c-h	98.50 f-l	40.00 bc	158.90 a-d	33.00 d-m	2933.00 h-r	30.50 a-f
G29	6.00 a	64.50 c-h	106.50 a-j	47.00 abc	166.00 ab	33.80 b-m	5000.00 b-e	30.50 a-f
G3	7.00 a	62.00 d- i	97.00 h-j	40.00 bc	149.90 a-e	34.90 a-k	4000.00 c-l	31.50 a-f
G30	6.50 a	63.00 c-h	103.00 b-l	45.00 abc	154.50 a-d	33.40 c-m	3133.00 g-q	31.50 a-f
G31	6.00 a	64.00 c-h	109.00 a-f	50.00 a	156.40 a-d	30.80 j-n	3599.00 d-o	29.50 b-f
G32	6.50 a	62.50 c-i	99.00 f-l	41.50 abc	154.20 a-d	32.70 e-n	3334.00 e-p	29.00 a-f
G33	7.00 a	67.00 a-d	107.50 a-i	45.50 abc	144.20 a-g	36.50 a-g	3133.00 g-q	30.00 a-f
G34	6.50 a	64.50 c-h	102.50 b-l	43.00 abc	150.60 a-d	37.40 a-d	4367.00 b-j	30.50 a-f
G35	7.00 a	65.00 c-g	108.00 a-h	48.00 abc	153.90 a-d	33.60 c-m	2734.00 i-s	29.50 a-f
G36	6.50 a	61.00 c-i	102.00 c-l	46.00 abc	143.60 a-g	38.30 ab	4101.00 b-k	32.00 a-f
G37	6.50 a	63.00 c-h	101.50 d-l	43.50 abc	144.00 a-g	36.90 a-f	4000.00 c-l	28.50 b-f
G38	6.00 a	61.50 d-i	96.50 i-l	40.00 bc	152.40 a-e	35.30 a-j	3799.00 c-l	32.00 a-f
G39	6.50 a	62.50 c-i	103.50 b-l	46.00 abc	135.40 c-h	37.70 abc	3933.00 c-l	31.50 a-f
G4	7.00 a	65.50 b-f	108.50 a-g	48.00 abc	136.90 b-h	29.30 mn	4467.00 b-i	28.50 b-f
G40	6.50 a	63.00 c-h	97.00 h-l	39.00 c	148.50 a-f	34.90 a-k	5800.00 ab	34.00 a
G41	6.50 a	65.00 c-g	101.00 d-l	41.00 abc	148.00 a-f	36.10 a-h	3733.00 c-n	30.50 a-f
G42	6.50 a	61.50 d-i	99.50 e-l	43.00 abc	150.90 a-k	38.50 a	3002.00 h-r	28.50 b-f
G43	6.00 a	59.50 g-i	94.00 l	39.50 bc	142.80 b-g	37.20 a-e	3667.00 d-o	31.00 a-f
G44	6.50 a	59.00 hi	95.00 kl	41.00 abc	129.30 d-h	33.60 c-m	3266.00 ef	28.50 a-f
G45	6.50 a	64.50 c-h	102.00 c-l	42.50 abc	109.70 h	30.90 i-n	1665.00 p-t	30.50 a-f

Appendix Table 4. (continued) Mehoni

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G46	7.00 [a]	63.00 [c-h]	101.00 [d-l]	43.00 [abc]	116.50 [gh]	30.60 [k-n]	2001.00 [m-t]	28.50 [b-f]
G47	6.50 [a]	61.00 [e-i]	97.00 [h-l]	41.00 [abc]	119.70 [f-h]	31.40 [i-n]	2466.00 [k-t]	30.50 [a-f]
G48	6.50 [a]	71.00 [ab]	113.00 [abc]	47.00 [abc]	123.20 [e-h]	35.50 [a-i]	1533.00 [q-t]	27.50 [d-f]
G49	7.00 [a]	66.50 [a-e]	105.00 [a-l]	43.50 [abc]	157.00 [a-d]	31.50 [h-n]	6667.00 [a]	28.50 [b-f]
G5	7.00 [a]	65.50 [b-f]	106.00 [a-k]	45.50 [abc]	172.60 [a]	29.40 [l-n]	3200.00 [f-q]	28.00 [c-f]
G6	7.00 [a]	64.00 [c-h]	101.00 [d-l]	42.00 [abc]	165.30 [abc]	28.30 [n]	4467.00 [b-i]	32.50 [abc]
G7	6.00 [a]	60.00 [f-i]	94.50 [l]	39.50 [abc]	157.70 [a-d]	32.70 [e-n]	5267.00 [a-d]	29.50 [a-f]
G8	7.00 [a]	68.00 [abc]	110.50 [a-e]	47.50 [abc]	147.30 [a-f]	31.60 [h-n]	866.00 [t]	27.00 [ef]
G9	7.50 [a]	71.00 [ab]	115.50 [a]	49.50 [abc]	139.90 [b-g]	31.20 [i-n]	1067.00 [st]	31.50 [a-e]
Mean	6.60	64.14	102.65	43.51	148.81	33.34	3518.24	29.87
CV (%)	9.60	3.70	4.40	8.40	8.00	5.60	20.10	6.70

Sheraro

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G1	7.00 [abc]	59.00 [k-q]	97.00 [d-g]	43.00 [abc]	166.15 [f-j]	33.80 [b-g]	5233.00 [a-j]	33.50 [a-d]
G10	7.00 [abc]	68.00 [bc]	103.50 [ab]	40.50 [a-d]	172.80 [d-j]	30.10 [b-h]	1740.00 [op]	35.00 [abc]
G11	7.00 [abc]	67.00 [bc]	103.00 [abc]	41.00 [a-d]	175.40 [c-j]	30.60 [b-h]	2266.00 [n-p]	31.50 [b-e]
G12	7.00 [abc]	65.00 [c-h]	100.50 [a-f]	40.50 [a-d]	189.50 [b-f]	31.90 [b-h]	2620.00 [m-o]	33.00 [a-d]
G13	8.00 [a]	66.00 [c-g]	101.50 [a-c]	40.50 [a-d]	178.70 [c-j]	28.00 [b-h]	1906.00 [op]	34.50 [a-d]
G14	7.00 [abc]	72.00 [a]	103.00 [abc]	36.00 [a]	157.20 [h-j]	30.80 [b-h]	1100.00 [p]	31.00 [b-e]
G15	6.50 [abc]	63.00 [e-l]	97.50 [c-g]	39.50 [a-d]	184.90 [b-j]	34.70 [b-e]	5320.00 [a-j]	32.00 [a-e]

Appendix Table 4. (continued) Sheraro

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G16	5.50 abc	61.50 g-n	97.00 d-g	40.50 a-d	179.10 c-j	35.00 b-e	4920.00 b-k	31.50 b-e
G17	6.50 abc	63.50 d-k	98.50 b-f	40.00 a-d	174.65 c-j	33.40 b-h	4840.00 b-l	33.50 a-d
G18	6.00 abc	63.00 e-n	97.50 c-g	39.50 a-d	177.60 c-j	31.20 b-h	4886.00 b-k	31.50 b-e
G19	6.00 abc	62.00 g-n	97.00 d-g	40.00 a-d	193.70 b-e	33.70 b-g	6426.00 a	33.50 a-d
G2	6.00 abc	62.50 e-m	96.50 e-g	39.00 a-d	156.50 ij	33.70 b-g	3448.00 l-n	34.00 a-d
G20	6.00 abc	64.50 c-i	100.00 a-f	40.50 a-d	187.10 b-f	32.20 b-h	5286.00 a-j	27.50 e
G21	6.00 abc	60.50 h-o	97.00 d-g	41.50 a-d	200.30 abc	35.90 bc	5920.00 a-d	33.50 a-d
G22	6.50 abc	62.00 g-n	97.50 c-g	40.50 a-d	182.90 c-i	33.50 b-h	5833.00 a-e	29.50 de
G23	5.50 bc	60.00 i-p	95.50 c-g	40.50 a-d	195.40 bcd	32.10 b-h	4766.00 c-l	32.50 a-e
G24	6.50 abc	62.00 g-n	97.00 d-g	40.00 a-d	176.40 c-j	31.50 b-h	5227.00 a-j	34.00 a-d
G25	6.00 abc	65.00 c-h	100.50 a-f	40.50 a-d	193.90 b-e	31.70 b-h	4173.00 h-l	32.50 a-e
G26	7.50 abc	62.00 g-n	99.50 a-f	42.50 abc	191.40 b-f	34.70 b-g	4407.00 e-l	35.00 abc
G27	7.00 abc	58.50 i-q	96.00 e-h	42.50 abc	180.10 c-i	32.60 b-h	5007.00 b-k	33.00 a-d
G28	6.50 abc	59.50 j-o	96.50 e-g	42.00 a-d	184.30 c-h	34.40 b-h	5720.00 a-g	33.50 a-d
G29	6.00 abc	62.00 g-n	97.00 d-g	40.00 ab	201.30 abc	35.40 bcd	6187.00 abc	33.00 a-d
G3	6.50 abc	58.00 m-q	97.00 d-g	44.00 a-d	167.80 e-j	33.90 b-g	4820.00 b-l	35.50 abc
G30	7.00 abc	61.50 g-n	96.00 e-h	39.50 a-d	186.40 b-f	32.30 b-h	5386.00 a-i	33.50 a-d
G31	6.50 abc	57.50 n-q	95.50 c-g	43.00 abc	176.20 c-j	33.30 b-h	4600.00 d-l	33.00 a-d
G32	6.50 abc	57.50 n-q	95.00 c-g	42.50 abc	184.20 c-h	31.90 b-h	5386.00 a-i	34.50 a-d
G33	6.50 abc	61.50 g-n	98.00 b-f	41.50 a-d	165.70 f-j	33.50 b-h	5533.00 a-h	31.00 be

Appendix Table 4. (continued) Sheraro

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G34	6.50 abc	62.00 g-n	97.00 d-g	40.00 a-d	152.50 j	36.40 b	5720.00 a-g	32.50 a-e
G35	7.00 abc	62.00 g-n	98.00 b-f	41.00 a-d	171.20 d-j	32.70 b-h	3893.00 j-l	31.50 b-e
G36	6.50 abc	62.50 e-m	98.50 b-f	41.00 a-d	179.70 c-j	32.40 b-h	4926.00 b-k	32.50 a-e
G37	5.50 abc	61.50 g-n	98.50 b-f	42.00 a-d	165.40 f-j	34.60 b-f	5073.00 a-k	30.50 c-e
G38	6.00 abc	60.00 i-p	92.00 g-h	37.00 cd	172.70 d-j	30.80 b-h	4347.00 f-l	30.50 c-e
G39	6.50 abc	56.50 o-p	95.00 f-h	43.50 ab	157.60 g-j	32.90 b-h	4566.00 d-l	33.00 a-d
G4	6.50 abc	62.50 e-m	99.00 b-f	41.50 a-d	221.50 a	29.40 c-h	4933.00 b-k	31.00 b-e
G40	6.00 abc	62.00 g-n	96.00 e-h	39.00 a-d	170.70 d-j	32.40 b-h	4813.00 b-l	34.00 a-d
G41	5.50 bc	62.00 g-n	98.00 b-f	41.00 a-d	158.70 g-j	33.00 b-h	4673.00 d-l	31.00 b-e
G42	6.00 abc	60.50 h-o	97.00 d-g	41.50 a-d	196.60 a-d	34.80 b-e	5633.00 a-g	35.50 abc
G43	6.50 abc	55.50 q	95.50 f-h	45.00 a	183.20 c-i	35.00 b-e	4160.00 h-l	36.00 ab
G44	5.00 c	56.00 pq	95.50 f-h	44.50 ab	175.80 c-j	33.90 b-g	5773.00 a-f	34.50 a-d
G45	7.50 ab	63.00 e-n	96.50 a-f	38.50 bcd	155.90 ij	28.50 e-h	3673.00 k-m	37.00 a
G46	7.50 ab	63.00 e-n	98.50 b-f	40.50 a-d	158.10 g-j	28.10 f-h	4087.00 i-l	37.00 a
G47	7.50 ab	63.50 d-k	99.50 a-f	41.00 a-d	164.10 f-j	27.20 h	4520.00 d-l	35.50 abc
G48	7.00 abc	61.00 h-n	99.00 b-f	43.00 abc	121.90 k	32.00 b-h	3947.00 j-l	35.00 abc
G49	7.00 abc	67.50 bcd	101.50 a-e	39.00 a-d	170.00 d-j	29.60 c-h	6200.00 ab	35.50 abc
G5	6.00 abc	64.00 c-j	99.50 a-f	40.50 a-d	211.20 ab	28.50 c-h	4326.00 g-l	34.50 a-d
G6	6.00 abc	61.50 g-n	96.50 e-h	40.00 a-d	182.50 c-k	30.80 b-h	4740.00 d-l	33.50 a-d
G7	6.00 abc	57.50 n-q	91.00 h	38.50 bcd	201.85 abc	43.10 a	4533.00 d-l	34.00 a-d

Appendix Table 4. (continued) Sheraro

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G8	7.50 ^{ab}	70.50 ^{ab}	104.50 ^{a}	39.00 $^{a-d}$	176.50 $^{c-j}$	29.80 $^{c-h}$	1713.00 ^{op}	32.00 $^{a-e}$
G9	7.50 ^{ab}	67.00 $^{b-f}$	102.50 $^{a-d}$	40.50 $^{a-d}$	178.50 $^{c-j}$	28.90 $^{d-h}$	1680.00 ^{op}	34.00 $^{a-e}$
Mean	6.51	62.16	97.95	40.79	177.67	32.46	4507.86	33.19
CV (%)	14.40	3.00	2.30	6.00	6.20	8.10	12.80	6.60

Appendix Table 5. Mean squares of different traits in respective environments

			Traits							
Location	SV	DF	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
Humera	Gen.	48	0.50***	52.64*	17.93^{ns}	16.14*	621.79***	8.50^{ns}	141035***	9.93^{ns}
	Rep.	1	0.041^{ns}	154.38^{ns}	96.01^{ns}	6.898^{ns}	1111.90^{ns}	287.38^{ns}	290540^{ns}	424.65^{ns}
	Error	48	0.166	28.71	13.74	9.606	91.81	8.50	18525	11.59
Kobo	Gen.	48	0.662^{ns}	11.04***	9.73^{ns}	18.82**	313.8*	10.87*	8330547***	23.67***
	Rep.	1	0.367^{ns}	12.50^{ns}	15.52^{ns}	0.16^{ns}	226.5^{ns}	111.64^{ns}	400512^{ns}	13.97^{ns}
	Error	48	0.472	4.40	8.90	9.60	161.40	6.28	57193	6.47
Fedis	Gen.	48	0.537^{ns}	14.01^{ns}	27.29^{ns}	34.70^{ns}	281.20***	9.68^{ns}	542764***	12.77^{ns}
	Rep.	1	0.367^{ns}	11.80^{ns}	695.11^{ns}	525.81^{ns}	1875.00^{ns}	540.92^{ns}	171029^{ns}	6.38^{ns}
	Error	48	0.597	13.15	29.47	40.97	114.40	8.185	83956.	12.15
Mehoni	Gen.	48	0.312^{ns}	19.90***	62.86***	19.53^{ns}	346.2***	11.45***	3323198***	5.06^{ns}
	Rep.	1	1.235^{ns}	50.00^{ns}	52.90^{ns}	0.04^{ns}	75.5^{ns}	12.36^{ns}	17139^{ns}	0.50^{ns}
	Error	48	0.401	5.65	20.42	13.23	142.9	3.50	499468	4.00
Sheraro	Gen.	48	0.843^{ns}	23.68***	14.67***	6.17^{ns}	574.20***	14.83*	3289622***	7.288^{ns}
	Rep.	1	4.082^{ns}	11.80^{ns}	1.24^{ns}	5.40^{ns}	506.10^{ns}	0.24^{ns}	6498^{ns}	0.01^{ns}
	Error	48	0.873	3.48	5.07	5.98	122.5	6.83	333685	4.82

*, **,*** = significant at P≤ 0.05, P≤ 0.01 and P≤ 0.001, respectively, SV= source of variation, DF = degree of freedom, DTE = Days to emergence (days), DTF = Days to flowering (days), DTM = Days to maturity (days), PTH = plant height (cm), PL= panicle length (cm), GY = grain yield (kg ha-1), TGW= thousand grain weight (g), CV (%) = coefficient of variation in percent.

Appendix Table 6. Mean performances for yield and yield related traits of 49 sorghum genotypes evaluated at five environments in Ethiopia.

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G1	6.00^{ns}	60.60^{h-m}	97.90^{c-i}	39.30^{ns}	133.50^{l-o}	29.56^{a-h}	2692^{b-f}	26.60^{a-e}
G10	7.10^{ns}	67.80^{ab}	106.00^{a}	40.20^{ns}	151.80^{a-i}	28.72^{b-h}	1000^{pq}	26.40^{a-e}
G11	7.10^{ns}	67.40^{abc}	104.10^{ab}	38.70^{ns}	142.30^{g-m}	28.26^{c-h}	932^{pq}	25.00^{a-e}
G12	6.60^{ns}	62.90^{d-k}	101.30^{b-f}	40.40^{ns}	152.50^{a-i}	29.72^{a-h}	1561^{m-o}	25.50^{a-e}
G13	7.10^{ns}	66.40^{a-d}	100.90^{b-f}	36.50^{ns}	148.20^{c-j}	27.60^{f-h}	1159^{o-q}	27.50^{abc}
G14	6.40^{ns}	68.90^{a}	101.70^{a-e}	34.80^{ns}	144.40^{f-l}	28.68^{b-h}	838^{q}	25.90^{a-e}
G15	6.70^{ns}	61.40^{f-m}	99.80^{b-h}	40.40^{ns}	153.50^{a-h}	30.30^{a-h}	2249^{e-j}	26.50^{a-e}
G16	6.20^{ns}	62.20^{e-m}	98.50^{c-i}	38.30^{ns}	156.00^{a-f}	29.92^{a-h}	2658^{b-f}	25.80^{a-e}
G17	6.10^{ns}	63.00^{d-k}	98.30^{c-i}	37.30^{ns}	156.30^{a-f}	29.46^{a-h}	2251^{e-i}	27.80^{abc}
G18	6.30^{ns}	63.20^{d-j}	99.20^{c-i}	38.00^{ns}	156.10^{a-f}	30.40^{a-h}	2623^{b-f}	28.10^{ab}
G19	6.20^{ns}	62.70^{d-l}	98.90^{c-i}	38.20^{ns}	158.50^{a-e}	29.63^{a-h}	2456^{c-g}	28.30^{a}
G2	6.10^{ns}	63.60^{d-h}	99.50^{b-i}	37.90^{ns}	132.60^{l-o}	28.70^{b-h}	1898^{h-m}	24.50^{c-e}
G20	6.00^{ns}	63.00^{d-k}	99.30^{b-i}	38.30^{ns}	160.70^{abc}	29.04^{b-h}	2894^{abc}	24.70^{b-e}

Appendix Table 6. (continued)

Genotypes	DTE	DTF	DTM	GFP	PHT	PL	GY	TGW
G21	6.20^{ns}	61.70^{e-m}	98.50^{c-i}	38.80^{ns}	162.30^{ab}	30.52^{a-f}	2828^{abcd}	27.00^{a-e}
G22	6.00^{ns}	61.50^{f-m}	99.80^{b-h}	40.30^{ns}	142.00^{g-m}	28.94^{b-h}	2652^{b-f}	26.40^{a-e}
G23	5.80^{ns}	62.10^{e-m}	100.20^{b-h}	40.10^{ns}	147.00^{e-k}	29.04^{b-h}	2175^{e-l}	25.70^{a-e}
G24	6.10^{ns}	64.20^{c-h}	101.00^{b-f}	38.80^{ns}	143.00^{g-m}	29.10^{b-h}	2679^{b-f}	25.30^{a-e}
G25	5.70^{ns}	63.70^{d-h}	100.00^{b-h}	38.30^{ns}	154.70^{a-g}	28.02^{d-h}	2410^{c-h}	26.10^{a-e}
G26	6.50^{ns}	59.40^{j-m}	98.30^{c-i}	40.90^{ns}	151.50^{a-i}	29.94^{a-h}	2274^{efgh}	26.30^{a-e}
G27	6.30^{ns}	60.70^{g-m}	97.90^{c-i}	39.20^{ns}	151.30^{a-i}	30.22^{a-h}	2303^{d-h}	27.90^{abc}
G28	6.10^{ns}	59.60^{i-m}	98.50^{c-i}	40.90^{ns}	156.20^{a-f}	30.56^{a-f}	2567^{b-g}	26.90^{a-e}
G29	6.20^{ns}	61.10^{f-m}	98.50^{c-i}	39.40^{ns}	159.80^{a-d}	31.42^{a-d}	3051^{ab}	24.70^{b-e}
G3	6.20^{ns}	61.80^{e-m}	96.90^{e-i}	37.10^{ns}	134.80^{k-o}	29.31^{a-h}	2244^{e-k}	27.70^{abc}
G30	6.50^{ns}	62.00^{e-m}	98.50^{c-i}	38.50^{ns}	152.80^{a-h}	29.96^{a-h}	2200^{e-k}	26.80^{a-e}
G31	5.90^{ns}	60.60^{h-m}	100.30^{b-h}	41.70^{ns}	150.60^{b-j}	30.48^{a-g}	2197^{e-k}	26.30^{a-e}
G32	6.00^{ns}	59.10^{lm}	95.70^{hi}	38.60^{ns}	160.60^{abc}	30.22^{a-h}	2377^{c-h}	26.00^{a-e}
G33	6.40^{ns}	64.50^{b-g}	102.00^{a-d}	39.50^{ns}	139.70^{i-n}	30.58^{a-f}	2172^{e-l}	25.30^{a-e}
G34	6.40^{ns}	64.50^{b-g}	98.70^{c-i}	36.20^{ns}	141.30^{h-m}	31.68^{abc}	2510^{c-g}	26.40^{a-e}
G35	6.50^{ns}	63.60^{d-h}	100.60^{b-g}	39.00^{ns}	152.30^{a-i}	29.56^{a-h}	2040^{g-m}	28.30^{a}
G36	6.20^{ns}	63.30^{d-i}	99.60^{b-i}	38.30^{ns}	144.80^{f-l}	31.42^{a-d}	2458^{c-g}	26.10^{a-e}
G37	6.20^{ns}	64.10^{c-h}	100.60^{b-g}	38.50^{ns}	133.30^{l-o}	31.04^{a-f}	2179^{e-l}	25.60^{a-e}
G38	6.00^{ns}	61.50^{f-m}	95.80^{g-i}	36.30^{ns}	149.50^{c-j}	31.08^{a-f}	2305^{d-h}	27.10^{a-e}
G39	6.40^{ns}	58.70^{m}	97.90^{c-i}	41.20^{ns}	140.80^{h-m}	31.32^{a-e}	2374^{c-h}	25.10^{a-e}

Appendix Table 6. (continued)

G4	6.40^{ns}	62.30^{e-m}	99.70^{b-h}	39.40^{ns}	156.50^{a-f}	26.86^{gh}	2713^{b-f}	23.70^{e}
G40	6.20^{ns}	62.00^{e-m}	97.40^{d-i}	37.40^{ns}	138.00^{j-n}	29.96^{a-h}	2726^{b-f}	27.20^{a-d}
G41	5.70^{ns}	61.50^{f-m}	97.80^{c-i}	38.30^{ns}	142.20^{g-m}	30.38^{a-h}	2354^{c-h}	25.60^{a-e}
G42	6.00^{ns}	63.50^{d-h}	99.40^{b-i}	37.90^{ns}	156.00^{a-f}	32.81^{a}	2258^{e-h}	27.40^{a-d}
G43	5.90^{ns}	60.70^{g-m}	97.60^{c-i}	38.90^{ns}	146.10^{e-k}	31.95^{ab}	2321^{d-h}	26.40^{a-e}
G44	6.20^{ns}	59.30^{k-m}	96.50^{f-i}	39.20^{ns}	147.50^{d-j}	31.84^{abc}	2352^{c-h}	25.90^{a-e}
G45	6.60^{ns}	62.00^{e-m}	99.60^{b-i}	39.60^{ns}	123.70^{op}	27.99^{d-h}	1673^{l-n}	25.50^{a-e}
G46	6.90^{ns}	64.70^{b-f}	100.70^{b-f}	38.00^{ns}	131.00^{m-o}	27.72^{e-h}	1718^{i-n}	27.30^{a-d}
G47	6.70^{ns}	61.40^{f-m}	97.60^{c-i}	38.20^{ns}	127.90^{no}	29.62^{a-h}	1899^{h-m}	26.90^{a-e}
G48	6.90^{ns}	63.00^{d-k}	100.80^{b-f}	39.80^{ns}	117.20^{p}	30.82^{a-f}	1353^{n-p}	24.00^{de}
G49	6.60^{ns}	66.20^{a-d}	101.90^{a-d}	37.70^{ns}	142.10^{g-m}	29.04^{b-h}	3278^{a}	26.30^{a-e}
G5	6.50^{ns}	64.30^{b-h}	101.50^{b-e}	39.20^{ns}	163.30^{a}	26.82^{h}	2170^{f-l}	26.60^{a-e}
G6	6.40^{ns}	61.40^{f-m}	96.60^{f-i}	37.20^{ns}	152.90^{a-h}	27.92^{d-h}	2732^{b-e}	26.70^{a-e}
G7	6.00^{ns}	59.10^{lm}	94.80^{i}	37.70^{ns}	149.90^{b-j}	30.76^{a-f}	2650^{b-f}	24.60^{cde}
G8	6.80^{ns}	65.50^{a-e}	102.50^{abc}	39.00^{ns}	147.80^{d-j}	28.25^{c-h}	735^{q}	24.70^{b-e}
G9	7.00^{ns}	64.90^{b-f}	102.30^{a-d}	39.40^{ns}	144.70^{f-l}	26.79^{h}	858^{q}	27.60^{abc}
Mean	6.34	62.71	100	38.71	147.00	29.70	2184.00	26.25
CV (%)	11.20	5.40	4.40	10.00	7.80	10.90	20.40	16.60

DTE = Days to emergence (days), DTF = Days to flowering (days), DTM = Days to maturity (days), PTH = plant height (cm), PL=panicle length (cm), GY = grain yield (kg ha^{-1}), TGW= thousand grain weight (g), LS= level of significance, CV (%) = coefficient of variation in percent.