EVALUATION AND GENOME WIDE ASSOCIATION MAPPING OF ETHIOPIAN SORGHUM LANDRACES (*Sorghum Bicolor* (L.) MOENCH) UNDER MOISTURE STRESS CONDITION AT SHERARO, NORTH ETHIOPIA

MSc. THESIS

BY

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NOVEMBER 2019

JIMMA, ETHIOPIA

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A Thesis
Submitted to School of Graduate Studies
College of Agriculture and Veterinary Medicine
Jimma University

In Partial Fulfillment of the Requirements for the Degree of Master of Science in Plant Biotechnology

By;

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November 2019
Jimma, Ethiopia

DEDICATION

This thesis is dedicated to my mother as she always eagers and prays to see the final fruitful of this work.

STATEMENT OF THE AUTHOR

First, I declare that this thesis is my original work and that all sources of materials used for this thesis is duly acknowledged. This thesis is submitted for partial fulfillment of the requirements for the award of the Degree of Master of Science in Plant Biotechnology at Jimma University and it can be deposited at the University Library to be made available to borrowers under rules of the library. I solemnly declare that this thesis is not submitted to any other institution anywhere for the award of any academic degree, diploma, or certificate.

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Name: Mewuleddeg Zebro

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BIOGRAPHY

Mewuleddeg Zebro was born in December 1992 in Sebeta, South West of Shewa in Oromia Regional state, Ethiopia. He attended his elementary school at Dimma Guranda elementary school from 2001 to 2008. He pursued his secondary and preparatory school education at Sebeta high and preparatory school from 2009 to 2012. He joined University of Gonder in 2013 and graduated with BSc. Degree in Biotechnology in 2015. After graduation, he is working in Jimma University College of Agriculture and Veterinary Medicine under sorghum improvement project since August, 2016. He joined the school of graduate studies of Jimma University College of Agriculture and Veterinary Medicine in 2017 to pursue his MSc. Study in Plant Biotechnology.

ACKNOWLEDGMENT

Above all, praised and glorified be the supreme God. Then, I would like to thanks my major advisor Prof. Kassahun Bantte for his great support and guidance. His valuable constructive criticism had built my confidence to undertake the activities with patience and optimism. Next I would like to thanks my co-advisor Mr. Temesgen Matiwos for his grateful guidance and continuous support throughout my thesis study.

I also have grateful thanks to the director of sorghum improvement project, Prof. Kassahun Bantte who gave me a chance to do my research under his project and financial supports.

I would like to thanks Mr. Zeleke Wendemu, Mr. Mihretie Getenet, Mr. Goyitom Berihun, Mr. Gezahegn Tefera, Mr. Tesfaye Mitiku, Mrs. Lula Kemal and all my MSc. classmate students in Plant Biotechnology of JUCAVM for their good will, comments, support and encouragement during those times.

Finally, I am so gratefully thanks my mother for her exhortation and pray to see my fruitful successes.

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ACRONYMS AND ABBREVIATION

BLINK	Bayesian Information and Linkage Disequilibrium Interatively Nested Keyway
DNA	Deoxyribonucleic Amino Acid
EBI	Ethiopia Biodiversity Institute
FAOSTAT	Food and Agriculture Organization Statistics
FarmCPU	Fixed and Random Model Circulating Probability Unification
GAPIT	Genome association and prediction integrated tool
GBS	Genotype by Sequence
GCV	Genotypic Correlation Coefficient
GWAS	Genome Wide Association Study
IBPRG	International Plant Genetic Resource Institute
ICRISAT	International Crop Research Institute in Sem-Arid Tropics
LD	Linkage Disequilibrium
m.a.s.l	Meter Above Sea Level
SMARC	Shire Maitsebri Agricultural Research Center
Mpb	Mega Base Pair
SNP	Single Nucleotide Polymorphism
USDA	United State Department of Agriculture
AM	Association Mapping

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ABSTRACT

Drought is one of the most important environmental challenges farmers face around the globe including in Ethiopia and it is the main cause of yield reduction. Improvement of the crop for drought tolerance related traits requires studying the genetics of the traits. Therefore, the present study was initiated to evaluate the performance of sorghum genotypes and to identify chromosomal regions associated with drought tolerance and other agronomic traits using genome wide association studies (GWAS). The field experiment was conducted at Sheraro, Northern Ethiopia, in 2018/19 growing season. The experimental materials consisted of 945 genotypes and the experiment was laid out in an alpha lattice design replicated twice. The experimental materials were genotyped with a total of 25,634 SNPs markers (minor allele frequency > 0.01) to perform GWAS. Analysis of variance revealed that there was highly significant difference ($p<0.01$) among the genotypes for all the traits. Genotypic coefficient of variation (GCV) ranged from 2.75 % (days to maturity) to 29 % (leaf angle), whereas phenotypic coefficient of variation (PCV) ranged from 3.81 % (days to maturity) to 31.53 % (leaf angle). Heritability ranged from 47.78 % (number of tillers) to 92.55 % (number of leaves) and genetic advance as percentage of mean (GAM) ranged from 4.09 % (days to maturity) to 57.38 % (leaf angle). Traits like panicle length, leaf angle and chlorophyll content at maturity had high GCV and PCV. High heritability coupled high GAM was observed for leaf area, leaf angle, panicle length, chlorophyll content at maturity, plant height and number of leaves. The studied genotypes were grouped into five subgroups with 73.62% of individuals had ancestry membership coefficient greater than 60% and the remaining 26.38% of the individuals were admixed. A total of 98 different SNPs having significant associations with 15 traits were detected. The identified marker-trait associations could be useful in marker-assisted selection. In General, this study had contributed to the characterization of genes and alleles controlling drought related traits, and will serve as a source of markers for molecular breeding.

Keywords: Sorghum, GWAS, Drought, SNPs

1. INTRODUCTION

Sorghum (*Sorghum bicolour* (L.) Moench), a C4 grass belongs to the family Poaceae and tribe Andropogoneae (Doggett, 1988). The origin of this crop is Ethiopia and surrounding countries (Dillon *et al*., 2007). It is predominantly self-pollinated and also readily outcrosses (Mullet *et al*., 2014). It is diploid crop (2n=2x =20) with a genome size of about 730 Mbp (Paterson, 2009). This crop is well adapted to withstand harsh environmental conditions due to its extensive root system and waxy bloom on its leaves (Paterson, 2008)

Sorghum is the fifth most economically important cereal crop grown worldwide following wheat (*Triticum* spp.), rice (*Oryza* spp.), maize (*Zea mays*) and barley (*Horedum vulgare*) and serves as a dietary staple food for people living in arid and semi-arid environmental conditions (FAOSTAT, 2018). In addition, the grain is also used as livestock feed and production of local beverages, while the stalk is used for animal feed, firewood and as a construction material (Krupa *et al*, 2017). Industrially, sorghum is also used to make sugar, starch, syrup, alcohol and molasses (Kleih *et al*., 2000). The other use of sorghum in the developed world is as a wheat substitute for people allergic to gluten (Fenster, 2003).

Sorghum is most widely produced in the semi-arid tropics where water availability is limited and frequently subjected to drought (Dep *et al*., 2004). The world sorghum production was 59.34 metric tons in 2017/18 production season. The top sorghum producing countries in the world are USA (11.5 million metric tons), India (7.5 million metric tons), Nigeria (7.4 million metric tons) and Mexico (6.1 million metric tons) (FAOSTAT, 2019). In Africa, Ethiopia is the third country following Nigeria and Sudan. In Ethiopia, a total of 4.48 million tons of sorghum was produced on 1.8 million hectares in 2017/18 production season (FAOSTAT, 2019). The major sorghum production regions in Ethiopia are Oromia (38.5 %), Amhara (32.9 %), Tigray (14.1 %) and Southern Nations and Nationalities People (7.6 %) (Kinfe and Tesfaye, 2018).

However, the productivity of the crop in Ethiopia is significantly low due to biotic and abiotic factors (Geremew *et al*., 2004; Ejeta, 2007). Among abiotic factors, drought is the major problem that reduces the productivity of sorghum (Besufekad and Bantte, 2013). Drought is the main limiting factor that reduces production worldwide and continues to be a challenge to

plant breeders despite many decades of research (Krupa *et al*., 2017). Drought occurs at any developmental stage of the crop. In the arid and semi-arid tropics, the probability of occurrence is high at the start and end of the growing season (Blum, 1999). When it occurs at the beginning of the growing season, it severely affects plant establishment and results in reduced yield, or complete crop failure when it occurs at flowering or grain filling stages (Blum, 1996). Drought at the vegetative stage and reproductive stage can reduce yield by more than 36% and 55% respectively (Assefa *et al*., 2010). In the world, total yield loss due to drought is estimated around 10 billion $US in each year (Mutava, 2009).

One of the solutions to minimize the effects of drought on crops is to develop drought tolerant crop varieties that are well adapted to moisture limited areas. Sorghum is a relatively drought tolerant crop that withstands moisture stresses (Belay and Meresa, 2017) which requires relatively less water than other important cereals such as maize and wheat (Asfaw, 2007; Krupa *et al*., 2017).

However, response of different sorghum genotypes to drought is variable in relation to the developmental stage, duration of drought, and evolutionary adaptation of the crop (Sanchez *et al*., 2002). Therefore, availability of diverse sorghum germplasm is vital for the development of drought tolerant varieties to identify appropriate genotypes. Previously, assessment of genetic variation and QTL identification in sorghum has been reported by several authors (Adugna, 2014; Besufekad and Bantte, 2013; Higgins *et al*., 2014; Murphy *et al*., 2014). Better understanding of the genetic basis of traits contributing to drought tolerance is important for the improvement of this crop. Traditionally, the identification of genomic regions and loci underlying traits of interest in crops were primarily based on evaluation of genetic populations derived from bi-parental crosses. However, this approach has yielded limited genomic resolution and restricted allelic diversity as only allelic segregates between and among the parents of the particular recombinant progenies can be assayed (Korte and Farlow, 2013).

Genome wide association mapping (GWAS) is an alternative approach that does not require development of biparental crosses and several generations of progeny (Rafalski, 2010). GWAS has become a routinely used method to investigate the genetic mechanisms underlying genetic variation due to the advancement of genotyping and sequencing technologies (Zhao *et al*., 2016). The uses of GWAS to delineate genomic regions associated with important traits in sorghum have been done by different authors. Morris *et al*. (2013) performed GWAS on plant height and inflorescence architecture and reported several loci related to plant height and inflorescence. Cuevas *et al*. (2017) studied Ethiopian sorghum germplasm and reported several loci for plant height and flowering time. Girma *et al*. (2019) also studied Ethiopian sorghum germplasm and identified markers associated with several traits.

Ethiopia is the center of diverse for sorghum germplasm and is an important source of genes for several agronomic traits (Doggett, 1988; Kebede, 1991). There are around 11,353 sorghum accessions collected and conserved in the gene bank of the Ethiopian Biodiversity Institute (EBI). However, the gene bank collections have not been systematically evaluated for drought related traits and to identify chromosomal regions associated with drought tolerance and other agronomic traits. Evaluating the germplasm based only on morphological characters for drought tolerance may not provide accurate and reliable information. The use of DNA-based markers for the genetic analysis and manipulation of important agronomic traits has become an increasingly useful tool in plant breeding and increases the efficiency of selection for difficult traits like drought tolerance. Therefore, the objectives of this study were:

- To evaluate the performance of sorghum genotypes for drought tolerance and other agronomic traits.
- To identify chromosomal regions associated with drought tolerance and other important traits

2. LITERATURE REVIEW

2.1. Origin, Taxonomy and Distribution of Sorghum

For the first time sorghum was domesticated in northen Africa, most likely in Ethiopia and Sudan (Doggett, 1988). Sorghum was taken from Africa to the Middle East and India (900 - 700 BC) and Far East through shipping and trade routes. This crop also transported into North America from Eastern parts Africa in the late 1800s in conjunction with slave trade (De Wet and Harlan, 1971; Doggett, 1988).

Sorghum is the C4 crop belongs to the grass family *Poaceae*, subfamily Panicoideae, tribe *Andropogoneae*, subtribe *Sorghinae* (Clayton and Renvoize, 1986). It has a very diverse group which has made the classification of domesticated and wild sorghums difficult (Wiersema and Dahlberg, 2007). Sorghum consists of 25 recognized species that are classified into five subgenera: *Chaetosorghum*, *Heterosorghum*, *Parasorghum*, *Stiposorghum* and *Eusorghum* (Price *et al*, 2005). Number of chromosomes which exist in the genus sorghum are 2n=2x=10, 20, 30 or 40, among this *Sorghum bicolor* has 2n=2x=20. Number of chromosomes in sorghum reflects the complexity of the species to be belonging to different subgenera (Price *et al*, 2005).

Sorghum is highly distributed in the arid and semi-arid tropics where availability of water is limited and repeatedly subjected to drought (Deb *et al.*, 2004). Globally, more than fifty percent of sorghum is grow in semi-arid parts of Africa and India which is used for food (Mehmood *et al.*, 2008). The crop is also found in temperate regions at altitudes of up to 2300 meters in the tropics and even in low rainfall areas (Craufurd et al., 1999). It is named as "Nature-cared crop" or "the crop camel" because of its strong resistance to harsh environments such as dry weather and high temperature in comparison to other crops. This indicates that sorghum has a potential to adapt itself to the given natural environment. Its ability to produce in areas with marginal rainfall (400 – 600 mm) and high temperatures (i.e. semiarid tropics and subtropical regions of the world) where it is difficult to grow any other cereal makes the crop highly valued (Shewale, 2008).

Sorghum also found in India, Pakistan, Thailand, in central and northern China, Australia, in the dry areas of Argentina and Brazil, Venezuela, USA, France and Italy where it has been given various names. For example, sorghum is known *dawa* in Housa, *sorgho* in French, *durra* Arabic, *mashela* in Amharic, *mtama* in Swahili, *jowa*r in Hindi, *Kaolian* in Chineese *milo* in Spanish and *sorgo* in portuguese (Dicko *et al*., 2006).

In Africa, sorghum is highly grown in West Africa, South of Sahara, East Africa (Dicko *et al*., 2006). In Ethiopia, sorghum grows over a wide range of ecological habitats, in the range of 400-3000 m.a.s.l. (Teshome *et al*., 2007). It is special crop in the lowland area of the country due to its drought tolerance ability. Sorghum is highly produced in north central, northwestern, western and the eastern mid-altitude areas of Ethiopia (Wortmann *et al*., 2006).

2.2. Uses of Sorghum

Sorghum is used as staple food for millions of people; as animal feed and industrial raw material (Agrama and Tuinstra, 2003). Sorghum is grown developed nations essentially for animal feed. However, in developing nations especially in Africa and Asia the grain is used both for human food and animal feed. million people from developing countries essentially rely on sorghum as a source of energy (Godwin and Gray, 2000). The main foods prepared from sorghum are: tortillas (Latin America), thin porridge, e.g. bouillie (Africa and Asia), stiff porridge (West Africa), couscous (Africa), injera (Eritrea and Ethiopia), nasha and kisra (Sudan) (Abraha *et al.*, 2015). In the USA and Japan, sorghum was considered as animal feed, however, utilization as human food is increasing because of its use in snacks and cookies (Rooney and Waniska, 2004). The future promise of sorghum in the developed world is for wheat substitution for people allergic to gluten (Fenster, 2003). In addition, pasta products, such as spaghetti and macaroni made from semolina or wheat could be made with mixtures of composite flour consisting of 30-50% sorghum in wheat (Hugo *et al*., 2003). The grain sorghum plays a dominant role in the traditional beer brewing, at household and industrial levels (House *et al*., 2000).

2.3. Sorghum Production Limiting Factors

Beside its importance, there are different constraints those decrease the production. Among production decreasing constraints; poor soils fertility, erratic rainfall, birds, poor stand establishment, disease (fungal), insects (stem borer) and striga (Geremew *et al*., 2004; Ejeta, 2007). In addition to biotic and abiotic problem lack of improved varieties also significantly affect the production (Wortmann *et al.*, 2009). Among the given problem drought is the main factor that reduces the production of sorghum in the world as well as in Ethiopia (Kebede *et al*., 2001; Besufekad and Bantte, 2013; Amelework *et al*., 2015).

Drought is one of the major global problems affecting crop production worldwide (Jie *et al.*, 2002). In the semi-arid tropics, drought is often the main production factor causing a significant yield loss (Matthews *et al.*, 1990). It is defined as a meteorological event during which precipitation is inadequate to meet crop water requirements that results in a loss of yield below that expected under optimal water supply (Thomas, 1997). It is a normal recurrent feature of climate that can occur in virtually all climatic zones; however, its feature varies significantly from region to region. In the semi-arid tropics where dry land farming is practiced, drought is a common phenomenon that occurs at different periods during the growing season (Blum, 2004). There is also a high season-to-season variability of rainfall, temperature, and radiation in the tropics. Besides, locations are greatly variable in topographic, soil, existing agricultural practices, and other associated biotic stress factors (Chapman *et al.*, 2000).

Drought is a combination of temperature (Prasad *et al.*, 2008) and water (Campos *et al.*, 2004) stress effects, in which evapo-transpiration is the major driving force that affects the soil, plant, and atmospheric continuum of the hydrologic cycle (Kramer, 1983). In earlier studies, predictions of drought were mainly based on the amount and distribution of precipitation (Blum, 2011). However, in recent studies soil moisture balance and soil characteristics were introduced in the assessment of drought. Lack of adequate soil moisture or water deficit, affects the ability of plants to grow and complete a normal life cycle (Moussa and Abdel-Aziz, 2008). Drought can have major consequences on growth, development and yield of plants by affecting several physiological, morphological and biochemical processes (Simpson,

1981). It is the major cause of poor crop performance and low yield, and sometimes it causes total crop failure. In the tropics, the probability of drought is highest at the start and end of the growing season.

Drought can occur at both pre-flowering and post-flowering stages of development, and has the most adverse effect on yield (Kebede *et al.,* 2001). Drought stress at the seedling stage of development will severely affect plant establishment (Baalbaki *et al.,* 1999). If it occurs at pre-flowering, flowering, or grain filling stages, it may result in reduced yield, or complete crop failure (Blum, 1996). Researchers have analyzed drought tolerance as pre-and post-flowering stresses and the reaction of genotypes to these stresses are variable and controlled by different genetic mechanisms (Rosenow *et al.,* 1996). Pre-anthesis moisture stress has effects on yield components such as stand count, tillering capacity, number of heads and number of seeds per head, while post-anthesis moisture stress has influences on transpiration efficiency, CO2 fixation and carbohydrate translocation. The latter, in turn, results in low yield and premature plant senescence (Xin *et al.,* 2008).

2.4. Mechanisms of Drought Adaptation in Sorghum

Sorghum is one of the most drought tolerant crop species and is an important model system for studying physiological and molecular mechanisms underlying drought tolerance (Krupa *et al*., 2017). Drought resistance mechanisms like drought avoidance, recovery, survival and tolerance, are associated with plant survival and production (Levitt, 1980). Drought avoidance is defined as the ability of plants to conserve water at the whole plant level through decreasing water loss from the shoots or by more efficiently extracting water from the soil (Ludlow and Muchow, 1990). However, drought tolerance is defined as the ability of plants to withstand water deficit while maintaining appropriate physiological activities to stabilize and protect cellular and metabolic integrity at tissue and cellular level (Xiong *et al*., 2006). Survival is the ability of the crop to survive drought, irrespective of the yield it produces, while production is the ability of the crop to grow and yield under water stress conditions (Amelework *et al*., 2015).

2.4.1. Physiological Adaptation

Ability to maintain key physiological processes, such as photosynthesis, during drought stress is indicative of the potential to sustain productivity under water deficit. Sorghum exhibits physiological responses that allow a continued growth under water stress (Dugas *et al*., 2011). High chlorophyll content, delayed senescence and chlorophyll fluorescence as well as low high transpiration efficiency and canopy temperature are physiological traits that confer drought tolerance to sorghum (Harris *et al*., 2007).

2.4.2. Morphological Adaptation

Plants constantly obtain water and nutrients from the soil through their roots. Therefore, the root system plays a critical role in response to water deficit stress. Some plants have the robust ability to increase root growth at the early stage of drought stress to absorb the water in deep soil (Hu and Xiong, 2014). The root system is the plant organ in charge of capturing water and nutrients, besides anchoring the plant into the ground. It is naturally viewed as a critical organ to improve crop adaptation to water stress (Vadez, 2014). Long, narrow, pointy leaves reduce the contact surface area with direct sunlight during high temperatures, hence preventing desiccation. Sorghum leaves and stem are covered by a waxy cuticle and epicuticular wax (Saneoka and Ogata, 1987) preventing excessive water loss during water stress. Leaf rolling is a common response of plants to water deficit, and it is a mechanism to reduce water consumption when water stress is present (Begg *et al*., 1980). Stay-green is an integrated drought-adaptation trait in sorghum. Delayed leaf senescence during grain filling is an emergent consequence of dynamics occurring earlier in crop growth and is largely due to an improved balance between the supply and demand of water, as well as the efficiency with which the crop converts water to biomass and grain yield (Jordan *et al*., 2012). Tillering ability is commonly associated with sorghum in regions with limited rainfall. Tillering is generally recognized as one of the most plastic traits affecting biomass accumulation and ultimately grain yield in many field crops (Kim *et al*., 2010).

2.4.3. Phenological Adaptation

Drought occurs at any developmental stages of the crops but sorghum is highly affected at both pre- and post-flowering stages of development. Pre-flowering drought stress response occurs when plants are under significant water stress prior to flowering, particularly at or close to panicle differentiation and until flowering (Kebede *et al*., 2001). The most adverse effect of water stress on yield occurs during and after anthesis (Blum, 2004). Post flowering drought stress significantly reduces the number and size of the seeds per plant, which are the main causes for lower grain yield in sorghum (Assefa *et al*., 2010).

2.5. Screening of Sorghum Landraces for Drought Adaptation

Tolerance to drought is a quantitative trait, with a complex phenotype, often confounded by plant phenology (Blum, 1999). Breeding for drought tolerance is further complicated since several types of abiotic stress, such as high temperatures, high irradiance, and nutrient toxicities or deficiencies can challenge crop plants simultaneously. Sorghum genotypes with good tolerance during one of the developmental stages are typically found to be susceptible to drought during the other growth stages. This developmental interaction further complicates the phenomenon of drought tolerance and each of these has a different effect on the crop. Selection for drought tolerance is complicated by the lack of fast, reproducible screening techniques and the inability to routinely create defined and repeatable drought stress conditions when a large number of genotypes can be evaluated efficiently (Ramirez and Kelly, 1998). Achieving a genetic increase in yield under these environments has been recognized to be a difficult challenge for plant breeders while progress in yield grain has been much higher in favorable environments (Richards, 2004).

A lot of studies have been done to set selection criteria for drought tolerance. Khan *et al*. (2004) reported that drought adapted plants are often characterized by deep and vigourous root systems. Some other scientists focused on morpho-physiological flag leaf related characters especially leaf water relations and their considerable interaction with drought tolerance. Selection based on plant developmental traits such as plant phenology (days to

flowering and maturity), stay-green, leaf area, tillering, panicle size and peduncle exertions are conducive for drought tolerance in sorghum genotypes (Ali *et al*., 2011).

In addition, multivariate techniques also used to select several characters simultaneously which make it feasible to approximate the genetic divergence. These techniques include principal component and cluster analysis which have analogous efficacy to establish the most suitable selection combinations (Machado *et al*., 2000). In past, multivariate analysis had mostly been exploited to assess and differentiate the genotypes for various morphological traits in sorghum (Tesso, 2005). However, Ahlawat *et al*. (2002) utilized multivariate analysis to ascertain diversity for stay-green character in 36 wheat genotypes. Similarly, Tesso *et al*. (2005) reported multivariate analysis for drought tolerance in sorghum and Bibi *et al*. (2010), working on 80 sorghum genotypes, found osmotic potential as the most important physiological marker for drought tolerance in addition to root length.

2.6. Genetics of Drought Tolerance in Sorghum

Several genes are involved in drought stress tolerance in various plant species. The function of these genes is either protecting the cell from water deficit by the production of important metabolic proteins or regulation of genes for signal transduction. The expression of a dehydrin, *dhn1* gene in sorghum as a response to water deficit was reported by Wood and Goldsbrough (1997). Expression and accumulation of *dhn1* gene in seedlings and pre-flowering sorghum was identical among genotypes, but genotypes showed variation in timing of expression of the gene. This suggested that the expression of dehydrins is possibly an important drought adaptation mechanism in sorghum.

The expression of genes related to water deficit in plants is found to be induced by water stress, desiccation, and abscisic acid (ABA). Shinozaki *et al.* (2002) also observed wide variation in the timing of induction and expression of drought related genes. The authors classified these genes into two groups; the first groups are responsible for proteins which function directly in stress tolerance, and the second group gives protein factors involved in the regulation of signal transduction and gene expression under drought. Most of these drought inducible gene expressions are induced by ABA. However, various researchers reported the

existence of ABA-dependent, and ABA-independent signal transduction cascades between the initial signal of drought stress and the expression of the genes. Furthermore, Shinozaki, (2000) suggested that at least two independent pathways exist in plants.

The purpose of studying the genetics of drought resistance in plants is to identify genetic factors that determine the productivity of crops under drought stress conditions. Advances in crop improvement under water-limited conditions are only possible, if drought resistance traits are identified and selected in addition to yield (Sanchez *et al.,* 2002). The quantitative trait loci (QTLs) that have been mapped on the 10 linkage groups of sorghum so far are involved in controlling traits related to yield and yield components, root systems, stay-green, plant height, flowering, and maturity.

2.7. Quantitative Trait Loci (QTL) for Drought Tolerance

Quantitative trait loci (QTL) mapping is used to determine quantitative traits which are related with drought and any other stresses at molecular level. Almost 6000 QTL were discovered over last decades in 150 studies for more than 220 traits in sorghum. These studies have produced a large body of information concerning the genetic basis of these traits including their allelic effects, genomic location and epistatic interactions (Mace *et al*., 2019). Among the identified QTL some of them are, stay-green in sorghum (*Stg1-Stg4*) (Harris *et al*., 2007) and nodal root angle are an important traits indicated an association between stay-green, grain yield, and nodal root angle QTLs (Mace *et al*., 2012). Stay-green QTLs (*Stg1-Stg4*) has positively associated with grain yield under drought conditions through its effect on leaf area dynamics and temporal and spatial water use patterns and also showed reduced tillering by increasing the size of lower leaves, reducing the size of upper leaves, and by decreasing the number of leaves per culm thereby more effectively harvesting light energy. Stay-green QTLs reduce the canopy development during pre-anthesis stage and reduce water demand, resulting in higher post-anthesis water use (Borrell *et al*., 2014). The other important trait in studying drought is days of flowering. Flowering time is an adaptive trait that determines the extent of the distribution of a crop in different climatic conditions, its reproductive success, and breeding methodology to be used (Yang *et al*., 2014). Sorghum is a short day plant and is sensitive to photoperiod (Childs *et al*., 1997). Several loci (*Ma1* to *Ma6*) related to flowering

time and maturity has been identified in sorghum (Higgins *et al*., 2014; Murphy *et al*., 2014). Despite those successes, QTL mapping suffers from two fundamental limitations; only allelic diversity that segregates between the parents of the particular population can be assayed and the allele frequencies and combinations present in any such population will differ from those in the natural population (Korte and Farlow, 2013).

2.8. Genome Wide association Study (GWAS) and Linkage Disequilibrium (LD)

GWAS is an alternative approach that does not require development of biparental crosses and several generations of progeny (Rafalski, 2010) and used to identify marker trait relationships (Flint-Garcia *et al*., 2003). With association mapping, statistical assessments are made for associations between genotypes based on molecular markers and phenotypes of various traits in reference germplasm sets (Buntjer *et al*., 2005).

GWAS usually emphasize associations between SNPs and traits, for example, DNA of plant varieties is compared with different phenotypes for a particular trait. GWAS implementation is based on designs, genotyping technologies, and statistical concepts for analysis, replication, interpretation, and follow-up of association results. GWAS is now more widely-used to identify candidate genes underlying traits of interest. With its power in overcoming the major limitations of bi-parental populations, it is becoming a more common approach in trait identification (Brachi *et al*., 2011) particularly with recent advances in high throughput DNA sequencing technologies, and large-scale precision-phenotyping. Genotyping-by-sequencing (GBS) is a next-generation sequencing (NGS) based genotyping procedure that represent high-marker density approaches, and frequently used genotyping approach in GWAS. The GBS approach works by reducing genome complexity with restriction enzymes, combined with multiplex NGS for high-density single nucleotide polymorphism (SNP) marker discoveries (Elshire *et al*., 2011). The process associated with GBS including genome-wide molecular marker discovery, highly multiplexed genotyping, flexibility and low cost make it an excellent tool in studies of plant genetics and breeding (Poland and Rife, 2012). Understanding population genetic structure and familial relatedness among individuals of study materials are important procedure to undertake prior to GWAS analysis as these are sources of possible false-positives. Failures to account for population stratification and

kinship diminish the revealing power of GWAS and can lead to spurious associations (Wu *et al*., 2011). It is therefore critical to choose appropriate models to reduce these two sources of false-positives.

The uses of GWAS to delineate genomic regions with important traits in sorghum have been shown in several studies. Morris *et al*. (2013) characterization using single nucleotide polymorphisms (SNPs) on accessions that have adapted from diverse agro-climatic conditions uses to facilitate gene discovery and molecular breeding in sorghum; they quantified variation in nucleotide diversity, linkage disequilibrium and recombination rates across the genome for better understanding of the genomic patterns of diversification in sorghum. Lasky *et al*. (2015) characterized genomic variation of 1943 sorghum accessions using 404,627 SNPs and quantified allelic associations with environmental variables. Their results suggest that genomic signatures of environmental adaptation may be useful for crop improvement, enhancing germplasm identification and marker-assisted selection. Maina *et al*. (2018) analyzed 516 Nigerien accessions using 144,299 single nucleotide polymorphisms (SNPs) generated by genotyping-by-sequencing library and showed the existence of significant association. In addition, GWAS was conducted by (Li *et al.*, 2018; Girma *et al*., 2019; Cuevas *et al*., 2017) and reported significant results on sorghum germplasm.

Linkage disequilibrium is a nonrandom association of alleles and determines the allelic linkage relationship at different loci, and linkage equilibrium (LE) is random association of alleles (Flint-Garcia *et al.,* 2003) and also defines the route of association mapping either at whole genome level or candidate gene level. The extent of LD estimates the resolution power and also suggests number of markers for AM (Association Mapping) (Whitt and Buckler, 2003). Extent of LD is the true determinant of power of AM (Remington *et al*., 2001). High resolution of AM indicates that with increasing genetic distances the LD will decline rapidly. Population structure and LD gives proper information for the efficient and accurate AM and marker assisted selection (Zhang *et al*., 2010). However, LD needs lot of genomic markers to detect linked markers with concerned character (Yu and Buckler, 2006).

Linkage disequilibrium can be affected by many factors like mutation, recombination, selection, epistasis, gene flow, co-adaptation of alleles at distinct loci and mating system

between different genotypes (Buckler and Thornsberry, 2002). Linkage disequilibrium will increase due to different factors like genetic drift, population structure, admixture, genomic rearrangements, mating system, kinship and selection (Oraguzie *et al.,* 2007) and decreased due to high rates of recurrent mutation, out crossing, recombination and gene conversion (Salvi and Tuberosa, 2007). If LD level is low, number of markers required in specific proximity will be high. High value of LD between unlinked and linked loci is the indication of presence of population selection, relatedness and genetic drift (Gupta *et al.,* 2005). On average, LD decays to 50% of its initial value by 1 kb and to background levels ($r^2 < 0.1$) within 150 kb. LD decay in sorghum estimated to be 15–20 kb (Hamblin *et al*., 2005) and 50–100 kb (Bouchet *et al*., 2012). The extent of LD in sorghum is similar to that in rice (~75–150 kb) (Mather *et al*., 2007). The average recombination rate in sorghum (1.4 ρ/kb) is intermediate as compared to estimates in plants such as Arabidopsis (0.8 ρ/kb) (Kim *et al*., 2007) and maize (2.2 ρ/kb) (Yan *et al*., 2009).

2.9. Genetic Parameters

2.9.1. Phenotypic and Genotypic Variations

Differences between individuals which rose due to differences in their genetic composition or environment are called variability (Allard, 1960). The degree of variation is measured and expressed as the variance, in which components are subdivided in to: the genotypic variance, which is the variance of genotypic value, and the environmental variance, which is the variance of environmental deviation. The phenotypic variance, or the variance of phenotypic values, is the total variance, and is the sum of the above separate variance components. The subdividing of the variances into components allows us to estimate the relative importance of the various determining factor of the phenotype, particularly the role of heredity versus environment; the relative importance of heredity in determining phenotypic value is called the heritability of character (Falconer, 1989).

High GCV (Genotypic coefficient of variation) alongside high heritability and hereditary progress give preferable data over different parameters alone. Stay-green parameters, yield per plant, panicle exertion, head length and 1000 seed weight are the most essential quantitative characters to be considered for powerful choice in sorghum. Chances to enhance these

characteristics give off an impression of being likely however the degree changes relying upon H^2 and GCV values (Addissu, 2012).

Bello *et al*. (2007) reported high value of PCV for panicle length and 100 seed weight and high GCV for panicle length. Amare *et al*. (2015) also reported high value of PCV and GCV for leaf area. In addition, Kalpande *et al*. (2018) reported high value of PCV and GCV for 100 seed weight and moderate value for plant height. Leaf length, days of flowering and days of maturity recorded low GCV and PCV. These traits are not used for genetic improvement because of low genetic variation and they may highly influenced by environmental factors. Further, low GCV was recorded by Gebrie and Genet (2019) for days of maturity and leaf width. Addisu (2011) reported the lowest genotypic and phenotypic coefficients of variation for days to maturity and in addition low GCV and PCV was recorded by Godbharle *et al.* (2010) for days of flowering.

2.9.2. Heritability

Heritability in broad sense is the ratio of the genotypic variance to the phenotypic variance and it can also be defined as a quantitative measure which provides information about correspondence between genotypic variance and phenotypic variance. The broad sense heritability expresses the proportion of the total variance that is attributable to the average effects of genes, and is useful if interest is in relative importance of genotype and environment in the determination of phenotypic value. It is a proportion ranging from 0 to 1.0 or in percentage from 0 to 100. A heritability of 0 means that genes do not contribute to individual differences in the trait, while a heritability of 1.0 means that trait variance is due mainly to heredity (Dabholkar, 1992).

When the broad sense heritability ranged from 23.76-98.65% over locations; high heritability was observed for days to heading (98.65%), days to flowering (98.64%), days to maturity (98.3%), plant height (96.77%), panicle length (91.31%) and 1000 seed weight (84.71%) across locations (Amare *et al*., 2015).

Mulualem *et al*. (2018) tested 110 sorghum genotypes in Sheraro and Mieso and reported that there were heritability ranges from 0.03 for grain yield to 0.93 for plant height at Meiso and

from 0.02 for plant height to 0.19 for number of panicles per plot at Sheraro. Traits those are highly heritable (> 0.60) were days to maturity, plant height, panicle length, hundred grain weight. According to Mofokeng *et al* (2019) there were high heritability for the traits plant height (90.1%), thousand seed weight (80.9%), intermediate for panicle length (62.7%), rachis number (64.2%), and low for panicle exertion (27.85), panicle weight (24.52) and grain yield per panicle (22.16). Nyadanu and Dikera (2014) reported high genetic advance as percent of mean for weight of 100 grains and plant height. High genetic advance as percent mean for days to flowering, leaf area, plant height and panicle length were reported by Amare *et al*. (2015). Mahajan *et al*. (2011) also reported high genetic advance as percent of mean for panicle length and plant height.

2.9.3. Genetic Advance

Genetic advance measures the expected genetic progress that would result from selecting the best performing genotype for a given character. It indicates the improvement of the performance of the selected genotype over the original. It is an indicator for the genetic improvement made in a population under selection (Allard, 1960).

Tomar *et al*. (2012) reported that moderate genetic advance as percentage of mean was observed for days to 50% flowering (16.01 percent), number of leaves (11.32) and low genetic advance attributable to non-additive gene action was noticed for days to maturity (7.92). High genetic advance (GA) was observed for number of days to flowering, weight of grains per panicle, and days to maturity (Nyadanu and Dikera, 2014). High genetic advance as percent mean for days to flowering, leaf area, plant height and panicle length were reported by Amare *et al*. (2015). Mahajan *et al*. (2011) also reported high genetic advance as percent of mean for panicle length and plant height.

2.9.4. Correlation Coefficients

Correlation coefficient is used to measure the magnitude of association between two characters. Therefore, it determines the component characters of a complex trait, like yield. Such studies are useful to indicate the magnitude and direction of relationships between different characters and grain yield as well as among the characters themselves (Falconer and Mackay, 1996).

Generally, there are three types of correlations; phenotypic, genotypic and environmental correlations. The association between two characters that can be directly observed is the correlation of phenotypic values or phenotypic correlation. The phenotypic correlation measures the magnitude of the two observed characters which are linearly related whereas genetic correlation is the association of breeding values (additive genetic variance) of the two characters. The genetic causes of correlation are mainly pleiotropic effects of genes affecting different characters. Pleiotropy is the property of a gene where it affects two or more characters, so that the segregating gene causes simultaneous variation in the two characters (Falconer and Mackay, 1996).

According to Sowmy *et al*. (2015), the correlation coefficient revealed days to maturity at genotypic level and days to flowering at both genotypic and phenotypic levels showed highly significant negative correlation with grain yield. Negative correlation is desirable for these traits as less number of days to flower reduces the crop duration; this in turn is helpful in terms of economic cultivation of sorghum crop. At both phenotypic and genotypic levels, plant height exerted highly significant positive correlation with grain yield. Gebrie and Genet (2019) also reported higher significant positive correlation of Grain yield with panicle width and panicle length and a negative significant correlation with single leaf area and number of leaves. In addition, (Legesse, 2007); Deepalakshmi and Ganesamurthy (2007), and Mahajan *et al*. (2011) reported similar results.

3. MATERIALS AND METHODS

3.1. Description of the Study Area,

The experiment was conducted at Sheraro (Northern Ethiopia), the experimental station of Shire Maitsebri Agricultural Research Center (SMARC), in 2018/19 growing season. Sheraro is located at an altitude of 1006 m a.s.l., 14^{o} 24' 00" N latitude, 37^{o} 56' 00" E longitude. The area is characterized by a soil type of vertisol with a pH of 6-7. The mean annual maximum and minimum relative humidity during the experiment were 57% and 21% respectively, and the mean annual maximum and minimum temperatures were 34^{0}C and 25^{0}C, respectively. The average rainfall of the area during the cropping season was 186.23mm (World Online Weather, 2019).

3.2. Plant Materials

The experimental materials consisted of 945 genotypes including landraces, breeding lines and checks. The materials were obtained from Ethiopian Biodiversity Institute (EBI) and Melkasa Agricultural Research Center (MARC). The land races from EBI were systematically selected from about 10,000 collections, representing all sorghum growing regions and ecologies (altitudes) of the country. The list of genotypes is given in the appendix Table 1.

3.3. Experimental Design and Trial Management

The experiment was conducted using an alpha lattice design with two replications, having 63 blocks per replication and fifteen experimental units per block. The spacing was 70 cm between rows and 15 cm between plants. The length of the plot was 3m and a total of twenty plants were planted in each plot. Thinning was done 20 days after emergence to adjust plant to plant spacing. A fertilizer rate of 100kg/ha diammonium phosphate (DAP) was applied during sowing. Fifty kilograms per hectare of urea was applied at the knee height stage. The fertilizers (DAP and urea) were applied as per recommended rates for sorghum in the experiment area. All agronomic management like land preparation, weeds, insect pests control and ridging were done following research recommendation (Ayana, 2001).

3.4. Data Collected

Data were collected from five randomly selected plants per plot. The following phenotypic traits were measured based on sorghum descriptors (IBPRG/ICRISAT, 1993)

Chlorophyll content (SPAD): the chlorophyll content was measured from randomly selected plants on the flag leaf, three times (from tip, mid and near collar and then the average was taken) at flowering and maturity stages using chlorophyll meter (SPAD - 502 Plus).

Days to 50% flowering (days): The number of days from emergence to 50 % flowering of the plants per plot.

Days to maturity (days): The number of days from emergence to 95 % of physiologically maturity.

Plant height (cm): Height of the plant was measured from the base of the plant to the tip of the panicle at maturity

Leaf length (cm): the length was measured from the collar to the leaf tip of the sixth leaf using ruler.

Leaf width (cm): the width was measured from widest part of the sixth leaf using ruler.

Leaf area (cm^2): was calculated using the formula KxLxW, where K is the "adjustment factor" 0.69, L is length and W is the width (Stickler *et al*., 1961).

Number of leaves (number): Number of leaves was counted from the base to the flag leaf at the time of blooming.

Tiller number (number): a total number of tillers present on randomly selected plants

Panicle length (cm): it was measured from the base of the panicle to the tip of the panicle.

Panicle width (cm): measured the diameter of the panicle at its widest part.

Leaf angle (degree): leaf angle was measured using field scorer (an application that used to record field data like morphological, physiological and agronomic traits) by adjusting data type into angle.

Grain yield per unit area (g/m^2): grain yield per unit area was measured by changing the grain yield which was harvested from randomly selected plants into specific plant by dividing the total yield to number of panicles.

Hundred seeds weight (g): The weight of one hundred seeds obtained from the randomly selected plants.

3.5. DNA Extraction and Genotyping

DNA was extracted from 14 days old seedlings. The leaf samples were dried for 18 hours using a freeze drier (Christ, Alpha 1 – 2 LD plus). Grinding was done using geno-grinder (QIAGEN, Tissue Lyser II). Both genomic DNA extraction and sequencing were done at DArT P/L by outsourcing (http://www.diversityarrays.com). Initially, 54,080 SNP markers were generated from 940 sorghum germplasm. The total number of SNP markers was reduced to 50,367 after removing of some markers with unknown and *super*-contigs positions. These 50,367 SNP markers were imputed for removal of missing values. Based on the allele frequency distribution in the Ethiopia sorghum collection, 65.5% of the SNPs were rare (MAF < 0.05) as result, the markers were filtered MAF >0.01 produced which resulted in 25,634 robust SNP markers for the population molecular studies.

3.6. Phenotypic Data Analysis

3.6.1. Analysis of Variance (ANOVA)

The data collected for each trait was subjected to analysis of variance (ANOVA) for alpha lattice design. Analysis of variance was done using proc GLM procedures of SAS version 9.4 (SAS, 2015). Treatment comparisons were using Least Significance Difference (LSD) at 5% probability level using ggplot package on R software (R Core Team, 2019). The following model was used to analysis the variance.

$y_{ijk} = \mu + Rep_i + Bock_j (Repi) + Gen_k + \Sigma_{ijk}$

where: y = is the trait of interest; μ = is the mean effect; $Rep_{i=}$ is the effect of the i^{th} replicate; $Bock_j$(Repi) = is the effect of the j^{th} incomplete block with within the i^{th} replicate; $Gen_{k=}$ is the effect of k^{th} genotype and Σ_{ijk} = is the error associated with the i^{th} replication, j^{th} incomplete block and k^{th} genotype which is assumed to be normally and independently distributed with mean zero.

3.6.2. Estimation of Variance Components

The variability present in the population was estimated by calculating phenotypic and genotypic variance and coefficient of variation. The phenotypic and genotypic variances were estimated based on the formula of Syukur *et al*., (2014) as follow:

$$\sigma^2 g = [(MSG) – (MSE)] / r$$

$$\sigma^2 p = [\sigma 2\ G + (\sigma 2\ E/r)];$$

Where: σ^2 G = Genotypic variance; σ^2 P = Phenotypic variance; σ^2 E = environmental variance (error mean square from the analysis of variance); MSG = mean square of genotypes; MSE = error mean square; r = number of replications.

Based on the analysis of variance, the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated using formula by Burton and Devane (1953) as follows:

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma g}\ x\ 100}{\bar{X}};$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma p}\ x\ 100}{\bar{X}};$$

Where: σ^2G = Genotypic variance; σ^2P = Phenotypic variance; $\bar{X}$ = is grand mean of a character.

According to Deshmukh *et al*. (1986), PCV and GCV values greater than 20% are considered as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be medium.

3.6.3. Broad Sense Heritability

Broad sense heritability (h^2) of the all traits expressed as the percentage of the ratio of the genotypic variance to the phenotypic variance was calculated according to the formula as described by Allard (1960).

$$h^2bs= [(\sigma^2 G) / (\sigma^2 P)] \times 100;$$

Where: h^2 bs= heritability in broad sense; σ^2 G = Genotypic variance; σ^2 P = Phenotypic variance.

Heritability values are categorized as low, moderate and high Robinson (1949) as follows: 0-30%: Low; 30-60%: Moderate; 60% and above high.

3.6.4. Genetic Advance

Genetic advance and genetic advance as percentage of mean assuming selection of superior at 5% of the genotypes was determined as described by Johnson *et al*. (1955).

$$GA = K (\sigma P) h^2;$$

Where: K = the selection differential (K = 2.06 at 5% selection intensity); σP = the phenotypic standard deviation of the character; h^2 = broad sense heritability.

Genetic advance as percent of mean was computed using the formula given below to compare the extent of predicted genetic advance of different traits under selection

$$\text{Genetic advance as percentage of mean} = \frac{\text{genetic advance} * 100}{\text{population mean}} = \text{GAM} = \frac{\text{GA} * 100}{\bar{X}}$$

Then following the Johnson *et al*. (1955); genetic advance in percentage of mean categorized as low (0 – 10 %), moderate (11- 20 %) and high above 20%.

3.7. Molecular Data Analysis

Population structure of the genotypes was analyzed by loading landscape and Ecological Association (LEA) packages (Francois, 2016) on R program (R core Team, 2019). The

number of sub-population was decided at which k value where the cross entropy plot began to plateau.

Linkage disequilibrium analysis was performed using TASSEL 5 standalone software to explore association of 25634 SNP markers (flittered from 50367 at MAF > 0.01) by setting LD decay threshold value 0.1 (r^2 <0.1) (Shi *et al*., 2010), LD type sliding window and window size was 50.

Best linear unbiased prediction (BLUP) results obtained from 940 sorghum genotypes for all the traits and a total of 50,367 SNP markers were used for GWAS analysis. The association analysis was performed with a mixed linear model (MLM) using the Bayesian Information and Linkage Disequilibrium Interatively Nested Keyway (BLINK) packages (Huang *et al.*, 2018) in R software (R Core Team, 2019) with a MAF greater than 0.01. Log quantile-quantile plot of p-values were examined to determine how well the models accounted for the studied sorghum germplasm.

4. RESULTS AND DISCUSSION

4.1. Analysis of variance

In the present study, highly significant difference was observed among genotypes ($p<0.01$) for all traits (Table 1). This result indicates the presences of variation among the tested sorghum genotypes. This opens an opportunity for further improvement of the genotypes through selection for the desired trait. Ayana and Bekele (2000) reported highly significant difference among 415 landraces genotypes for number of leaves, leaf length, leaf width, leaf area, plant height, days to 50% flowering, panicle length, panicle width and thousand seed weight. Similarly, Mulualem *et al*. (2018) also reported significance differences among 110 sorghum collections for days to flowering, days to maturity, grain yield, hundred grain weight, panicle length and plant height. In addition, Mofokeng *et al*. (2019) reported significant differences among genotypes for panicle length, thousand seed weight and grain yield per panicle.

Table 1. Analysis of variance for 15 traits of 945 Sorghum genotypes

Traits	Rep	Block/rep	Genotype	MSE	R-Square
DTF	210.33**	140.16	23.99**	10.90	0.85
DTM	843.74**	19.731	32.97**	15.81	0.85
PH	28218.97**	1139.88**	2884.97**	462.40	0.94
TN	0.01	0.22	0.42**	0.22	0.79
LN	23.03**	1.22**	4.36**	0.70	0.93
ChCF	263.29**	43.98**	56.35**	11.45	0.94
ChCM	14.24	21.80	87.43**	17.09	0.94
PL	55.21**	5.61	70.99**	5.98	0.96
PW	0.23	0.79**	1.30**	0.44	0.88
LW	0.39	0.38**	1.34**	0.28	0.87
GYPUA	1191.70	1349.12**	2284.51**	827.31	0.99
HSW	2.32**	0.14	0.36**	0.12	0.89
LA	2514.62**	104.96**	597.06**	63.18	0.93
LeA	59170.48**	1934.80**	8682.90**	1017.00	0.92
LL	59170.48**	45.69**	120.05**	26.12	0.86

DTF = days of 50% flowering (days); DTM = days of maturity (days); PH = plant height (cm); TN = tiller number (number); LN = leaf number (number); ChCF = Chlorophyll content at flowering (SPAD reading); ChCM = Chlorophyll content at maturity (SPAD reading); PL = panicle length (cm); PW = panicle width (cm); GYPUA = grain yield unit area (g); HSW = hundred seed weight (g); LA = leaf angle (degree); LeA = leaf area (cm^2); LL = leaf length (cm) and LW = leaf width (cm).

4.2. Mean performance of the genotypes

The tested genotypes showed wide range of variability for most of the traits (Table 2). The mean value of grain yield was 262.88g per plants; genotype JUS163330 showed the maximum (815.45g) and genotype JUS173037 showed the minimum (20.61g). The existence of genotypes with better yield performance is an indication of the possibility of developing high yielding varieties from the available materials. The mean value for days to 50% flowering was 74.41 and JUS171203 had the maximum (95 days) and Dagnew (local check) showed the minimum (62 days). The mean value for days to 95% maturity was 106.54 days; JUS173295 had the maximum (123 days) and Dagnew (local check) showed the minimum (92 days). Under moisture stress condition, short days to flowering and maturity have an advantage for escaping harsh conditions and increasing grain yield. Delay in flowering and maturity is a strong indication of sensitivity and is caused by growth retardation during soil drying in response to stress (Blum *et al*., 1999).

The mean value of leaf area was 414.93 cm^2; JUS171454 showed the maximum (651.30 cm^2) and JUS171494 showed the minimum (216.09 cm^2). The mean value for number of leaves was 16.72; JUS171056 had the maximum (20.67 cm) and JUS173640 had the minimum (12 cm). Optimum leaf area, leaf length and number of leaves are required for carrying out enough photosynthesis to run the essential processes of the plant (Ali *et al*., 2009). Because, more leaf area and number of leaves might cause more water loss due to more evapo-transpiration from the surface and finally causing desiccation. The mean value of plant height was 281.7cm; JUS173819 had the maximum (375 cm) and JUS163338 had the minimum (121.5cm). A genotype with shorter plant height is recommended under drought stress condition as genotypes with taller plant height may utilize the available soil water for vegetative development, leaving no moisture for the grain filling stage concomitant with lower current photosynthesis during post flowering stages and decreased grain yield. The mean value for chlorophyll content (SPAD reading) at maturity was 18.67; JUS173364 had the maximum (47.90) and JUS173341 had the minimum (8.43). High chlorophyll content confers drought tolerance to sorghum by giving more chance for grain filling during water stress post-flowering conditions (Harris *et al*., 2007).

Therefore, the existence of wider variability among sorghum genotypes implies the potential to improve the crop and the need to conserve these resources. Many researchers conducted similar works on genotypes which were collected from different agro-ecologies and their results revealed the existence of variability. Among these studies, Geleta and Labuschagne (2005) reported the existence of morphological variation among sorghum accessions using 10 morphological traits. Similarly, Abreha *et al*. (2015) reported the presence of morphological variation among the studied sorghum genotypes using 16 morphological traits.

Table 2. Five Genotypes with the Highest and Lowest Values

Top Five											
		Trait			Trait			Trait			Trait
No.	Genotype	GY	No.	Genotype	DTF	No.	Genotype	DTM	No.	Genotype	LeA
1	JUS163330	815.45	1	JUS171203	95.00	1	JUS173295	123.00	1	JUS173586	413.83
2	JUS173773	791.48	2	JUS173090	95.00	2	JUS173215	120.00	2	JUS173365	414.18
3	JUS171267	727.99	3	JUS173215	90.00	3	JUS161326	120.00	3	JUS171380	414.18
4	JUS173480	693.46	4	JUS173295	90.00	4	JUS173063	120.00	4	JUS173795	414.48
5	JUS171325	692.02	5	JUS161326	90.00	5	JUS171705	120.00	5	JUS171625	414.65
Bottom Five											
1	JUS173037	20.61	1	Dagnew (Local check)	62.00	1	Dagnew (Local check)	92.00	1	JUS171454	621.31
2	JUS173451	36.57	2	JUS171176	63.50	2	JUS171176	92.50	2	JUS171623	619.93
3	JUS173206	37.51	3	JUS163348	64.00	3	JUS163348	94.00	3	JUS171030	618.47
4	JUS173808	44.09	4	JUS163434	64.50	4	JUS163434	95.50	4	JUS173004	617.10
5	JUS173765	46.20	5	JUS173625	65.00	5	JUS171666	95.50	5	JUS171378	616.13
	Mean	262.88			74.41			106.54			414.93

DTF = days of 50% flowering (days); DTM = days of maturity (days); PH = plant height (cm); TN = number of tillers (number); LN = number of leaves (number); GYPUA = grain yield per unit (g); ChcM = Chlorophyll content at maturity (SPAD); LeA = leaf area and HSW = hundred seed weight (g)

Table 1 (continued)

Top Five												
No.	Genotype	Trait LN	No.	Genotype	Trait PH	No.	Genotype	Trait ChCM	No.	Genotype	Trait HSW
1	JUS173005	16.71	1	JUS163338	125.75	1	JUS173364	47.90	1	JUS173519	3.92
2	JUS173212	16.63	2	JUS163345	138.13	2	JUS173711	46.43	2	JUS173515	3.42
3	JUS173315	16.63	3	JUS173640	150,00	3	JUS171773	45.80	3	JUS171711	3.35
4	JUS173304	16.63	4	JUS163342	152.00	4	JUS173187	44.27	4	JUS173709	3.23
5	JUS173675	16.63	5	JUS173347	157.25	5	JUS171008	43.45	5	JUS173096	3.22
Bottom Five											
1	JUS171056	20.67	1	JUS173819	375.00	1	JUS173341	8.43	1	JUS173713	0.76
2	JUS173732	20.50	2	JUS173298	375.00	2	JUS173634	8.78	2	JUS171329	0.73
3	JUS173240	20.50	3	JUS173783	375.00	3	JUS173106	8.80	3	JUS173490	0.72
4	JUS173145	20.50	4	JUS173226	374.00	4	JUS163341	8.92	4	JUS173467	0.61
5	JUS173779	20.25	5	JUS171489	370.38	5	JUS171447	9.13	5	JUS173295	0.48
	Mean	16.72			281.70			18.67			2.08

4.3. Variance components and coefficient of variation

Genotypic coefficient of variation (GCV) ranged from 2.75 % for days to maturity to 29 % for leaf angle. Similarly, phenotypic coefficient of variation (PCV) ranged from 8.09 % for days of maturity to 31.53 % for leaf angle (Table 3).

According to Deshmukh *et al*. (1986), PCV and GCV values greater than 20% are considered as high, whereas values less than 10% as low and values between 10% and 20% are moderate. Based on this, chlorophyll content at maturity, panicle length and leaf angle recorded high GCV. Moderate GCV was recorded for traits like plant height, number of leaves, chlorophyll content at flowering, grain yield per unit area, panicle width, leaf area, number of tillers and hundred seed weight. Chlorophyll content at maturity, panicle length, leaf angle, tiller number and hundred seed weight recorded high PCV. Plant height, number of leaves, chlorophyll content at flowering, grain yield, panicle width, leaf width and leaf area had moderate PCV. The PCV was relatively greater than GCV for the traits recorded in this study. Even though; the magnitude of the differences was low. This shows that the influence of environmental factors for the phenotype expression of genotypes was low. Because of this reason, there is higher chance of improvement of these traits through selection based on the phenotypic performance. Therefore, traits with high and moderate phenotypic and genotypic coefficients of variation could be used for selection as their phenotypic expression is a good indication of genetic potential of genotypes. Bello *et al*. (2007) reported a similar high value of PCV for panicle length and hundred seed weight and high GCV for panicle length. Amare *et al*. (2015) also reported high value of PCV and GCV for leaf area. In addition, Kalpande *et al*. (2018) reported high value of PCV and GCV for hundred seed weight and moderate value for plant height.

Leaf length, days of flowering and days of maturity recorded low GCV and PCV. These traits are not used for direct selection in genetic improvement because of low genetic variation and they might be influenced by environmental factors. Further, low GCV was recorded by Gebrie and Genet (2019) for days to maturity and leaf width. Addisu (2011) reported the lowest genotypic and phenotypic coefficients of variation for days to maturity and low GCV and PCV was reported by Godbharle *et al.* (2010) for days to flowering.

4.4. Heritability and genetic advance

The efficiency with which genotypic variability can be exploited by selection depends upon heritability of individual traits (Bilgin *et al*., 2010). In addition, it gives an indication as to how a given trait or agronomic character will respond to selection (Falconer and Mackey, 1996).

Heritability ranged from 47.78 % for number of tillers to 92.55 % for number of leaves (Table 3). According to Robinson (1949), heritability values greater than 60 % are high, values from 30-60 % are moderate and less than 30 % are low. Accordingly, plant height, number of leaves, chlorophyll content at flowering, chlorophyll content at maturity, panicle length, panicle width, grain yield, hundred seed weight, leaf angle, leaf area, leaf length and leaf width showed high heritability. High heritability indicates that the environmental influence is minimal on the expression of the trait. Therefore, traits with high heritability can be used for selection. Similar results were reported for leaf area, plant height, number of leaves, leaf length and leaf width by Gebrie and Genet (2019). High heritability in broad sense was also reported by Ali *et al.* (2006) for plant height, grain weight, and hundred seed weight. Amare *et al*. (2015) also reported high heritability for leaf area, plant height, panicle length and hundred seed weight. In addition, Mofokeng *et al*. (2019) reported high heritability for plant height, hundred seed weight and panicle length. Furthermore, Nyadanu and Dikera, (2014) reported high heritability values for grain weight per panicle, hundred grain weight and plant height.

Medium heritability was recorded for days to flowering, days to maturity and number of tillers and these traits are also used for selection even if there is more environmental influence as compared to high heritability. Generally, high heritability estimates indicate that the selection for these traits will be effective as they are less influenced by environmental effects. Heritability estimates have been found to be useful in indicating the relative value of selection based on phenotypic expression of traits.

Genetic advance as percent of mean is very important for selection than heritability estimate alone (Najeeb *et al*., 2009). Therefore, high genetic gain coupled with high heritability estimates offers the most suitable condition for selection. In addition, genetic advance also

shows the degree of gain obtained in a character under a particular selection pressure. Jonson *et al*. (1955) classified genetic advance as percentage of mean (GAM) as values from 0%-10% are low, 10% -20% moderate and 20% and above as high.

In this study, the range for GAM was from 4.09% for days to flowering to 57.38% for leaf angle. High genetic advance as percentage of mean was recorded for tiller number, chlorophyll content at flowering, chlorophyll content at maturity, panicle length, panicle width, hundred seed weight, leaf angle, number of leaves and leaf area. Moderate GAM was recorded for grain yield, leaf length and leaf width. The traits with high and moderate GAM have high degree of gain under a particular selection pressure. Therefore, the traits with high and moderate genetic advance as percentage of mean can be used for selection. Nyadanu and Dikera (2014) reported similar high genetic advance as percent of mean for hundred grain weight and plant height. High genetic advance as percent of mean for days to flowering, leaf area, plant height and panicle length were reported by Amare *et al*. (2015). Mahajan *et al*. (2011) also reported high genetic advance as percent of mean for panicle length and plant height. Lower genetic advance as percentage of mean was recorded for days to flowering and maturity. These traits might be affected by environmental factors because of their quantitative nature; hence improving such traits by direct selection is very difficult.

Table 3. Estimates of genetic parameters for 15 traits of 945 genotypes evaluated at Sheraro in 2019 cropping season

Traits	Ranges	Mean	CV	σ2g	σ2p	GCV (%)	PCV (%)	H^2(%)	GA	GAM (%)
DTF	62.00-95	74.41	6.50	6.54	11.99	3.44	4.65	54.57	3.89	5.23
DTM	92.00-123	106.54	7.83	8.58	16.49	2.75	3.81	52.05	4.35	4.09
PH	125.75-375	281.70	7.63	1211.29	1442.49	12.35	13.48	83.97	65.70	23.32
TN	1.00-3.67	1.65	28.19	0.10	0.21	19.08	27.61	47.78	0.45	27.17
LN	12.00-20.67	16.72	5.00	4.33	4.68	12.45	12.94	92.55	4.12	24.66
ChCF	16.43-53.43	74.41	9.51	22.45	28.18	13.31	14.91	79.68	8.71	24.47
ChCM	8.43-47.90	18.67	18.67	35.17	43.71	26.79	29.87	80.46	10.96	49.50
PL	2.13-7.00	4.86	13.61	32.51	35.50	23.42	24.47	91.58	11.24	46.17
PW	7.88-43.63	24.35	13.61	0.43	0.65	13.49	16.56	66.34	1.10	22.64
GYPUA	20.61-815.45	262.88	10.94	728.60	1142.26	10.27	12.86	63.79	44.41	16.89
HSW	0.48-3.92	2.08	16.48	0.12	0.18	16.48	20.13	67.06	0.58	27.81
LA	20.75-95.50	50.03	15.89	212.56	240.60	29.64	31.53	88.34	28.23	57.38
LeA	216.09-651.3	414.93	7.63	3832.95	4341.45	14.92	15.88	88.29	119.83	28.88
LL	36.25-120.25	78.15	6.54	46.97	60.02	8.77	9.91	78.25	12.49	15.98
LW	4.00-19.46	7.65	6.86	0.53	0.67	9.53	10.70	79.47	1.34	17.51

DTF = days of 50% flowering (days); DTM = days of maturity (days); PH = plant height (cm); TN = tiller number (number); LN = leaf number (number); ChCF = Chlorophyll content at flowering (SPAD reading); ChCM = Chlorophyll content at maturity (SPAD reading); PL = panicle length (cm); PW = panicle width (cm); GYPUA = grain yield unit area (g); HSW = hundred seed weight (g); LA = leaf angle (degree); LeA = leaf area (cm^2); LL = leaf length (cm) and LW = leaf width (cm).

4.5. Correlation among studied traits

Correlation coefficient uses to measure the magnitude of association between two traits. Therefore, it determines the component traits of a complex trait, like yield and drought. Such studies are useful to indicate the magnitude and direction of relationships between different traits and grain yield as well as among the traits themselves (Falconer and Mackay, 1996).

In this study, the traits showed highly significant and significant positive and negative correlation coefficient (Table 4). Trait like number of leaves was positively correlated with leaf width, leaf area and leaf length. Similarly, Tesso *et al.* (2011) reported the positive association of leaf traits. Under drought condition these traits are critical for the development of the plants (Saneoka and Ogata, 1987). Selection of sorghum genotypes those have optimum number of leaves, leaf area, leaf length and width could be selected for drought tolerance because, narrow, pointy leaves reduce the contact surface area with direct sunlight during high temperature, hence preventing desiccation (Vadaz, 2014).

Grain yield showed highly significant negative correlated with days to maturity, leaf length, chlorophyll contents at maturity and number of leaves (Table 2). To improve grain yield per unit area under drought stress condition short days to maturity and optimum number of leaves should be selected in order to escape and reduce evapo-transpiration respectively. Sellamuthu *et al*., (2011) also reported that delay in flowering and maturity during the reproductive stage could affect starch accumulation in grains by reducing photosynthesis and altering sink structure, this finally brings grain yield reduction. On the other hand, grain yield per unit area had highly significant positive correlation with hundred seed weight, panicle width, panicle length and chlorophyll contents at flowering. Therefore, in order to increase grain yield, hundred seed weight, panicle length and chlorophyll contents at flowering should be selected because they have direct relation with this trait. Similarly, Gebrie and Genet (2019) reported higher significant positive correlation of grain yield with panicle width and panicle length and a negative significant correlation with single leaf area and number of leaves. In addition, Legesse (2007); Deepalakshmi and Ganesamurthy (2007), and Mahajan *et al*. (2011) reported similar results.

Table 4. Correlation among 15 traits studied for 945 genotypes evaluated at Sheraro in 2019 cropping season

	LL	DTF	DTM	GYPUA	HSW	LA	LeA	LN	LW	PH	PL	PW	ChCF	ChCM	TN
LL	1														
DTF	0.25**	1													
DTM	0.22**	0.74**	1												
GYPUA	-0.07ns	-0.10ns	-0.12**	1											
HSW	-0.04ns	-0.21**	-0.23**	0.20**	1										
LA	-0.04ns	0.04ns	0.02ns	-0.02ns	0.05ns	1									
LeA	0.75**	0.22**	0.22**	0.01ns	-0.04ns	-0.10**	1								
LN	0.42**	0.38**	0.38**	-0.24**	-0.06ns	0.14**	0.37**	1							
LW	0.29**	0.12**	0.16**	0.03ns	0.01ns	-0.10**	0.76**	0.20**	1						
PH	0.09*	0.12**	0.12**	0.04ns	-0.04ns	0.08ns	0.06ns	0.21**	-0.02ns	1					
PL	0.00ns	-0.16**	-0.16**	0.06ns	0.02ns	-0.03ns	-0.09*	-0.33**	-0.11*	0.25**	1				
PW	-0.10*	-0.26**	-0.24**	0.32**	0.23**	0.08ns	0.01ns	-0.28**	0.06ns	0.23**	0.23**	1			
ChCF	0.00ns	-0.04ns	-0.07ns	0.16**	0.32**	0.10*	-0.05ns	0.01ns	-0.01ns	0.11*	0.10*	0.26**	1		
ChCM	0.30**	0.32**	0.31**	-0.23**	0.01ns	-0.02ns	0.25**	0.55**	0.17**	0.19**	-0.13**	-0.25**	0.31**	1	
TN	0.04ns	0.03ns	-0.01ns	-0.01ns	-0.03ns	0.03ns	0.00ns	-0.04ns	-0.05ns	-0.08ns	0.16**	-0.04ns	-0.04ns	-0.05ns	1

Where, * =significant at 5% probability; ** highly significant at 1% probability; DTF = days of 50% flowering (days); DTM = days of maturity (days); PH = plant height (cm); TN = tiller number (number); LN = leaf number (number); ChCF = Chlorophyll content at flowering (SPAD reading); ChCM = Chlorophyll content at maturity (SPAD reading); PL = panicle length (cm); PW = panicle width (cm); GYPUA = grain yield unit area (g); HSW = hundred seed weight (g); LA = leaf angle (degree); LeA = leaf area (cm^2); LL = leaf length (cm) and LW = leaf width (cm)

4.6. Principal components

In this study, out of total 15, six principal components were extracted having Eigen values >1. These six PCs contributed 69.56% of the total variability amongst the genotypes assessed for various morph-physiological traits (Table 5). However, the remaining 9 components contributed only 30.44% towards the total morph-physiological diversity for this set of genotypes. PC1 contributed the maximum towards the variability (20.59%) followed by PC2 (14.06%), PC3 (10.98%), PC4 (8.95%), PC5 (7.94%) and PC6 (7.01%).

Table 5. Principle component analysis of various morpho-physiological traits in sorghum genotypes under moisture stress condition

Traits	PC1	PC2	PC3	PC4	PC5	PC6
LL	-0.36	0.24	-0.21	0.15	-0.17	0.14
DTF	-0.37	-0.20	0.18	0.28	0.39	-0.04
DTM	-0.37	-0.19	0.18	0.27	0.39	-0.05
GYPUA	0.15	0.35	0.05	0.05	0.51	0.05
HSW	-0.05	0.33	0.20	-0.40	0.06	0.17
LA	-0.03	-0.05	0.31	-0.12	0.11	0.53
LeA	-0.37	0.37	-0.35	0.06	-0.02	0.04
LN	-0.43	-0.07	0.16	-0.13	-0.18	0.16
LW	-0.26	0.34	-0.32	-0.04	0.09	-0.13
PH	-0.02	0.16	0.44	0.41	-0.21	-0.24
PL	0.18	0.22	0.10	0.51	-0.35	0.00
PW	0.15	0.45	0.16	0.14	0.21	-0.01
ChCF	-0.03	0.32	0.45	-0.24	-0.06	-0.01
ChCM	-0.36	0.00	0.25	-0.16	-0.35	-0.14
TN	0.04	-0.01	-0.09	0.30	-0.12	0.74
Eigen value	3.09	2.11	1.65	1.34	1.19	1.05
standard deviation	1.76	1.45	1.28	1.16	1.09	1.03
percent of total variance	20.60	14.06	10.98	8.96	7.95	7.01
comulative variance	20.60	34.66	45.65	54.60	62.55	69.56

DTF = days of 50% flowering (days); DTM = days of maturity (days); PH = plant height (cm); TN = tiller number (number); LN = leaf number (number); ChCF = Chlorophyll content at flowering (SPAD); ChCM = Chlorophyll content at maturity (SPAD reading); PL = panicle length (cm); PW = panicle width (cm); GYPUA = grain yield unit area (g); HSW = hundred seed weight (g); LA = leaf angle (degree); LeA = leaf area (cm^2); LL = leaf length (cm) and LW = leaf width (cm)

Among the six principal components, the first two axes of the PCA were used to draw a biplot to visualize the contribution of traits (Fig. 1). The most important traits in PC 1 (20.6%) was due to variations among the genotypes mainly for leaf length, days to flowering, days to maturity, leaf area, number of leaves, leaf width, grain yield, panicle width and chlorophyll content at maturity. Besides, grain yield per unit area and panicle width had considerable positive factor loadings on PC1. The second principal component (14.1%) was dominated by traits such as panicle width, grain yield, leaf width, leaf area, leaf length, number of leaves, days to flowering, days to maturity and chlorophyll content at maturity. Traits like chlorophyll content at maturity, number of leaves, days to flowering and days to maturity had considerable negative factor loadings on PC2. This implies that these traits are vital for the variation in the genotypes. Since, this experiment was conducted under water stress conditions, the above mentioned traits are reported to be crucial for moisture stress tolerance (Tesso *et al.*, 2011; Sellamuthu *et al.*, 2011). Hence due consideration should be given to the high contributor traits while planning a breeding strategy for improving drought related traits in sorghum. Comparative results were reported by Abraha *et al*. (2015), Ali *et al*. (2011) and Mujaju and Chakuya, (2008) who worked on different agro-morphological traits in sorghum genotypes.

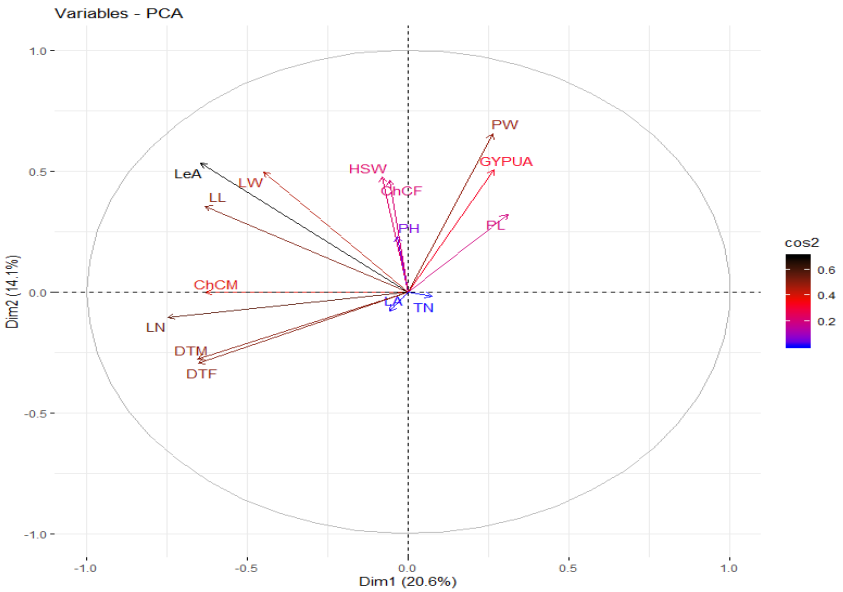

Fig.1. Biplot generated from principal component 1 (PC1) and principal component 2 (PC2) to visualized their contribution level (the color intensity shows their contribution level)

4.7. Population structure

Population structure analysis of 940 genotypes was performed using 5000 SNPs (random subset from 50367). The k value where the cross entropy plot began to plateau was selected as the true k (Francois, 2016). Based on this, genotypes were divided into five subgroups (Fig. 2).

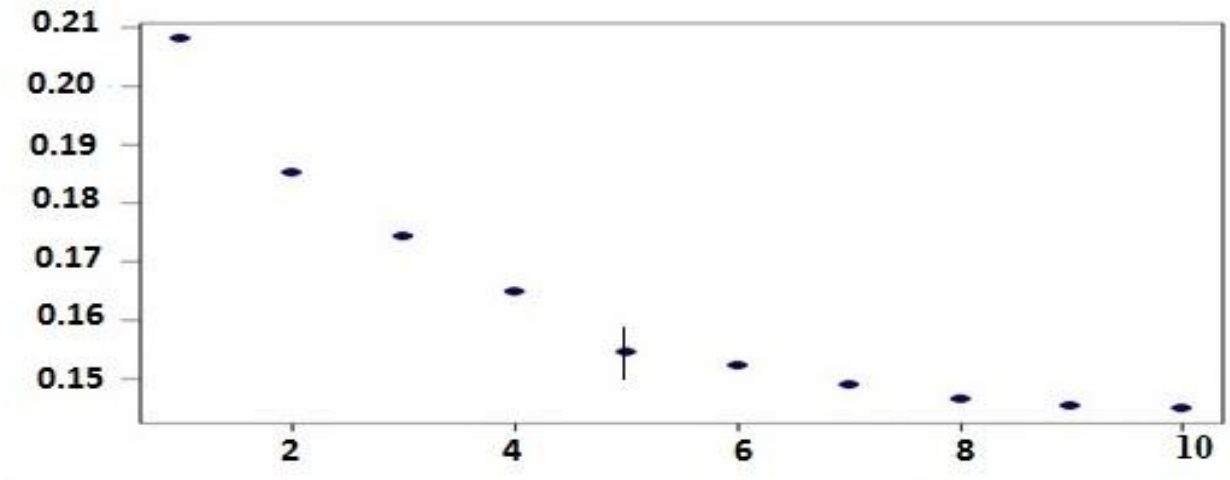

Fig. 2. K values for population grouping, the retained value of k is k = 5

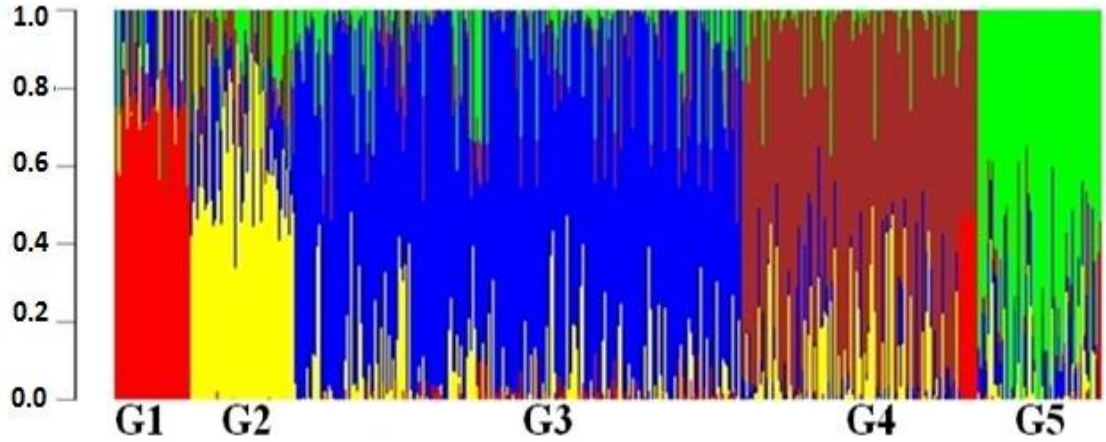

Fig. 3. Population genetic structure of the 940 Ethiopian sorghum genotypes collected from all over the country (G1 = sub population 1 (74 genotypes), G2 = sub-population 2 (98 genotypes), G3 = sub population 3 (425 genotypes), G4 = sub-population 4 (225 genotypes) and G5 = sub-population 5 (118 genotypes))

Genotypes assigned to either one of the 5 sub-populations (Fig. 3); 73.62% of individuals had ancestry membership coefficient greater than 60% and the remaining 26.38% of the individuals represented admixed. The first group (red) consisted of 74 genotypes of which 15 were from Amhara, 30 from Oromia, one from SNNP, one from Afar, 14 from Tigray, three from Gambela four from Benishangul, three from Somali and two from Dire Dawa. The second group (yellow) consisted of 98 genotypes of which nine were from Amhara, 22 from Oromia, 14 from SNNP, one from Afar, 16 from Tigray, 32 from Gambela, one Dire Dawa, one from Somali and two unknown. The third group (blue) consisted of 425 genotypes from which 128 were from Amhara, 88 from Oromia, 33 from SNNP, 22 from Afar, 14 from Tigray, five from Gambela, 25 Dire Dawa, 26 from Somali, five from Benishangul and three unknown. The fourth group (brown) consisted of 225 genotypes of which 56 were from Amhara, 105 from Oromia, 24 from SNNP, three from Afar, 22 from Tigray, nine from Gambela, three Dire Dawa, two from Somali and one unkown. The fifth group consisted of 118 genotypes of which 18 were from Amhara, 14 from Oromia, 26 from SNNP, two from Afar, 12 from Tigray, two from Benishangul, 41 from Gambela and three unknown. The grouping of genotypes does not reflect the region of collection which indicates the presence of wide variations among genotypes within a region as well as absence of strong regional differentiation. The cause might be due to gene flow among the regions, through seed exchange among farmers and migration (movement) of people with seeds from one region to another. (Girma *et al*., 2019; Cuevas et al., 2017 and Atnafu and Bantte, 2010) also reported the existence of different groups of population structure similar to the results of this study.

4.8. Linkage disequilibrium

Linkage disequilibrium (LD) is critical for the design of association studies (Kim *et al*, 2007; Mather *et al.*, 2007), interpretation of association peaks (Huang *et al*., 2010) and the transfer of alleles in marker-assisted selection (Thomson *et al*, 2009). In the present study, the mean r^2 in each chromosome was between 0.11 and 0.13. Based on the threshold r^2 value 0.1, the mean r^2 value started to decay between 50 to 100kb (Fig. 4). The previously published value of LD decay in sorghum was 15-20kb (Hamblin *et al.*, 2005) and 50-100kb (Bouchet *et al*., 2012).

The present results were in agreement with Bouchet *et al*. (2012) but in contrast with that of Hamblin *et al*. (2005). The difference may be due to low genome coverage of markers. As sorghum is a predominantly selfing species, we expect a greater extent of LD than in out-crossing species (Flint-Garcia *et al*., 2003). As LD is broken down by recombination and recombination is not distributed homogeneously across the genome, blocks of LD are expected. Inter-chromosomal LD variation has been reported in maize (Yan *et al*., 2009) and wheat (Zhang *et al*., 2010).

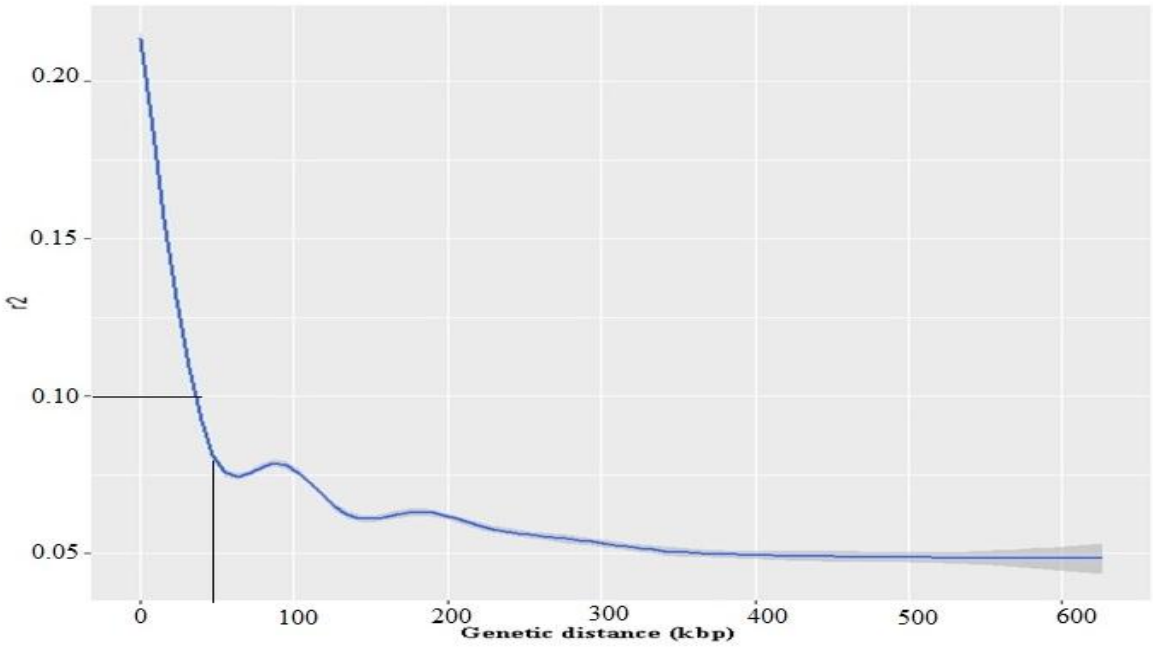

Fig. 4. Linkage disequilibrium decay plot generated by SNP markers (where threshold r^2 value = 0.1)

4.9. GWAS for important drought related traits

Genome wide association studies have been useful in detecting novel marker trait-associations for quantitative traits in various plant species (Korte and Farlow, 2013) including sorghum (Morris *et al*., 2013).

Genome wide association study (GWAS) identified a total of 98 different SNPs with significant association with chromosomal regions for 15 traits with R^2 ranging from 4.88 % to 32.67 % (Table 6 and Fig. 5). Identified SNP markers in the present study may serve as source of markers for the improvement of the crop for drought tolerance related traits after

proper validation. Previously, QTL controlling days to flowering , days to maturity, plant height, leaf area, leaf number, panicle length, panicle width and grain yield were identified on different chromosomes (Reddy *et al*., 2013; Higgins *et al*., 2014; Murphy *et al*., 2014 and Thurber *et al*., 2013). Several GWAS studies also have been done on important traits in sorghum. Zhao *et al*. (2016) reported marker-trait association for plant height, panicle length, leaf angle, flowering time and tiller number on different chromosomes. Morris *et al*. (2013) performed GWAS for plant height and maturity and they reported several loci for plant height and candidate genes for inflorescence. Cuevas *et al*. (2017) studied on Ethiopian sorghum genotypes and reported several loci for plant height and flowering time. Girma *et al*. (2019) also reported significant associations of markers with several traits in Ethiopian sorghum genotypes.

Days to 50% flowering: Four ($p < 5.21E-5$) markers were associated with days to 50 % flowering. Of which, one SNP was from chromosome one, one on chromosome three and two from chromosome five. The SNP explains up to 7.63 % of the phenotypic variation for days of flowering. In total, 4 regions across the genome were identified as having significant associations with days to 50 % flowering. Among these, 13 genes were identified on chromosome three in the interval of 55.85 Mbp and 55.90 Mbp and three on chromosome five between 63.06 Mbp and 63.16 Mbp using sorghum genome Assembly online data base (NCBIv3.1) (Fig. 5). The identified regions were hypothetical in their functions. Therefore, further study will be needed to know the function of identified genes. Previously, 60 QTL were identified on chromosome one, 34 QTL on three and 19 QTL on chromosome five (https://aussorgm.org.au › sorghum-qtl-atlas). The present results are similar to identified QTL earlier.

Plant height: a total of six SNP markers were associated with plant height. Of which, one SNP was from chromosome one, two on chromosome three, one on chromosome four, one on chromosome five and one on chromosome 10. These SNPs accounted for up to 21.85 % of the total phenotypic variance for the trait. Using sorghum genome Assembly online data base (NCBIv3.1) 23 genes were identified in the plant height associated regions on chromosome three with linkage group between 11.91 Mbp and 12.01 Mbp (Fig. 6). The identified genes were hypothetical; their functions are not yet known. Therefore, further study will be needed

to know the function of these genes. Previously, 28 QTL on chromosome one, 21 on chromosome three, 20 on chromosome four, nine on chromosome five and 14 on chromosome ten were reported (https://aussorgm.org.au › sorghum-qtl-atlas). These reported results are in agreement with the results of the present study.

Numbers of leaves: a total of nineteen ($p < 5.21E-5$) SNP markers were associated with number of leaves. Of which, four SNPs were from chromosome one, two on chromosome two, two on chromosome three, one on chromosome four, four on chromosome five, two on chromosome six, one on chromosome seven, one on chromosome nine and two on chromosome 10. These SNPs accounted for up to 26.54% of the total phenotypic variance for number of leaves. Among identified SNPs, on chromosome three SBRI-3003G301800 was detected between 63,24Mbp and 63,34Mbp, which is homologous to the rice gene OSPPC3 on chromosome one between 31.85 Mbp – 31.86 Mbp linkage group (*sorghum bicolor* - Ensembl genome 45 - NCBIv3.1). The obtained gene produces phosphoenolpyruvate carboxylase (PEPCase) which has great role during C4 photosynthesis and involved and stomatal opening (Cousins *et al*., 2007). In addition, PEPCase plays a crucial role in modulating the balance of carbon and nitrogen metabolism in Arabidopsis leaves (Shi *et al*., 2015). Before twelve QTL, three on chromosome one, six on chromosome three, one on chromosome seven, one on chromosome nine and one chromosome ten were identified (https://aussorgm.org.au › sorghum-qtl-atlas). These reported results are similar to the present study.

Chlorophyll content at maturity: a total of eight ($p < 5.21E-5$) SNP markers were associated with chlorophyll content at maturity. Of which, one SNP was from chromosome one, two on chromosome four, one on chromosome five, three on chromosome nine and one on chromosome 10. These SNPs accounted for up to 14.38 % of the total phenotypic variance. Among identified markers, one gene on chromosome four encodes SBRI_3004G128500 between 16.20Mbp and 16.30Mbp and produce nucleolin protein (*sorghum bicolor* - Ensembl genome 45 - NCBIv3.1). The principal function of the nucleolin is rRNA synthesis and ribosome biogenesis and involved in many aspects of cell biology such as gene silencing, senescence and cell cycle regulation (Olson *et al*., 2000). The function of nucleolin protein has been previously reported on Arabidopsis by Patricka and Nelson (2007).

Hundred seed weight: a total of seven (p < 5.21E-5) SNP markers were associated with hundred seed weight. Of which, 3 SNPs were from chromosome one, one on chromosome five, one on chromosome six, one on chromosome seven and one on chromosome 10. These SNPs accounted for up to 21.16 % of the total phenotypic variance for the trait. From the identified regions, on chromosome 10, SORBI_3010G170600 gene was detected between 50.20Mbp and 50.30Mbp; which is homologous to rice HSFA6 gene (21.761Mbp to 21.762Mpb) (*sorghum bicolor* - Ensembl genome 45 - NCBIv3.1). The product of the obtained gene is heat stress transcription factor A-6 protein, which play a crucial role in plants response to several abiotic stresses by regulating the expression of stress-responsive genes, such as heat shock proteins (*Hsps*) (Guo *et al*., 2016). Heat shock proteins are crucial in protecting plants against stress by reestablishing normal protein conformation (Wang *et al*., 2004). It has been reported that high temperature changed the properties of membranes of nucleus, endoplasmic reticulum, mitochondria and chloroplasts of rice (*Oryza sativa*) (Shah *et al*., 2011). Cho and Hong, (2006) have been reported that higher levels of heat shock protein in tobacco showed more resistant to drought stress.

Panicle length: a total of thirteen (p < 5.21E-5) SNP markers were associated with panicle length. Of which, one SNP was from chromosome one, one on chromosome two, two on chromosome three, five on chromosome six, one on chromosome seven, one on chromosome eight, one on chromosome nine and one on chromosome 10. These SNPs accounted for up to 32.67 % of the total phenotypic variance for the trait. Among identified SNP regions, SORBI_3006G176700 gene was identified on chromosome 6 between 53.192 Mbp and 53.194 Mbp interval which is homologous to rice OsPIP1 gene on chromosome 2 (27.04Mbp - 27.047Mbp) (*sorghum bicolor* - Ensembl genome 45 - NCBIv3.1). PIP1 proteins are usually present in the plasma membrane (Wayne and Tazawa, 1990) and are considered to have low water permeability (Chaumont *et al*., 2000). In tobacco (*Nicotiana tabacum*) plant, reducing the expression of NtAQP1, a member of the PIP1 family, caused a decline of root hydraulic conductivity and decreased resistance of plants to water stress. In pea (*Pisum sativum*), PIP1 was demonstrated to play an important role in water absorption during seed water uptake (Kaldenhoff and Fisher, 2006). In addition, 33 QTL were identified on chromosome one, 25 on chromosome two, 20 on chromosome three, 21 on chromosome six, 20 on chromosome

seven, 11 on chromosome eight, 8 on chromosome nine and 13 on chromosome ten were reported. These are similar to the results of the present study.

Number of tillers: Three ($p < 5.21E-5$) SNP markers were associated with number of tillers. Of which, one SNP was from chromosome two, one on chromosome four and one on chromosome seven. These SNPs accounted for up to 8.32 % of the total phenotypic variance for the trait. Among identified markers, on chromosome four between 3.55Mbp and 3.56Mbp SORBI_3004G044000 gene was identified which is homologous to rice YL1 (2:2922461-2925073bp) gene (*sorghum bicolor* - Ensembl genome 45 - NCBIv3.1). This gene produces Nucleus-encoded chloroplast protein, which is important in chloroplast development and biogenesis of chloroplast ATP (Chen *et al*., 2016). In addition, 14 QTL on chromosome two, 15 on chromosome four and eight on chromosome seven were reported (https://aussorgm.org.au › sorghum-qtl-atlas). These results are in agreement with the present study.

Leaf angle: Three ($p < 5.21E-5$) SNP markers were associated with leaf angle. Of which, one SNP was on chromosome four, one on chromosome five and one on chromosome nine. These SNPs accounted for up to 6.99 % of the total phenotypic variance for the trait. Previously, one QTL was identified on chromosome four, one on chromosome five and one on chromosome nine (https://aussorgm.org.au › sorghum-qtl-atlas). These results are in agreement with the present study.

Numbers of leaves: A total of nineteen SNP markers were associated with number of leaves. Of which, four SNPs were from chromosome one, two on chromosome two, two on chromosome three, one on chromosome four, four on chromosome five, two on chromosome six, one on chromosome seven, one on chromosome nine and two on chromosome 10. These SNPs accounted for up to 26.54 % of the total phenotypic variance for the trait. Twelve QTL; three on chromosome one, six on chromosome three, one on chromosome seven, one on chromosome nine and one chromosome ten were previously identified (https://aussorgm.org.au › sorghum-qtl-atlas). These reported results are similar to the present study.

Leaf area: A total of 10 ($p < 5.21E-5$) SNP markers were associated with leaf area. Of which, two SNPs were from chromosome one, one on chromosome two, three on chromosome three,

one on chromosome four, two on chromosome six, one on chromosome seven and one on chromosome nine. These SNPs accounted for up to 21.55 % of the total phenotypic variance for the trait. Previously, 17 QTL were identified on chromosome one, 13 QTL on chromosome two, 15 on chromosome three, nine on chromosome four, four on chromosome six and one on chromosome seven (https://aussorgm.org.au › sorghum-qtl-atlas). These reported results were in agreed with the present study at chromosomal level.

Grain yield: Two significant ($p < 5.21E-5$) SNP markers were associated with grain yield per unit area. Of which, one SNP was from chromosome four and one on chromosome five. These SNPs accounted for up to 5.83% of the total phenotypic variance for the trait. Previously, six QTL were found for grain yield; three on chromosome 9 and one on chromosome 3, 4 and 6 (Reddy *et al*., 2013).

Leaf width: A total of seven SNP markers were associated with leaf width. Of which, three SNPs were from chromosome one, two on chromosome two, one on chromosome five and one on chromosome six. These SNPs accounted for up to 20.17 % of the total phenotypic variance for the trait. No QTL were detected for leaf width in the previous study.

Panicle width: One SNP marker located on chromosome nine was associated with panicle width. This SNP accounted for up to 4.88 % of the total phenotypic variance. Previously, two QTL on chromosome nine were reported (https://aussorgm.org.au › sorghum-qtl-atlas). This result is similar to ours.

Chlorophyll content at flowering: A total of four significant SNPs markers were associated with chlorophyll content at flowering. Of which, one SNP was from chromosome one, one on chromosome four, one on chromosome six and one on chromosome eight. These SNPs accounted for up to 12.58 % of the total phenotypic variance for the trait.

Leaf length: A total of eight significant SNPs markers were associated with leaf length. Of which, one SNP was from chromosome one, one on chromosome three, one on chromosome four, one on chromosome five, one on chromosome six, two on chromosome eight and one on chromosome nine. These SNPs accounted for up to 12.01 % of the total phenotypic variance. Previously, nine QTL were identified on chromosome one, two on chromosome

three, five on chromosome four, one on chromosome six, four on chromosome eight and one on chromosome nine were reported(https://aussorgm.org.au › sorghum-qtl-atlas). These reported results are in agreement with the present study at chromosomal level.

Table 6. Summary of significant single nucleotide polymorphisms (SNPs) representing different regions across sorghum chromosome for the 15 traits

Traits	QTL	Chr	Marker position	P.value	R^2
DTF	QTLDTF1.1	1	20561181	1.593E-05	0.072244
	QTLDTF3.1	3	55904203	1.022E-05	0.069443
	QTLDTF5.1	5	33883660	3.304E-06	0.076285
	QTLDTF5.2	5	63115586	4.8E-05	0.076305
DTM	QTLDTM1.1	1	54747637	2.15E-07	0.129389
	QTLDTM2.1	2	66843065	6.688E-07	0.13458
	QTLDTM9.1	9	5932168	4.669E-05	0.129182
LeA	QTLLeA1.1	1	16484825	1.912E-10	0.210163
	QTLLeA1.2	1	21735985	7.443E-11	0.215537
	QTLLeA2.1	2	6235899	3.427E-05	0.207981
	QTLLeA3.1	3	4872822	8.144E-06	0.209756
	QTLLeA3.2	3	8976977	1.807E-06	0.207933
	QTLLeA3.3	3	60693861	1.838E-05	0.207855
	QTLLeA4.1	4	16552112	3.172E-05	0.212167
	QTLLeA6.1	6	8636143	5.389E-06	0.206446
	QTLLeA6.2	6	38732636	2.777E-05	0.203624
	QTLLeA7.1	7	61272200	2.429E-07	0.203269
LN	QTLLN1.1	1	8248365	4.117E-05	0.254172
	QTLLN1.2	1	8254890	2.001E-05	0.254034
	QTLLN1.3	1	18246011	2.767E-06	0.260014
	QTLLN1.4	1	60848821	6.611E-11	0.260594
	QTLLN2.1	2	2174885	1.002E-05	0.258155
	QTLLN2.2	2	47362865	9.487E-08	0.253683
	QTLLN3.1	3	56373218	4.072E-06	0.25944
	QTLLN3.2	3	63291023	6.307E-12	0.248926
	QTLLN4.1	4	18704309	4.451E-06	0.256668
	QTLLN5.1	5	56933525	7.167E-10	0.261964
	QTLLN5.2	5	69914317	5.279E-10	0.265447
	QTLLN5.3	5	70344913	5.389E-07	0.262357
	QTLLN5.4	5	70541274	1.427E-08	0.252666
	QTLLN6.1	6	1301680	1.577E-07	0.263449
	QTLLN6.2	6	50806153	1.75E-09	0.264828
	QTLLN7.1	7	735933	1.679E-06	0.262689
	QTLLN9.1	9	56055915	9.578E-07	0.259634
	QTLLN10.1	10	2411592	2.832E-08	0.261075
	QTLLN10.2	10	57210251	8.74E-14	0.260547

Table 6 (continued)

Traits	QTL	Chr	Marker position	P.value	R^2
LA	QTLLA4.1	4	51084190	2.754E-05	0.064833
	QTLLA5.1	5	59563978	1.102E-05	0.067364
	QTLLA9.1	9	462461	3.168E-05	0.069919
ChCM	QTLChCM1.1	1	30269892	2.866E-05	0.143715
	QTLChCM4.1	4	5437839	2.581E-05	0.137643
	QTLChCM4.2	4	16256273	4.51E-06	0.128563
	QTLChCM5.1	5	71680491	4.323E-05	0.143784
	QTLChCM9.1	9	4072754	2.273E-05	0.135446
	QTLChCM9.2	9	41434687	5.049E-05	0.135077
	QTLChCM9.3	9	55592996	4.279E-05	0.140972
	QTLChCM10.1	10	7439036	1.666E-06	0.134898
PH	QTLPH1.1	1	9570516	1.302E-06	0.215998
	QTLPH3.1	3	11960865	1.426E-07	0.212738
	QTLPH3.2	3	68619359	7.777E-07	0.216683
	QTLPH4.1	4	53337251	4.647E-05	0.210651
	QTLPH5.1	5	65930956	3.079E-05	0.20603
	QTLPH10.1	10	12119168	1.884E-06	0.218496
TN	QTLTN2.1	2	59202176	4.446E-05	0.07909
	QTLTN4.1	4	3608487	1.124E-06	0.065713
	QTLTN7.1	7	61831543	1.161E-05	0.083226
LL	QTLLL1.1	1	73656429	1.565E-05	0.109396
	QTLLL3.1	3	7101805	2.808E-07	0.11531
	QTLLL4.1	4	53812009	3.961E-05	0.115674
	QTLLL5.1	5	68952399	3.602E-05	0.109878
	QTLLL6.1	6	51365781	2.613E-07	0.104356
	QTLLL8.1	8	38511324	1.167E-05	0.108069
	QTLLL8.1	8	55644540	9.816E-11	0.120111
	QTLLL9.1	9	2663496	2.047E-05	0.111932
LW	QTLLW1.1	1	16484825	5.21E-06	0.194461
	QTLLW1.2	1	21735985	5.178E-08	0.201695
	QTLLW1.3	1	75298487	9.542E-06	0.186875
	QTLLW2.1	2	5745493	2.278E-07	0.187838
	QTLLW2.2	2	76427071	1.003E-07	0.197641
	QTLLW5.1	5	4321731	7.456E-06	0.193069
	QTLLW6.1	6	390629	3.447E-07	0.188756
PL	QTLPL1.1	1	79767363	9.458E-07	0.315223
	QTLPL2.1	2	387787	8.124E-07	0.327557
	QTLPL3.1	3	56295971	3.821E-06	0.321172
	QTLPL3.2	3	60215678	3.633E-06	0.327325
	QTLPL6.1	6	42392329	2.789E-07	0.324118
	QTLPL6.2	6	45084509	1.772E-06	0.325424
	QTLPL6.3	6	47613362	1.799E-10	0.323842
	QTLPL6.4	6	49801708	6.502E-08	0.323716

Table 6 (continued)

Traits	QTL	Chr	Marker Position	P.value	R^2
PL	QTLPL6.5	6	53235367	2.04E-13	0.326744
	QTLPL7.1	7	57661917	9.467E-07	0.322895
	QTLPL8.1	8	1748926	1.764E-06	0.32318
	QTLPL9.1	9	48960463	4.312E-05	0.315816
	QTLPL10.1	10	40204351	4.356E-06	0.31749
PW	QTLPW9.1	9	3321322	4.723E-05	0.048829
ChCF	QTLChCF1.1	1	53454401	3.865E-08	0.109634
	QTLChCF4.1	4	9482945	2.376E-08	0.125831
	QTLChCF6.1	6	1783682	7.88E-09	0.111765
	QTLChCF8.1	8	54819764	2.153E-06	0.108017
GY	QTLGY4.1	4	59499734	5.637E-06	0.056845
	QTLGY5.1	5	485978	7.893E-06	0.058277
HSW	QTLHSW1.1	1	22035494	6.466E-09	0.210568
	QTLHSW1.2	1	30569756	1.861E-05	0.198925
	QTLHSW1.3	1	71717987	3.571E-05	0.20595
	QTLHSW1.4	1	80849846	5.239E-07	0.210278
	QTLHSW5.1	5	2879991	2.46E-05	0.207631
	QTLHSW6.1	6	60296888	5.338E-07	0.201987
	QTLHSW7.1	7	6527837	7.078E-06	0.202046
	QTLHSW10.1	10	50253862	5.142E-14	0.211609

DTF = days to 50% flowering (days); DTM = days to maturity (days); PH = plant height (cm); TN = tiller number (number); LN = leaf number (number); ChCF = Chlorophyll content at flowering (SPAD reading); ChCM = Chlorophyll content at maturity (SPAD reading); PL = panicle length (cm); PW = panicle width (cm); GYPUA = grain yield unit area (g); HSW = hundred seed weight (g); LA = leaf angle (degree); LeA = leaf area (cm^2); LL = leaf length (cm) and LW = leaf width (cm)

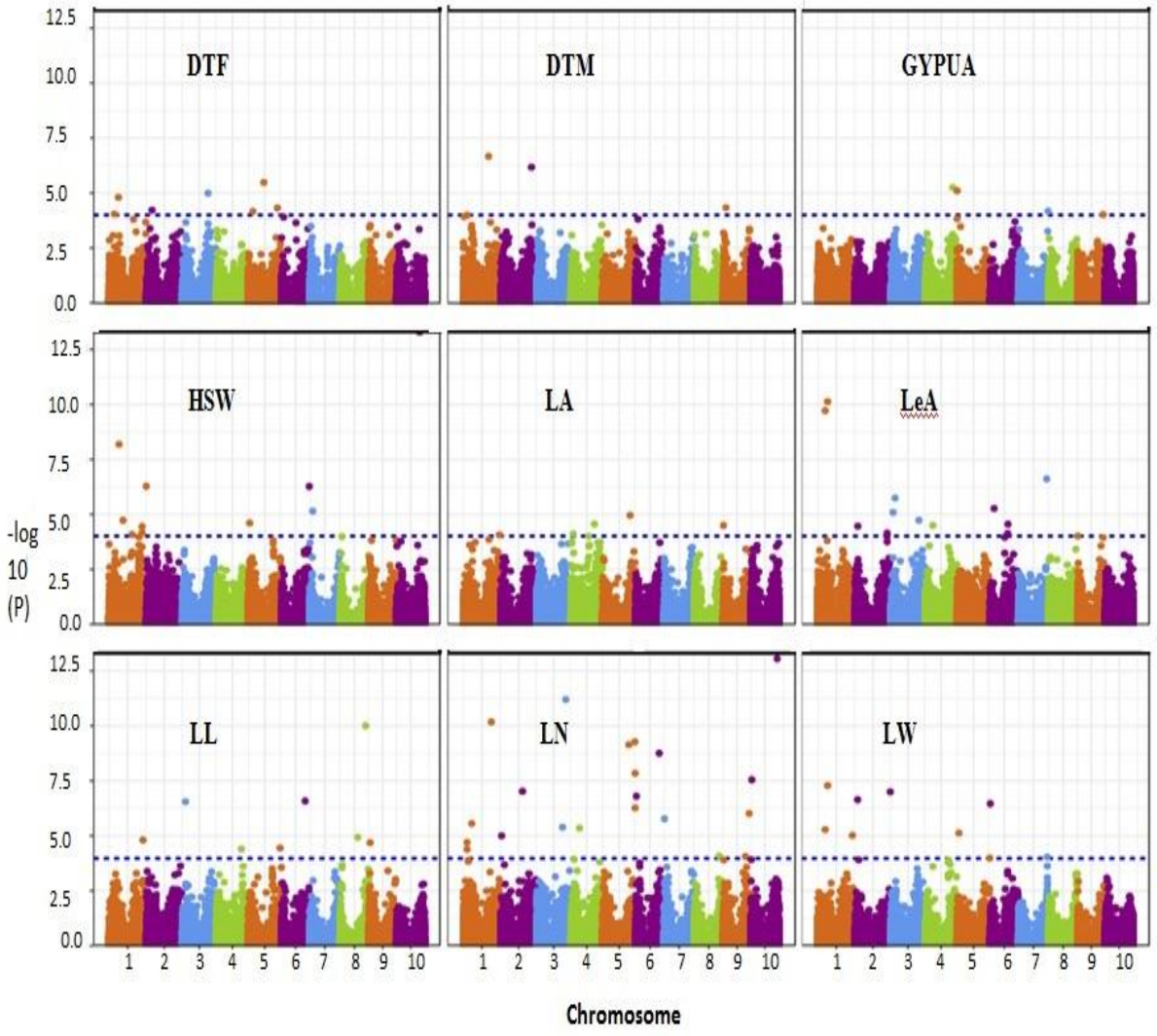

Fig. 5. GWAS across 940 Ethiopian sorghum genotypes using 25637 SNP markers and Manhattan plots showing significant SNP markers at MAF > 0.01 for 15 traits.

DTF = days to 50% flowering (days); DTM = days to maturity (days); PH = plant height (cm); TN = tiller number (number); LN = leaf number (number); ChCF = Chlorophyll content at flowering (SPAD reading); ChCM = Chlorophyll content at maturity (SPAD reading); PL = panicle length (cm); PW = panicle width (cm); GYPUA = grain yield unit area (g/m^2); HSW = hundred seed weight (g); LA = leaf angle (degree); LeA = leaf area (cm^2); LL = leaf length (cm) and LW = leaf width (cm).

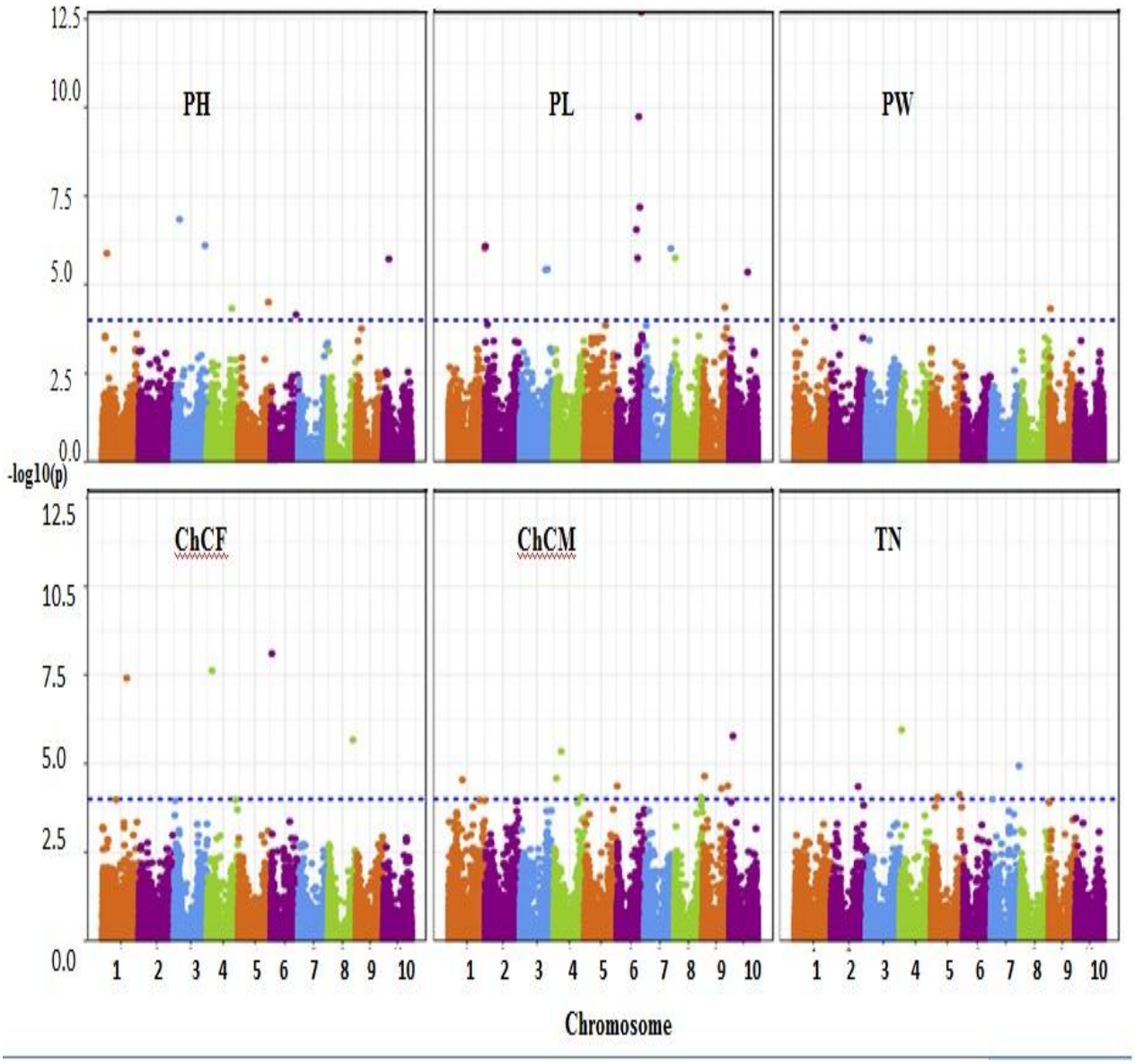

Fig. 5 (continued)

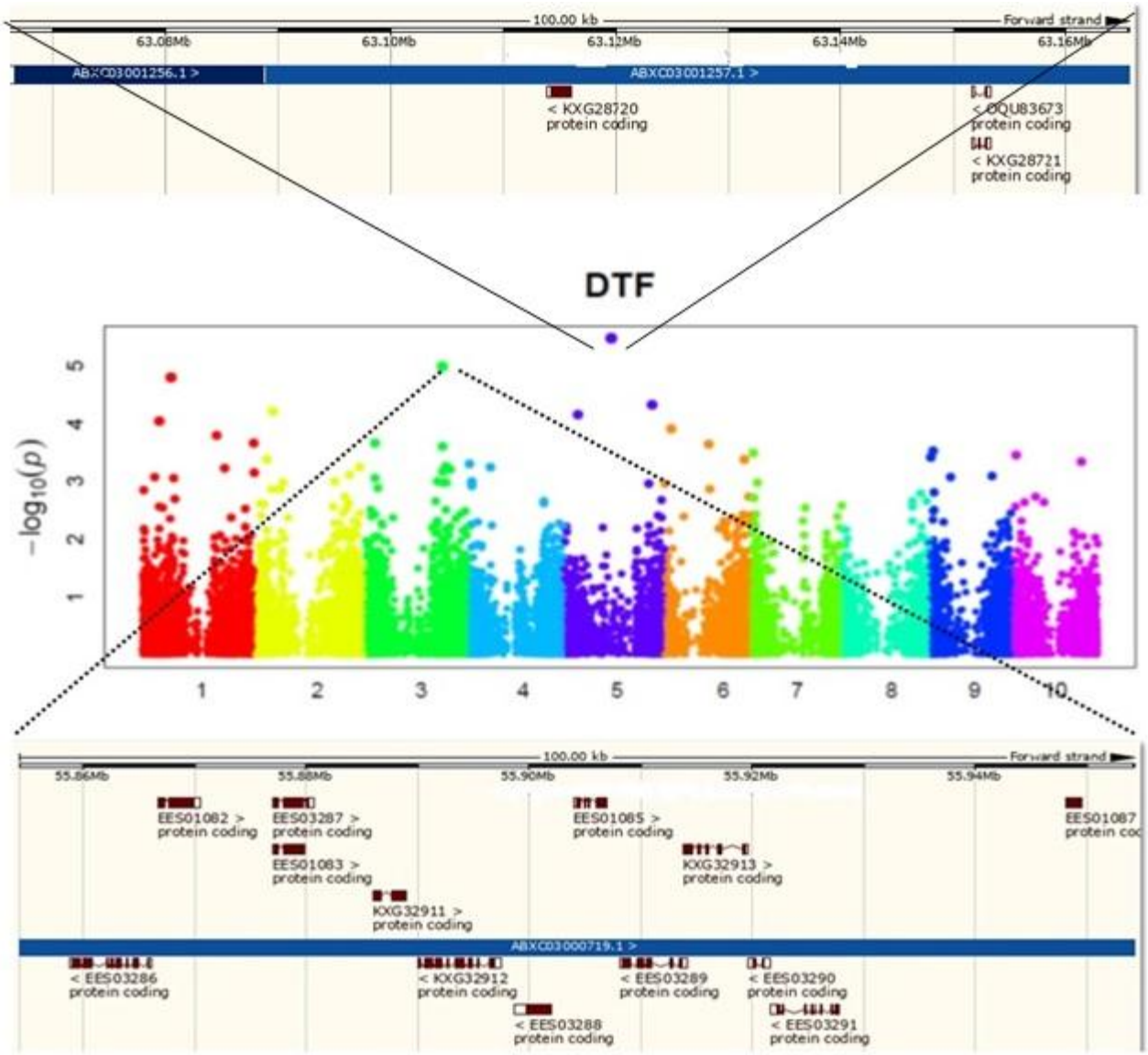

Fig. 6. The gene identified from day to flowering at chromosome three and five at highly significant p-value

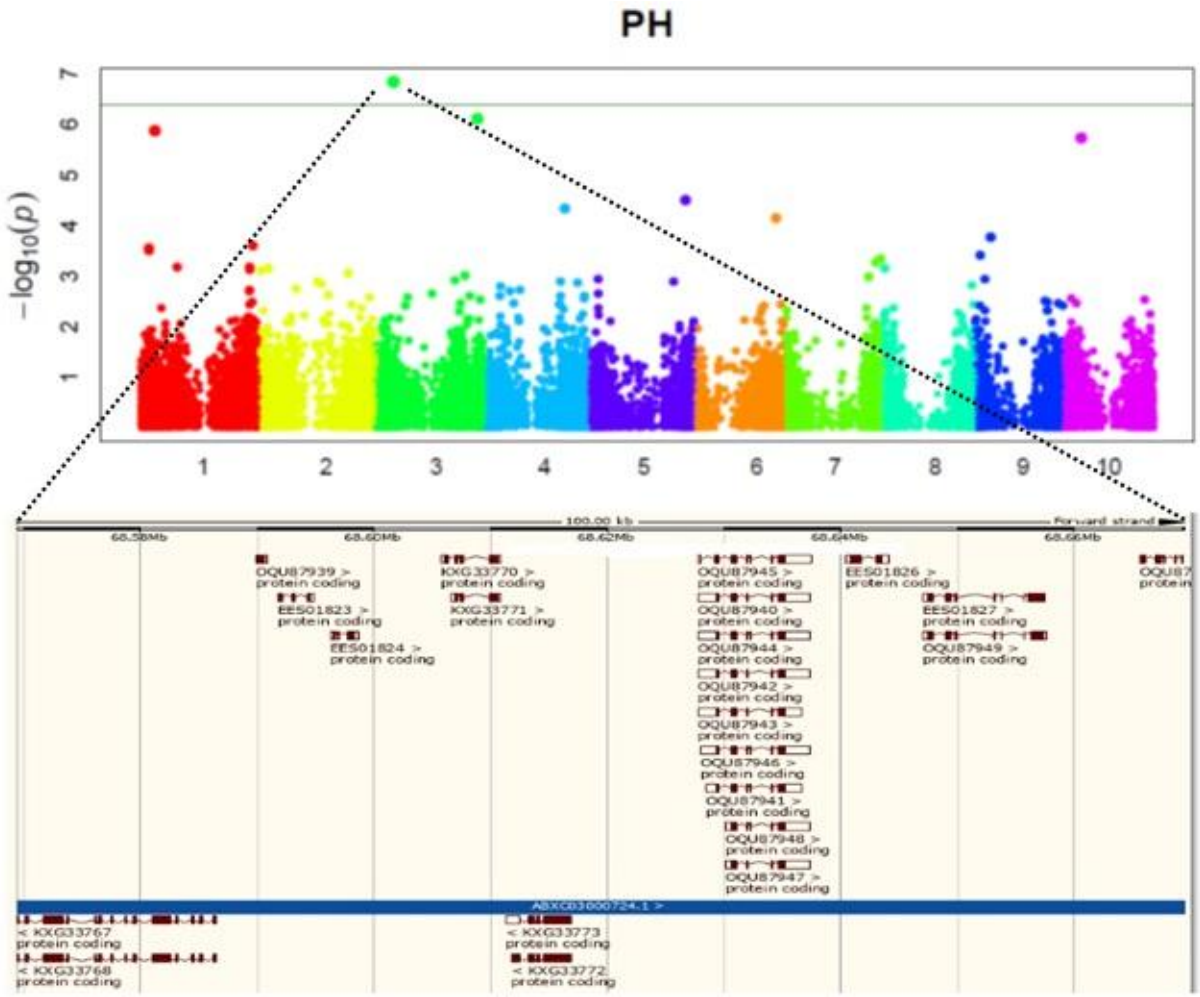

Fig. 7. The gene identified from plant height on chromosome three at highly significant p-value

5. SUMMARY AND CONCLUSIONS

Sorghum (*Sorghum bicolor* (L.) Moench) is the most important food cereal in Ethiopia next to maize and teff with a total production of 4.48 million tons in 1.8 million hectare. It has a lot of uses; in making *injera*, traditional pancake bread, porridge, local beverages and the stalk also uses for construction, animal feed and fire wood. However, the production of this crop is limited due to various biotic and abiotic factors. Among abiotic factors, drought is the main problem that affects the production and productivity of sorghum.

Drought is a complex trait which is controlled by many genes coding for various characters. Knowledge of genetic variability for drought related traits is the key component in selecting genotypes that withstand drought for the future breeding program. In addition, genetic improvement of quantitative trait like drought depends on the nature and amount of variability present in any genetic stock. Therefore, systematically evaluating the genotypes uses to know the difference of the studied genotypes and increases our potential genetic resources which has important role in improving quantitative traits. So, using genome wide association study it is easy to identify significantly associated marker for each drought related traits and this help us to minimize the challenge faced by drought.

In the present study, 945 sorghum genotypes was evaluated using alpha lattice design with two replications having 63 blocks per replication and fifteen experimental units per block. Five plants per plot were randomly selected from each genotype to record morphological data which is related to drought tolerance. The recorded morphological data were Chlorophyll contents, days to flowering, days to maturity, plant height, leaf length, leaf width, single leaf area, number of tillers, panicle length, panicle width, leaf angle, number of leaves, grain yield and hundred seeds weight were collected based on sorghum descriptor IBPGR and ICRISAT, 1993.

The analysis of variances showed highly significant difference for all the traits ($p<0.01$) indicating the presences of subtential variation among the tested sorghum genotypes. Moderate to high phenotypic and genotypic coefficient of variation was observed for most traits.

The GCV ranged from 2.75 % for days of maturity to 29 % for leaf angle while PCV ranged from 3.81 % for days of maturity to 31.53 % for leaf angle. The PCV was relatively greater than GCV for all the traits recorded in this study but the magnitude was low. This shows that the influences of environmental factors for the phenotype expression of genotypes were low. As a result, there is high chance of improvement of these traits through selection based on the phenotype performance. The heritability in broad sense runs from 52.05 % for days to maturity to 92.55 % for Number of leaves. All of the traits showed high and moderate heritability. High heritability shows the minimum environmental influence. Therefore, any of traits (Table 2) with high and moderate heritability can be used for selection. The other very important in estimating genetic variability is genetic advance. It shows the degree of gain obtained in a character under a particular selection pressure. High genetic advance as percent of mean was recorded for leaf angle (57.38 %) and low for days of maturity (4.09 %). High values of genetic advance indicate the presence of additive gene actions while low values for non-additive gene action but for effective selection both heritability and genetic gain should be considered. The correlation coefficient showed significant positive and negative association along traits. In the principal component analysis, the first six principal components with eigen values greater than one accounted for 69.56 % of the total genotypic variation and the genotypes were grouped into five sub-groups.

For genome wide association studies, Markers with MAF <1 % were filtered out. The remaining 25634 SNPs were used by for genome-wide association study (GWAS). A total of 98 different SNPs were associated with different 15 studied traits. From the studied traits, the highest marker trait association was recorded for leaf number (19) followed by panicle length (13), while the lowest number of marker trait association was recorded for panicle width (1). These identified marker trait association which could be useful in marker assisted selection.

Generally, the analysis of genetic parameters in the current study indicated that there are heritability of quantitative traits that control morpho-physiological traits with related to drought were there. Traits like days to flowering, days to maturity, number of leaves and leaf length showed highly negative correlation with grain yield. Negative correlation is desirable

for these traits; less number of days to flowering and days to maturity reduce the crop duration which are helpful interims of economic cultivation of sorghum genotypes. On the other hand, genome wide association study indentifies 98 significant SNPs. These SNPs were identified from different drought related traits and agronomic traits at different chromosome and regions. Therefore, the identified markers serve as a source for future breeding program to improve traits which are related to drought and other agronomic traits. Finally, based on present investigation, the following recommendations were suggested.

- In the studied sorghum genotypes trait like days to flowering, days to maturity, number of leaves, leaf area and chlorophyll content at maturity are major contributors to total variation under moisture stress condition; hence, these traits could be potential candidates for further evaluation and selection.
- The studied sorghum genotypes were grouped into five subgroups with regional independency. Therefore, further studies should be done based on their altitude variation.
- A number of marker-trait associations were identified in GWAS. The identified marker-trait association need to be validated and finally can be used by breeder(s) for sorghum drought tolerance and other agronomic trait improvement.

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7. APPENDIX

Appendix Table 1. List of sorghum genotypes used in the study arranged according to their collection regions and zone

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
1	JUS171645	Amara	Misrak Gojam	25	JUS171369	SNNP	Bench Maji
2	JUS171639	Amara	Semen Gondar	26	JUS171746	Amara	Semen Gondar
3	JUS171480	Oromiya	Mirab Shewa	27	JUS171223	Amara	Debub Wello
4	JUS171325	Amara	Semen Shewa	28	JUS171435	Oromiya	Misrak Shewa
5	JUS171380	Oromiya	Semen Shewa	29	JUS171241	Affar	Zone 1
6	JUS171741	Amara	Semen Gondar	30	JUS171538	Amara	Semen Gondar
7	JUS171403	Oromiya	Arsi	31	JUS171321	Tigray	Debubawi
8	JUS171757	Amara	Debub Wello	32	JUS171779	Amara	Semen Gondar
9	JUS171422	SNNP	Hadiya	33	JUS171599	Amara	Semen Gondar
10	JUS171509	Gambella	Zone 1	34	JUS171597	SNNP	Bench Maji
11	JUS171289	Tigray	Mirabawi	35	JUS171463	Oromiya	Semen Shewa
12	JUS171358	Amara	Semen Shewa	36	JUS171506	Gambella	Zone 1
13	JUS171475	Oromiya	Semen Shewa	37	JUS171784	Amara	Debub Wello
14	JUS171259	Amara	Semen Wello	38	JUS171472	Oromiya	Semen Shewa
15	JUS171700	Oromiya	Mirab Shewa	39	JUS171316	Tigray	Debubawi
16	JUS171622	Oromiya	Misrak Wellega	40	JUS171378	SNNP	Bench Maji
17	JUS171560	Amara	Semen Wello	41	JUS171627	Oromiya	Misrak Shewa
18	JUS171534	Amara	Semen Gondar	42	JUS171792	Tigray	Mehakelegnaw
19	JUS171521	Amara	Debub Wello	43	JUS171666	Tigray	Mirabawi
20	JUS171290	Tigray	Mirabawi	44	JUS171660	Tigray	Mehakelegnaw
21	JUS171615	Tigray	Mehakelegnaw	45	JUS171520	Oromiya	Illubabor
22	JUS171503	SNNP	Bench Maji	46	JUS171677	Tigray	Debubawi
23	JUS171711	Tigray	Mehakelegnaw	47	JUS171547	Tigray	Mehakelegnaw
24	JUS171782	Amara	Semen Gondar	48	JUS171344	Amara	Semen Shewa

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
49	JUS171508	Oromiya	Misrak Shewa	73	JUS171291	Tigray	Mirabawi
50	JUS171638	Amara	Debub Gondar	74	JUS171766	Oromiya	Misrak Harerge
51	JUS171460	Amara	Misrak Gojam	75	JUS171640	Amara	Semen Gondar
52	JUS171544	Amara	Debub Gondar	76	JUS171352	Amara	Semen Shewa
53	JUS171637	Amara	Semen Gondar	77	JUS171252	Amara	Semen Wello
54	JUS171537	Amara	Debub Gondar	78	JUS171387	Oromiya	Mirab Shewa
55	JUS171649	Amara	Agew Awi	79	JUS171505	Gambella	Zone 1
56	JUS171754	Amara	Oromiya	80	JUS171464	Oromiya	Semen Shewa
57	JUS171519	Oromiya	Mirab Harerge	81	JUS171515	Amara	Semen Wello
58	JUS171542	Amara	Debub Gondar	82	JUS171349	Amara	Semen Shewa
59	JUS171385	Oromiya	Mirab Shewa	83	JUS171786	Amara	Debub Wello
60	JUS171625	SNNP	Sidama	84	JUS171562	Amara	Semen Wello
61	JUS171500	Oromiya	Misrak Wellega	85	JUS171574	Amara	Debub Wello
62	JUS171478	Oromiya	Semen Shewa	86	JUS171623	Oromiya	Illubabor
63	JUS171556	Oromiya	Mirab Harerge	87	JUS171345	Amara	Semen Shewa
64	JUS171652	Oromiya	Bale	88	JUS171641	Tigray	Debubawi
65	JUS171414	Oromiya	Misrak Shewa	89	JUS171512	SNNP	Bench Maji
66	JUS171163	Tigray	Debubawi	90	JUS171686	Oromiya	Borena
67	JUS171441	SNNP	Sidama	91	JUS171280	Tigray	Mirabawi
68	JUS171248	Affar	Zone 1	92	JUS171368	SNNP	Bench Maji
69	JUS171496	Amara	Debub Wello	93	JUS171807	Amara	Semen Gondar
70	JUS171329	Amara	Semen Shewa	94	JUS171447	Oromiya	Semen Shewa
71	JUS171665	Tigray	Mirabawi	95	JUS171459	Amara	Misrak Gojam
72	JUS171808	Somali	Jigjiga	96	JUS173351	Oromiya	Mirab Harerge

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
97	JUS173360	SNNP	Bench Maji	121	JUS173343	Tigray	Debubawi
98	JUS173389	Tigray	Debubawi	122	JUS173391	Tigray	Mirabawi
99	JUS171251	Amara	Semen Wello	123	JUS171395	Amara	Semen Gondar
100	JUS161002	Oromiya	Mirab Shewa	124	JUS161004	Oromiya	Mirab Harerge
101	JUS161329	SNNP	Bench Maji	125	JUS161331	Tigray	Misrakawi
102	JUS173221	Gambella	Zone 1	126	JUS173219	Affar	Zone 1
103	JUS173421	SNNP	Bench Maji	127	JUS173214	Affar	Zone 1
104	JUS173361	Tigray	Debubawi	128	JUS173358	Tigray	Mirabawi
105	JUS173367	Tigray	Mirabawi	129	JUS173368	Tigray	Mirabawi
106	JUS173373	SNNP	Bench Maji	130	JUS173376	Tigray	Mirabawi
107	JUS171590	Tigray	Misrakawi	131	JUS171334	Amara	Semen Shewa
108	JUS173350	Tigray	Debubawi	132	JUS173356	Tigray	Mirabawi
109	JUS173344	Tigray	Debubawi	133	JUS173372	Tigray	Debubawi
110	JUS173390	SNNP	Bench Maji	134	JUS171168	Oromiya	Mirab Harerge
111	JUS171593	Amara	Semen Gondar	135	JUS171298	Tigray	Mirabawi
112	JUS161003	Oromiya	Misrak Wellega	136	JUS161325	Oromiya	Illubabor
113	JUS161330	Oromiya	Arssi	137	JUS161332	Dire Dawa provision	Dire Dawa
114	JUS173241	Affar	Zone 1	138	JUS173312	Tigray	Debubawi
115	JUS173423	SNNP	Bench Maji	139	JUS173420	SNNP	Bench Maji
116	JUS173363	SNNP	Bench Maji	140	JUS173355	SNNP	Bench Maji
117	JUS173369	Tigray	Mirabawi	141	JUS173216	Gambella	Zone 1
118	JUS173375	Tigray	Mirabawi	142	JUS173374	Tigray	Debubawi
119	JUS171497	Tigray	Debubawi	143	JUS171336	Amara	Semen Shewa
120	JUS173354	Tigray	Debubawi	144	JUS173347	SNNP	Bench Maji

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection	
		Region	Zone
145	JUS173342	Tigray	Debubawi
146	JUS173236	Affar	Zone 1
147	JUS171256	Amara	Semen Wello
148	JUS161326	Affar	Zone 1
149	JUS161333	Oromiya	Illubabor
150	JUS173311	Oromiya	Mirab Wellega
151	JUS173419	SNNP	Bench Maji
152	JUS173357	SNNP	Bench Maji
153	JUS173379	SNNP	Bench Maji
154	JUS173377	Tigray	Mirabawi
155	JUS171601	SNNP	Semen Omo
156	JUS173346	SNNP	Bench Maji
157	JUS173341	Tigray	Debubawi
158	JUS173225	Affar	Zone 1
159	JUS171526	Amara	Debub Gondar
160	JUS161327	Amara	Misrak Gojam
161	JUS173227	Gambella	Zone 1
162	JUS173305	Gambella	Zone 1
163	JUS173424	Oromiya	Mirab Harerge
164	JUS173364	Tigray	Debubawi
165	JUS173380	Tigray	Mirabawi
166	JUS173352	Tigray	Debubawi
167	JUS171365	Amara	Semen Shewa
168	JUS173359	SNNP	Bench Maji
169	JUS173340	SNNP	Bench Maji
170	JUS153001	Unknown	Unknown
171	JUS161008	Somali	Jigjiga
172	JUS173222	Gambella	Zone 1
173	JUS173310	Oromiya	Mirab Harerge
174	JUS173425	SNNP	Bench Maji
175	JUS173365	SNNP	Bench Maji
176	JUS173381	SNNP	Bench Maji
177	JUS173348	Tigray	Debubawi
178	JUS171619	Tigray	Mirabawi
179	JUS173345	Tigray	Mirabawi
180	JUS173215	Affar	Zone 1
181	JUS161001	Amara	Semen Wello
182	JUS161328	Oromiya	Mirab Shewa
183	JUS173226	Affar	Zone 1
184	JUS173309	Gambella	Zone 1
185	JUS173362	SNNP	Bench Maji
186	JUS173366	SNNP	Bench Maji
187	JUS173382	Somali	Jigjiga
188	JUS173349	Tigray	Debubawi
189	JUS173217	Affar	Zone 1
190	JUS173515	Tigray	Mirabawi
191	JUS173258	Gambella	Zone 1
192	JUS173244	Affar	Zone 1

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
193	JUS173207	Affar	Zone 1	217	JUS173205	Gambella	Zone 1
194	JUS173235	Gambella	Zone 1	218	JUS173238	Gambella	Zone 1
195	JUS173307	Gambella	Zone 1	219	JUS173303	Gambella	Zone 1
196	JUS173297	Gambella	Zone 1	220	JUS173294	Gambella	Zone 1
197	JUS173315	Oromiya	Mirab Harerge	221	JUS173317	Oromiya	Illubabor
198	JUS173330	Amara	Semen Wello	222	JUS173328	Gambella	Zone 1
199	JUS173525	Amara	Semen Wello	223	JUS173527	Amara	Semen Wello
200	JUS173506	Tigray	Debubawi	224	JUS173508	Affar	Zone 1
201	JUS173213	Amara	Debub Wello	225	JUS173211	Gambella	Zone 1
202	JUS173516	Amara	Semen Wello	226	JUS173518	Affar	Zone 1
203	JUS173254	Amara	Debub Wello	227	JUS173252	Affar	Zone 1
204	JUS173458	Gambella	Zone 1	228	JUS173460	Oromiya	Mirab Wellega
205	JUS173206	Affar	Zone 1	229	JUS173204	Amara	Debub Wello
206	JUS173237	Affar	Zone 1	230	JUS173231	Amara	Debub Wello
207	JUS173304	Gambella	Zone 1	231	JUS173302	Oromiya	Misrak Harerge
208	JUS173296	Oromiya	Misrak Harerge	232	JUS173295	Tigray	Debubawi
209	JUS173318	Oromiya	Misrak Harerge	233	JUS173333	Gambella	Zone 1
210	JUS173329	Oromiya	Jimma	234	JUS173313	Gambella	Zone 1
211	JUS173526	Tigray	Mirabawi	235	JUS173513	Amara	Semen Wello
212	JUS173507	Amara	Debub Wello	236	JUS173509	Amara	Semen Wello
213	JUS173212	Affar	Zone 1	237	JUS173210	Amara	Debub Wello
214	JUS173517	Amara	Semen Wello	238	JUS173519	Amara	Semen Wello
215	JUS173250	Amara	Semen Gondar	239	JUS173257	Gambella	Zone 1
216	JUS173459	Oromiya	Misrak Harerge	240	JUS173461	SNNP	Bench Maji

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
241	JUS173220	Amara	Debub Wello	265	JUS173240	Amara	Debub Wello
242	JUS173242	Affar	Zone 1	266	JUS173299	Gambella	Zone 1
243	JUS173301	Oromiya	Mirab Harerge	267	JUS173320	Tigray	Mirabawi
244	JUS173293	Oromiya	Misrak Harerge	268	JUS173316	Gambella	Zone 1
245	JUS173332	Unknown	Unknown	269	JUS173522	Tigray	Debubawi
246	JUS173521	Tigray	Debubawi	270	JUS173504	Amara	Semen Wello
247	JUS173514	Tigray	Mirabawi	271	JUS173512	Amara	Debub Wello
248	JUS173510	Amara	Semen Wello	272	JUS173208	Affar	Zone 1
249	JUS173230	Gambella	Zone 1	273	JUS161343	Amara	Mirab Gojam
250	JUS173306	Oromiya	Illubabor	274	JUS173229	Affar	Zone 1
251	JUS173251	Gambella	Zone 1	275	JUS173234	Gambella	Zone 1
252	JUS173462	Oromiya	Mirab Shewa	276	JUS173232	Affar	Zone 1
253	JUS173233	Affar	Zone 1	277	JUS173298	Gambella	Zone 1
254	JUS173239	Gambella	Zone 1	278	JUS173319	Gambella	Zone 1
255	JUS173300	Oromiya	Mirab Harerge	279	JUS173314	Gambella	Zone 1
256	JUS173334	Dire Dawa provisiona	Dire Dawa	280	JUS173524	Tigray	Debubawi
257	JUS173331	Tigray	Debubawi	281	JUS173505	Affar	Zone 1
258	JUS173523	Amara	Semen Wello	282	JUS173520	Tigray	Debubawi
259	JUS173503	Tigray	Debubawi	283	JUS173463	Oromiya	Misrak Harerge
260	JUS173511	Amara	Semen Wello	284	JUS173439	Gambella	Zone 1
261	JUS173209	Amara	Debub Wello	285	JUS173466	Gambella	Zone 1
262	JUS173308	Oromiya	Illubabor	286	JUS173622	Gambella	Zone 1
263	JUS173223	Affar	Zone 1	287	JUS173445	Oromiya	Misrak Harerge
264	JUS173228	Affar	Zone 1	288	JUS173449	Gambella	Zone 1

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
289	JUS173479	SNNP	Bench Maji	313	JUS173624	Amara	Debub Wello
290	JUS173588	Gambella	Zone 1	314	JUS173626	Gambella	Zone 1
291	JUS173575	Gambella	Zone 2	315	JUS173573	Gambella	Zone 1
292	JUS173596	Gambella	Zone 1	316	JUS173623	Gambella	Zone 1
293	JUS173572	Gambella	Zone 1	317	JUS173601	Amara	Semen Wello
294	JUS173594	Gambella	Zone 1	318	JUS173615	Oromiya	Mirab Harerge
295	JUS173464	SNNP	Bench Maji	319	JUS173442	Oromiya	Misrak Harerge
296	JUS173453	SNNP	Bench Maji	320	JUS173450	Somali	Shinile
297	JUS173485	Oromiya	Misrak Harerge	321	JUS173621	SNNP	Bench Maji
298	JUS173743	Amara	Debub Wello	322	JUS173727	Oromiya	Misrak Harerge
299	JUS173446	SNNP	Bench Maji	323	JUS173457	SNNP	Bench Maji
300	JUS173448	Oromiya	Misrak Harerge	324	JUS173469	Oromiya	Mirab Wellega
301	JUS161345	Oromiya	Arssi	325	JUS173616	SNNP	Bench Maji
302	JUS173589	Gambella	Zone 1	326	JUS173630	Gambella	Zone 2
303	JUS173574	Gambella	Zone 1	327	JUS173609	Gambella	Zone 1
304	JUS173597	Gambella	Zone 1	328	JUS173598	Gambella	Zone 1
305	JUS173604	Gambella	Zone 1	329	JUS173625	Gambella	Zone 1
306	JUS173610	Gambella	Zone 1	330	JUS173611	Gambella	Zone 1
307	JUS173465	Gambella	Zone 1	331	JUS173443	Oromiya	Misrak Harerge
308	JUS173444	Oromiya	Mirab Harerge	332	JUS173440	Oromiya	Misrak Harerge
309	JUS173578	Gambella	Zone 1	333	JUS173576	Oromiya	Mirab Shewa
310	JUS173728	Somali	Jigjiga	334	JUS173725	Oromiya	Misrak Harerge
311	JUS173456	Oromiya	Misrak Harerge	335	JUS173482	Oromiya	Mirab Wellega
312	JUS173468	SNNP	Bench Maji	336	JUS173470	Oromiya	Jimma

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
337	JUS173618	SNNP	Bench Maji	361	JUS173581	Gambella	Zone 1
338	JUS173590	Gambella	Zone 2	362	JUS173585	Gambella	Zone 1
339	JUS173587	SNNP	Bench Maji	363	JUS173600	Gambella	Zone 1
340	JUS173614	Gambella	Zone 2	364	JUS173591	Gambella	Zone 1
341	JUS173579	Gambella	Zone 1	365	JUS173617	Gambella	Zone 1
342	JUS173613	SNNP	Bench Maji	366	JUS173452	SNNP	Bench Maji
343	JUS173447	SNNP	Bench Maji	367	JUS173455	Oromiya	Illubabor
344	JUS173441	Oromiya	Mirab Wellega	368	JUS173620	Gambella	Zone 1
345	JUS173607	Gambella	Zone 1	369	JUS173481	Somali	Shinile
346	JUS173722	Dire Dawa provisiona	Dire Dawa	370	JUS173478	SNNP	Bench Maji
347	JUS173474	Oromiya	Mirab Shewa	371	JUS173584	Gambella	Zone 1
348	JUS173471	Gambella	Zone 1	372	JUS173580	Gambella	Zone 1
349	JUS173606	SNNP	Bench Maji	373	JUS173595	Gambella	Zone 2
350	JUS173582	Gambella	Zone 1	374	JUS173577	Gambella	Zone 1
351	JUS173608	SNNP	Bench Maji	375	JUS171191	Gambella	Zone 1
352	JUS173603	Gambella	Zone 1	376	JUS173454	Gambella	Zone 1
353	JUS173619	SNNP	Bench Maji	377	JUS173720	Amara	Debub Wello
354	JUS173612	Gambella	Zone 2	378	JUS173731	Somali	Jigjiga
355	JUS173451	Gambella	Zone 1	379	JUS173707	Amara	Oromiya
356	JUS173467	Amara	Semen Wello	380	JUS173695	Somali	Jigjiga
357	JUS173586	SNNP	Bench Maji	381	JUS173708	Somali	Jigjiga
358	JUS173480	Oromiya	Mirab Wellega	382	JUS173783	Tigray	Mehakelegnaw
359	JUS173472	SNNP	Bench Maji	383	JUS173762	Somali	Jigjiga
360	JUS173605	Gambella	Zone 1	384	JUS173663	Amara	Semen Wello

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
385	JUS173672	Benishangul Gumuz	Metekel	409	JUS173679	Oromiya	Mirab Wellega
386	JUS173666	Oromiya	Mirab Harerge	410	JUS173645	Oromiya	Jimma
387	JUS173735	Dire Dawa provisiona	Dire Dawa	411	JUS173632	Gambella	Zone 1
388	JUS173657	Oromiya	Mirab Wellega	412	JUS173659	SNNP	Bench Maji
389	JUS173702	Oromiya	Misrak Harerge	413	JUS173704	Amara	Debub Wello
390	JUS173734	Oromiya	Misrak Harerge	414	JUS173729	Oromiya	Misrak Harerge
391	JUS173705	Amara	Debub Wello	415	JUS173696	Amara	Debub Wello
392	JUS173701	Dire Dawa provisiona	Dire Dawa	416	JUS171171	Oromiya	Mirab Harerge
393	JUS173712	Oromiya	Mirab Harerge	417	JUS173714	Amara	Debub Wello
394	JUS173759	Somali	Jigjiga	418	JUS173755	Somali	Jigjiga
395	JUS173764	Somali	Jigjiga	419	JUS173782	Amara	Debub Wello
396	JUS173677	Oromiya	Mirab Harerge	420	JUS173648	Amara	Semen Wello
397	JUS173671	Amara	Semen Wello	421	JUS173639	Oromiya	Mirab Harerge
398	JUS173646	SNNP	Bench Maji	422	JUS173644	Amara	Debub Wello
399	JUS173633	Oromiya	Mirab Harerge	423	JUS173652	Gambella	Zone 2
400	JUS173658	Oromiya	Mirab Shewa	424	JUS173660	Oromiya	Mirab Harerge
401	JUS173726	Oromiya	Misrak Harerge	425	JUS173706	Somali	Jigjiga
402	JUS173733	Amara	Debub Wello	426	JUS173721	Amara	Debub Wello
403	JUS173703	Oromiya	Misrak Harerge	427	JUS173697	Oromiya	Misrak Harerge
404	JUS173694	SNNP	Bench Maji	428	JUS173692	Dire Dawa provisiona	Dire Dawa
405	JUS173713	Amara	Oromiya	429	JUS173715	Amara	Semen Wello
406	JUS173754	Benishangul Gumuz	Metekel	430	JUS173756	Tigray	Mirabawi
407	JUS173765	Benishangul Gumuz	Metekel	431	JUS173792	Oromiya	Jimma
408	JUS173664	Amara	Debub Wello	432	JUS173650	Tigray	Mehakelegnaw

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection	
		Region	Zone
433	JUS173638	Oromiya	Jimma
434	JUS173643	Unknown	Unknown
435	JUS173653	Amara	Debub Wello
436	JUS173661	SNNP	Bench Maji
437	JUS173724	DDP	Dire Dawa
438	JUS173744	Amara	Debub Wello
439	JUS173687	Amara	Semen Wello
440	JUS173700	Oromiya	Misrak Harerge
441	JUS173716	Oromiya	Misrak Harerge
442	JUS173757	DDP	Dire Dawa
443	JUS173767	Amara	Semen Wello
444	JUS173649	SNNP	Bench Maji
445	JUS173637	Amara	Oromiya
446	JUS173642	Gambella	Zone 1
447	JUS173654	Amara	Semen Wello
448	JUS173662	Amara	Semen Wello
449	JUS173723	Amara	Semen Wello
450	JUS173710	SNNP	Bench Maji
451	JUS173698	Oromiya	Mirab Harerge
452	JUS173717	Amara	Semen Wello
453	JUS173760	Benishangul Gumuz	Metekel
454	JUS173768	Somali	Jigjiga
455	JUS173668	Oromiya	Illubabor
456	JUS173636	Oromiya	Mirab Harerge
457	JUS173641	Tigray	Debubawi
458	JUS173655	Somali	Jigjiga
459	JUS173719	DDP	Dire Dawa
460	JUS173711	Oromiya	Mirab Harerge
461	JUS173709	Amara	Debub Wello
462	JUS173699	DDP	Dire Dawa
463	JUS173718	Somali	Jigjiga
464	JUS173758	Somali	Jigjiga
465	JUS161337	SNNP	Hadiya
466	JUS173670	Gambella	Zone 1
467	JUS173634	Oromiya	Jimma
468	JUS173640	Amara	Debub Wello
469	JUS173656	Amara	Oromiya
470	JUS173732	Amara	Debub Wello
471	JUS173688	Somali	Jigjiga
472	JUS173153	Oromiya	Illubabor
473	JUS173823	Gambella	Zone 1
474	JUS173817	Oromiya	Misrak Harerge
475	JUS173802	Somali	Jigjiga
476	JUS173807	Amara	Debub Wello
477	JUS173789	Tigray	Mehakelegnaw
478	JUS173780	Oromiya	Illubabor
479	JUS173777	Oromiya	Misrak Harerge
480	JUS173174	Tigray	Mehakelegnaw

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
481	JUS173856	Oromiya	Mirab Shewa	505	JUS173169	Oromiya	Mirab Shewa
482	JUS173149	Oromiya	Mirab Shewa	506	JUS173161	Tigray	Mirabawi
483	JUS173691	Amara	Semen Wello	507	JUS173689	Oromiya	Misrak Harerge
484	JUS173152	Oromiya	Mirab Shewa	508	JUS173158	Oromiya	Jimma
485	JUS173881	Oromiya	Jimma	509	JUS173829	Amara	Semen Wello
486	JUS173819	Amara	Debub Wello	510	JUS173831	Tigray	Mehakelegnaw
487	JUS173799	Amara	Debub Wello	511	JUS173801	Somali	Jigjiga
488	JUS173809	Somali	Jigjiga	512	JUS173811	Amara	Debub Wello
489	JUS173790	Oromiya	Misrak Harerge	513	JUS173885	Unknown	Unknown
490	JUS173770	Amara	Debub Wello	514	JUS173772	Oromiya	Illubabor
491	JUS173778	Tigray	Mehakelegnaw	515	JUS173781	Somali	Jigjiga
492	JUS173175	SNNP	Bench Maji	516	JUS173147	Oromiya	Mirab Shewa
493	JUS173155	Oromiya	Mirab Shewa	517	JUS173170	DDP	Dire Dawa
494	JUS173159	Oromiya	Mirab Shewa	518	JUS173160	Tigray	Mirabawi
495	JUS173690	DDP	Dire Dawa	519	JUS173797	Amara	Semen Shewa
496	JUS173151	Oromiya	Illubabor	520	JUS173150	DDP	Dire Dawa
497	JUS173826	Oromiya	Mirab Harerge	521	JUS173830	Tigray	Debubawi
498	JUS173820	Amara	Semen Wello	522	JUS173832	Oromiya	Jimma
499	JUS173800	DDP	Dire Dawa	523	JUS173803	Benishangul Gumuz	Metekel
500	JUS173810	Oromiya	Mirab Harerge	524	JUS173784	Oromiya	Jimma
501	JUS173791	DDP	Dire Dawa	525	JUS173793	Benishangul Gumuz	Metekel
502	JUS173771	Oromiya	Illubabor	526	JUS173773	Somali	Jigjiga
503	JUS173779	Somali	Jigjiga	527	JUS173191	Oromiya	Mirab Shewa
504	JUS173146	Tigray	Mehakelegnaw	528	JUS173148	DDP	Dire Dawa

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
529	JUS173171	Tigray	Debubawi	553	JUS173165	SNNP	Bench Maji
530	JUS173162	Tigray	Mehakelegnaw	554	JUS173763	Somali	Jigjiga
531	JUS173798	Amara	Semen Wello	555	JUS173824	Amara	Semen Wello
532	JUS161340	SNNP	Semen Omo	556	JUS173816	Tigray	Debubawi
533	JUS173814	Amara	Semen Wello	557	JUS173806	Benishangul Gumuz	Metekel
534	JUS173833	Gambella	Zone 1	558	JUS173788	DDP	Dire Dawa
535	JUS173804	Amara	Debub Wello	559	JUS173796	Oromiya	Illubabor
536	JUS173786	Oromiya	Illubabor	560	JUS173776	Somali	Jigjiga
537	JUS173794	Oromiya	Jimma	561	JUS173183	DDP	Dire Dawa
538	JUS173774	Benishangul Gumuz	Metekel	562	JUS173185	Tigray	Mehakelegnaw
539	JUS173190	Oromiya	Misrak Shewa	563	JUS173163	DDP	Dire Dawa
540	JUS173144	Tigray	Mirabawi	564	JUS173157	Oromiya	Mirab Shewa
541	JUS173172	Tigray	Mehakelegnaw	565	JUS173834	Oromiya	Jimma
542	JUS173164	Oromiya	Illubabor	566	JUS173143	Oromiya	Mirab Shewa
543	JUS173785	Amara	Oromiya	567	JUS173142	Tigray	Mirabawi
544	JUS173156	DDP	Dire Dawa	568	JUS171565	SNNP	Debub Omo
545	JUS173815	Oromiya	Jimma	569	JUS173129	Amara	Debub Wello
546	JUS173805	Somali	Jigjiga	570	JUS173098	Amara	Debub Wello
547	JUS173787	DDP	Dire Dawa	571	JUS161338	SNNP	Semen Omo
548	JUS173795	Oromiya	Mirab Harerge	572	JUS173113	Unknown	Unknown
549	JUS173775	Oromiya	Illubabor	573	JUS173840	Oromiya	Mirab Shewa
550	JUS173177	Oromiya	Misrak Shewa	574	JUS173186	DDP	Dire Dawa
551	JUS173145	DDP	Dire Dawa	575	JUS173184	DDP	Dire Dawa
552	JUS173166	DDP	Dire Dawa	576	JUS173167	Amara	Oromiya

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
577	JUS173835	Oromiya	Jimma	601	JUS173124	SNNP	Bench Maji
578	JUS173675	Amara	Oromiya	602	JUS173647	Gambella	Zone 1
579	JUS171425	SNNP	Hadiya	603	JUS171577	SNNP	Semen Omo
580	JUS171576	SNNP	Kembata Alabana Temb	604	JUS171116	Amara	Mirab Gojam
581	JUS173126	SNNP	Bench Maji	605	JUS173105	SNNP	Bench Maji
582	JUS173106	SNNP	Bench Maji	606	JUS171569	Oromiya	Arssi
583	JUS161335	SNNP	Debub Omo	607	JUS173121	Amara	Semen Wello
584	JUS173114	Oromiya	Misrak Harerge	608	JUS173111	Unknown	Unknown
585	JUS173841	Oromiya	Mirab Shewa	609	JUS173822	Oromiya	Jimma
586	JUS173187	DDP	Dire Dawa	610	JUS173179	Oromiya	Mirab Shewa
587	JUS173154	DDP	Dire Dawa	611	JUS173173	Tigray	Mirabawi
588	JUS173218	Amara	Debub Wello	611	JUS173173	Tigray	Mirabawi
589	JUS173116	Oromiya	Illubabor	612	JUS173095	Oromiya	Mirab Harerge
590	JUS173651	Tigray	Mehakelegnaw	613	JUS173117	Tigray	Debubawi
591	JUS171595	SNNP	Keficho Shekicho	614	JUS173676	Amara	Debub Wello
592	JUS171029	SNNP	Debub Omo	615	JUS171600	SNNP	Semen Omo
593	JUS173118	Oromiya	Illubabor	616	JUS171602	SNNP	Semen Omo
594	JUS173099	SNNP	Bench Maji	617	JUS173103	SNNP	Bench Maji
595	JUS173122	Amara	Semen Wello	618	JUS173808	Amara	Oromiya
596	JUS173112	SNNP	Bench Maji	619	JUS173110	SNNP	Bench Maji
597	JUS173821	Oromiya	Mirab Shewa	620	JUS173836	Tigray	Mehakelegnaw
598	JUS173188	Tigray	Mehakelegnaw	621	JUS173828	Gambella	Zone 1
599	JUS173180	Oromiya	Misrak Shewa	622	JUS173189	Tigray	Mirabawi
600	JUS173483	SNNP	Bench Maji	623	JUS173182	Unknown	Unknown

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
624	JUS173285	Oromiya	Illubabor	648	JUS173127	Oromiya	Illubabor
625	JUS173096	Amara	Debub Wello	649	JUS173203	Amara	Debub Wello
626	JUS173279	Gambella	Zone 1	650	JUS171424	SNNP	Hadiya
627	JUS171433	Amara	Bahir Dar Special	651	JUS173102	Tigray	Mehakelegnaw
628	JUS171089	SNNP	Semen Omo	652	JUS173100	Tigray	Mehakelegnaw
629	JUS173104	SNNP	Bench Maji	653	JUS173115	Oromiya	Illubabor
630	JUS173108	SNNP	Bench Maji	654	JUS173839	Oromiya	Mirab Shewa
631	JUS173120	Amara	Semen Wello	655	JUS173818	Amara	Semen Wello
632	JUS173837	Gambella	Zone 1	656	JUS173193	Tigray	Mehakelegnaw
633	JUS173813	Oromiya	Jimma	657	JUS173178	DDP	Dire Dawa
634	JUS173194	DDP	Dire Dawa	658	JUS171669	Tigray	Mehakelegnaw
635	JUS173181	Tigray	Mirabawi	659	JUS171016	Amara	Debub Wello
636	JUS173278	Tigray	Debubawi	660	JUS171017	Amara	Debub Wello
637	JUS173125	Tigray	Debubawi	661	JUS171323	Amara	Semen Shewa
638	JUS173761	Tigray	Mehakelegnaw	662	JUS171143	Oromiya	Mirab Harerge
639	JUS171511	SNNP	Gurage	663	JUS171077	Tigray	Mehakelegnaw
640	JUS173097	Oromiya	Misrak Harerge	664	JUS171106	Somali	Jigjiga
641	JUS173109	Amara	Semen Wello	665	JUS171429	Amara	Semen Shewa
642	JUS173119	Oromiya	Illubabor	666	JUS171250	Amara	Semen Wello
643	JUS173838	Oromiya	Misrak Harerge	667	JUS171319	Tigray	Debubawi
644	JUS173827	Oromiya	Mirab Shewa	668	JUS171462	Oromiya	Semen Shewa
645	JUS173195	Oromiya	Mirab Shewa	669	JUS171216	Oromiya	Mirab Harerge
646	JUS173192	Amara	Oromiya	670	JUS171176	Oromiya	Illubabor
647	JUS173593	Gambella	Zone 2	671	JUS171034	Gambella	Zone 1

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection	
		Region	Zone
672	JUS171510	Oromiya	Misrak Harerge
673	JUS171613	Tigray	Mehakelegnaw
674	JUS171728	Tigray	Debubawi
675	JUS171651	Oromiya	Misrak Wellega
676	JUS171030	Amara	Misrak Gojam
677	JUS171351	Amara	Semen Shewa
678	JUS171061	Gambella	Zone 1
679	JUS171240	Affar	Zone 1
680	JUS171183	Tigray	Mehakelegnaw
681	JUS171528	Tigray	Misrakawi
682	JUS171606	Amara	Misrak Gojam
682	JUS171606	Amara	Misrak Gojam
683	JUS171192	Gambella	Zone 1
684	JUS171684	Unknown	Unknown
685	JUS171626	Oromiya	Misrak Shewa
686	JUS171740	Amara	Semen Gondar
687	JUS171673	Amara	Semen Gondar
688	JUS171161	Tigray	Debubawi
689	JUS171056	SNNP	Bench Maji
690	JUS161339	SNNP	Semen Omo
691	JUS171107	Oromiya	Misrak Harerge
692	JUS171121	Oromiya	Misrak Harerge
693	JUS171297	Tigray	Mirabawi
694	JUS171549	Tigray	Mehakelegnaw
695	JUS171072	Oromiya	Misrak Harerge
696	JUS171635	Tigray	Mirabawi
697	JUS171580	SNNP	Bench Maji
698	JUS171267	Somali	Jigjiga
699	JUS171084	Oromiya	Misrak Harerge
700	JUS171126	Oromiya	Misrak Harerge
701	JUS171421	SNNP	Hadiya
702	JUS171076	Oromiya	Mirab Harerge
703	JUS171080	Oromiya	Misrak Shewa
704	JUS171181	Tigray	Mehakelegnaw
705	JUS171440	SNNP	Hadiya
706	JUS171454	Amara	Misrak Gojam
707	JUS171019	Oromiya	Mirab Harerge
708	JUS171753	Amara	Semen Shewa
709	JUS171653	Oromiya	Bale
710	JUS171135	Oromiya	Misrak Harerge
711	JUS171117	Oromiya	Misrak Harerge
712	JUS171794	Oromiya	Misrak Harerge
713	JUS171049	Gambella	Zone 2
714	JUS171548	Tigray	Debubawi
715	JUS171707	Tigray	Debubawi
716	JUS171672	Tigray	Debubawi
717	JUS171386	Oromiya	Mirab Shewa
718	JUS171791	SNNP	Bench Maji

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
719	JUS171810	Tigray	Mehakelegnaw	743	JUS171736	Tigray	Mirabawi
720	JUS171494	Gambella	Zone 1	744	JUS171088	Tigray	Misrakawi
721	JUS171219	Gambella	Zone 1	745	JUS171608	Amara	Bahir Dar Special
722	JUS171146	Oromiya	Misrak Harerge	746	JUS171170	Oromiya	Mirab Harerge
723	JUS171040	Gambella	Zone 1	747	JUS171361	Amara	Semen Shewa
724	JUS171265	Tigray	Mehakelegnaw	748	JUS171094	Oromiya	Misrak Harerge
725	JUS171432	Amara	Bahir Dar Special	749	JUS171575	Amara	Semen Gondar
726	JUS171773	Amara	Semen Gondar	750	JUS171139	Oromiya	Misrak Harerge
727	JUS171218	Oromiya	Jimma	751	JUS171705	Amara	Semen Shewa
728	JUS171332	Amara	Semen Shewa	752	JUS171366	Amara	Semen Shewa
729	JUS171003	Amara	Misrak Gojam	753	JUS173879	Oromiya	Jimma
730	JUS171458	Amara	Misrak Gojam	754	JUS171260	Amara	Debub Wello
731	JUS171588	Amara	Debub Gondar	755	JUS171199	Amara	Semen Gondar
732	JUS171255	Amara	Semen Wello	756	JUS171628	Oromiya	Misrak Shewa
733	JUS171809	Amara	Semen Gondar	757	JUS171207	Amara	Semen Gondar
734	JUS171008	Oromiya	Mirab Harerge	758	JUS171360	Amara	Semen Shewa
735	JUS171127	Oromiya	Misrak Harerge	759	JUS173394	Tigray	Debubawi
736	JUS171484	Oromiya	Misrak Shewa	760	JUS171018	Oromiya	Mirab Harerge
737	JUS171238	Amara	Debub Wello	761	JUS171763	Oromiya	Mirab Harerge
738	JUS171101	Oromiya	Misrak Harerge	762	JUS171379	Oromiya	Semen Shewa
739	JUS171737	Tigray	Mirabawi	763	JUS171717	SNNP	Gurage
740	JUS171559	Amara	Oromiya	764	JUS171747	Tigray	Debubawi
741	JUS171203	Amara	Semen Gondar	765	JUS173553	Amara	Semen Wello
742	JUS171167	Oromiya	Mirab Harerge	766	JUS171347	Amara	Semen Shewa

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
767	JUS171778	Amara	Semen Gondar	791	JUS171057	Amara	Semen Gondar
768	JUS171195	Gambella	Zone 1	792	JUS171322	Tigray	Mirabawi
769	JUS171776	Amara	Semen Gondar	793	JUS171706	Amara	Semen Shewa
770	JUS171453	Amara	Misrak Gojam	794	JUS171603	Amara	Debub Wello
771	JUS171035	Gambella	Zone 1	795	JUS171611	Oromiya	Mirab Harerge
772	JUS173861	Oromiya	Jimma	796	JUS173627	Oromiya	Mirab Harerge
773	JUS171450	Oromiya	Semen Shewa	797	JUS171132	Oromiya	Misrak Harerge
774	JUS171388	Oromiya	Mirab Shewa	798	JUS171487	Unknown	Unknown
775	JUS173392	Tigray	Mirabawi	799	JUS171295	Tigray	Mirabawi
776	JUS171296	Tigray	Mirabawi	800	JUS171664	Tigray	Mehakelegnaw
777	JUS171331	Amara	Semen Shewa	801	JUS171231	Amara	Debub Wello
778	JUS171335	Amara	Semen Shewa	802	JUS171530	Amara	Semen Gondar
779	JUS171594	Amara	Debub Gondar	803	JUS171050	Gambella	Zone 2
780	JUS171293	Tigray	Mirabawi	804	JUS171642	Oromiya	Borena
781	JUS173138	Amara	Debub Wello	805	JUS171208	Amara	Misrak Gojam
782	JUS171566	Amara	Misrak Gojam	806	JUS171632	Amara	Semen Gondar
783	JUS171169	Oromiya	Mirab Harerge	807	JUS171489	Oromiya	Mirab Harerge
784	JUS171724	Oromiya	Misrak Wellega	808	JUS171217	Oromiya	Mirab Harerge
785	JUS171096	Oromiya	Misrak Harerge	809	JUS171397	Oromiya	Arssi
786	JUS171443	Oromiya	Misrak Shewa	810	JUS171504	Oromiya	Misrak Shewa
787	JUS173261	Amara	Debub Wello	811	JUS171284	Tigray	Mirabawi
788	JUS171266	Tigray	Mehakelegnaw	812	JUS171716	Oromiya	Mirab Shewa
789	JUS171229	Amara	Debub Wello	813	JUS171631	Amara	Debub Wello
790	JUS171772	Amara	Semen Gondar	814	JUS171224	Amara	Debub Wello

Appendix Table 1 (Continued)

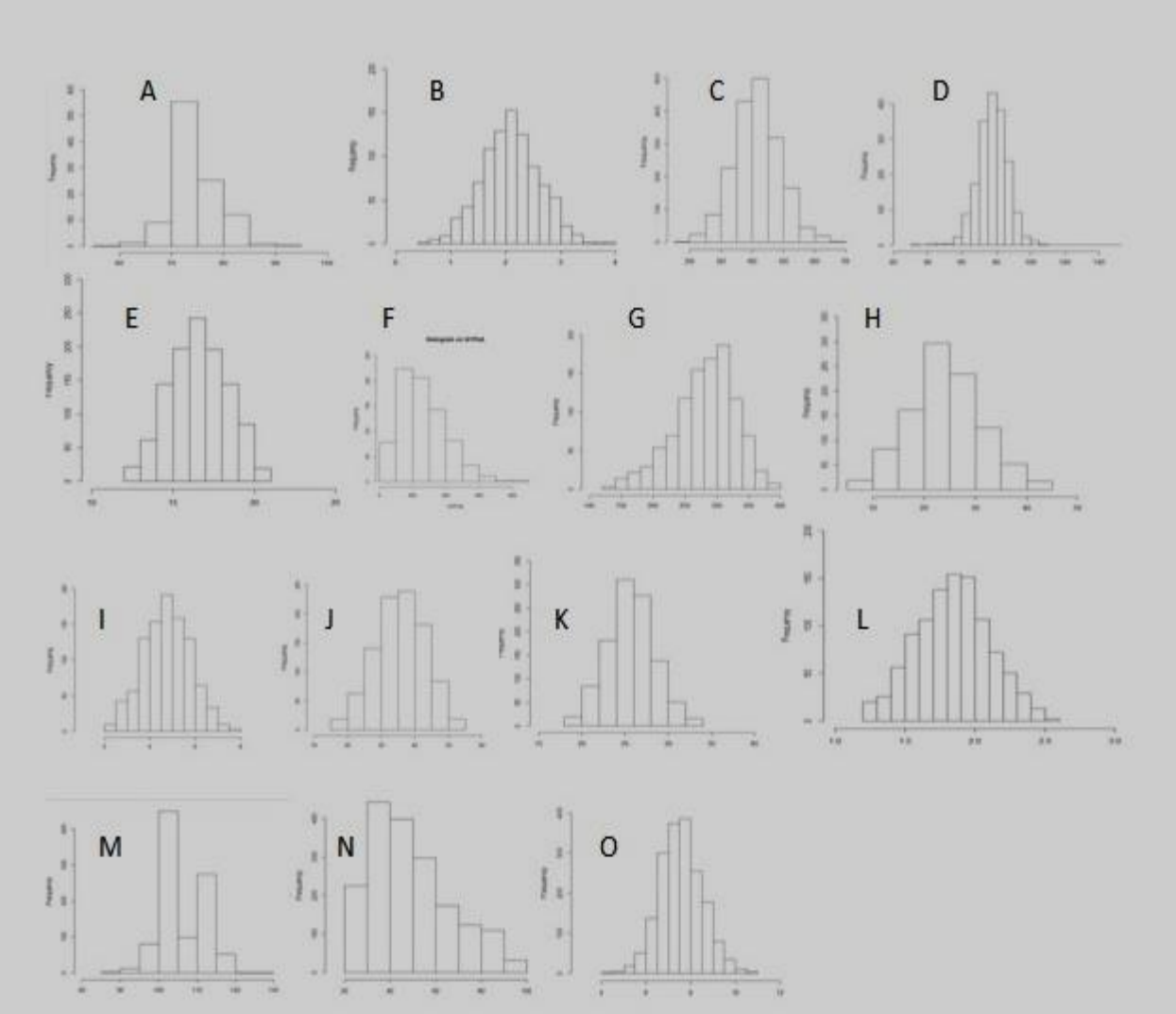
List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
815	JUS171190	Gambella	Zone 1	839	JUS171350	Amara	Semen Shewa
816	JUS173490	Oromiya	Mirab Harerge	840	JUS171755	Amara	Debub Wello
817	JUS171226	Amara	Debub Wello	841	JUS171444	Oromiya	Misrak Shewa
818	JUS171633	Amara	Bahir Dar Special	842	JUS171557	Oromiya	Mirab Harerge
819	JUS171436	Oromiya	Misrak Shewa	843	JUS171221	Oromiya	Misrak Harerge
820	JUS171095	Oromiya	Misrak Harerge	844	JUS171420	SNNP	Hadiya
821	JUS171093	Oromiya	Misrak Harerge	845	JUS171162	Tigray	Debubawi
822	JUS171555	Oromiya	Mirab Harerge	846	JUS171340	Amara	Semen Shewa
823	JUS171585	Tigray	Debubawi	847	JUS173090	Amara	Semen Wello
824	JUS171202	Amara	Semen Gondar	848	JUS173091	Tigray	Debubawi
825	JUS171644	Amara	Semen Gondar	849	JUS173086	Oromiya	Mirab Shewa
826	JUS171330	Amara	Semen Shewa	850	JUS173043	SNNP	Bench Maji
827	JUS171038	Gambella	Zone 1	851	JUS173044	Benishangul Gumuz	Metekel
828	JUS171341	Amara	Semen Shewa	852	JUS173042	Benishangul Gumuz	Metekel
829	JUS171696	Amara	Debub Wello	853	JUS173045	Amara	Oromiya
830	JUS171173	Oromiya	Mirab Harerge	854	JUS173046	Amara	Semen Wello
831	JUS171726	Oromiya	Misrak Wellega	855	JUS173047	Somali	Shinile
832	JUS171134	Oromiya	Semen Shewa	856	JUS173048	Amara	Debub Wello
833	JUS171765	Oromiya	Mirab Harerge	857	JUS173033	Amara	Semen Wello
834	JUS173682	Oromiya	Mirab Harerge	858	JUS173034	Amara	Debub Wello
835	JUS171346	Amara	Semen Shewa	859	JUS173035	Oromiya	Mirab Harerge
836	JUS171026	Amara	Misrak Gojam	860	JUS173085	Oromiya	Misrak Harerge
837	JUS171774	Amara	Semen Gondar	861	JUS173036	Oromiya	Mirab Wellega
838	JUS171193	Gambella	Zone 1	862	JUS173037	Gambella	Zone 1

Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
863	JUS173087	Gambella	Zone 2	887	JUS173006	Affar	Zone 1
864	JUS173038	SNNP	Bench Maji	888	JUS173001	Amara	Semen Wello
865	JUS173039	Oromiya	Mirab Shewa	889	JUS173002	Tigray	Mirabawi
866	JUS173040	Oromiya	Mirab Wellega	890	JUS173076	Amara	Semen Wello
867	JUS173012	Oromiya	Illubabor	891	JUS173075	Tigray	Debubawi
868	JUS173084	Oromiya	Illubabor	892	JUS173077	Oromiya	Mirab Shewa
869	JUS173013	Oromiya	Jimma	893	JUS173088	Oromiya	Misrak Harerge
870	JUS173014	Tigray	Mehakelegnaw	894	JUS173089	Somali	Jigjiga
871	JUS173016	Oromiya	Mirab Wellega	895	JUS173056	Oromiya	Illubabor
872	JUS173017	Oromiya	Jimma	896	JUS173054	Tigray	Debubawi
873	JUS173015	Oromiya	Mirab Harerge	897	JUS173021	Oromiya	Mirab Harerge
874	JUS173018	Oromiya	Misrak Harerge	898	JUS173057	Amara	Debub Wello
875	JUS173019	Somali	Shinile	899	JUS173022	Oromiya	Jimma
876	JUS173020	Oromiya	Mirab Wellega	900	JUS173055	Amara	Debub Wello
877	JUS173007	DDP	Dire Dawa	901	JUS173053	Gambella	Zone 2
878	JUS173008	Oromiya	Mirab Wellega	902	JUS173031	Oromiya	Jimma
879	JUS173092	Oromiya	Mirab Wellega	903	JUS173071	Oromiya	Jimma
880	JUS173009	Tigray	Mirabawi	904	JUS173049	Tigray	Debubawi
881	JUS173010	Tigray	Debubawi	905	JUS173032	Amara	Debub Wello
882	JUS173011	Oromiya	Illubabor	906	JUS173070	Oromiya	Jimma
883	JUS173083	Gambella	Zone 1	907	JUS173072	Oromiya	Jimma
884	JUS173003	Amara	Semen Gondar	908	JUS173051	Benishangul Gumuz	Metekel
885	JUS173004	Amara	Debub Wello	909	JUS173074	Oromiya	Misrak Harerge
886	JUS173005	Amara	Debub Wello	910	JUS173068	Oromiya	Illubabor

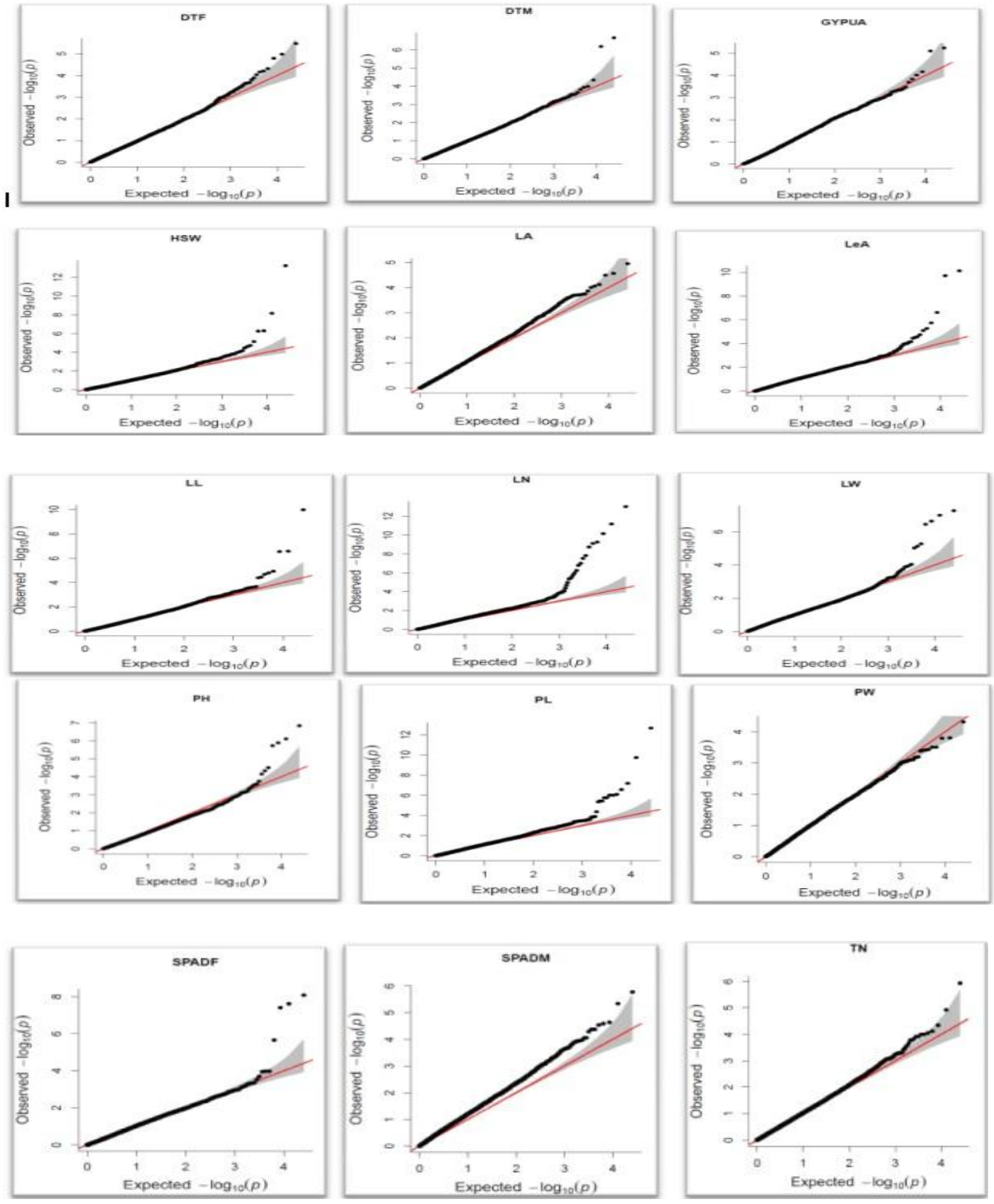
Appendix Table 1 (Continued)

List	Genotypes	Place of Collection		List	Genotypes	Place of Collection	
		Region	Zone			Region	Zone
911	JUS173073	Benishangul Gumuz	Metekel	935	JUS173094	Oromiya	Misrak Harerge
912	JUS173052	Oromiya	Misrak Harerge	936	JUS173080	Amara	Semen Wello
913	JUS173050	Tigray	Mehakelegnaw	937	JUS173079	Amara	Debub Wello
914	JUS173041	Tigray	Mehakelegnaw	938	JUS173082	Oromiya	Misrak Harerge
915	JUS173027	Tigray	Debubawi	939	JUS173081	Amara	Debub Wello
916	JUS173059	Tigray	Debubawi	940	JUS173078	Oromiya	Illubabor
917	JUS173024	Oromiya	Mirab Shewa	941	ICSR50	Realesed	variety
918	JUS173025	Amara	Semen Wello	942	S35	Realesed	variety
919	JUS173023	Tigray	Mirabawi	943	Gobiye	Realesed	variety
920	JUS173093	Oromiya	Misrak Shewa	944	ETS_2752	Realesed	variety
921	JUS173061	Oromiya	Mirab Shewa	945	Local check		
922	JUS173060	Oromiya	Mirab Shewa		(Danganw)		
923	JUS173065	Oromiya	Mirab Shewa				
924	JUS173062	Tigray	Mehakelegnaw				
925	JUS173026	Tigray	Mehakelegnaw				
926	JUS173058	DDP	Dire Dawa				
927	JUS173063	Amara	Debub Wello				
928	JUS173028	Amara	Semen Wello				
929	JUS173067	Oromiya	Mirab Harerge				
930	JUS173066	Oromiya	Mirab Harerge				
931	JUS173030	Oromiya	Mirab Harerge				
932	JUS173069	Oromiya	Mirab Harerge				
933	JUS173064	Oromiya	Misrak Harerge				
934	JUS173029	Oromiya	Misrak Harerge				



Appendix figure 1. Frequency distribution of 15 traits studied using sorghum germplasm

(A= days of flowering, B = Hundred seed weight, C = leaf area, D = leaf length, E = number of leaves, F = grain yield per unit area, G = plant height, H = panicle length, I = panicle width, J = ChCF at flowering, K = ChC at maturity, L = tiller number, M = days of maturity, N = leaf angle and O = leaf width)



Appendix figure 2. Log QQ plot of the FarmCPU results to determine how well the models accounted for the studied sorghum germplasm