GENETIC IMPROVEMENT FOR GRAIN YIELD UNDER DROUGHT STRESS, COMPOSITION AND GENE ACTION ON ELITE SORGHUM GENOTYPES OF KENYA

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DECLARATION

This thesis is my original work and has not been presented for award of a degree in any other university.

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DEDICATION

To the pillars of my life: God and my parents, without you, my life would fall apart. I might not know where the life's road will take me but walking with you, God, through this journey has given me Strength. To the loving memory of my father Jotham Arodi (1927-1995), for sowing in me the seed of discipline, self-respect, passion for better things in life.

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Father- in- law (Clement Abaya) you always told me to "aim at the stars." I think I got one. Thanks for inspiring my life for transformation. We made it…

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TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS AND ACRONYMS

ANOVA:	Analysis of variance
AOAC:	Association of Analytical Chemist
ASALs:	Arid and semi-arid lands
ASL:	Above Sea Level
BC:	Before Christ
BP:	Better Parent
BPH:	Better Parent Heterosis
CVD:	Cardiovascular Disease
DAP:	Di-Ammonium Phosphate
DMRT:	Duncan Multiple Range Test
EPZ:	Export Processing Zone
FAO:	Food and Agricultural Organization of the United Nations
GA:	Genetic Advance
GCV:	Genotypic Coefficient of Variation
H_2SO4:	Sulphuric Acid
HCL:	Hydrochloric Acid
ICRISAT:	The International Crops Research Institute for the Semi-Arid Tropics
IPGRI:	International Plant Genetic Resources Institute
KALRO:	Kenya Agricultural and Livestock Research Organization
KDHS:	Kenya Demographic and Health Survey
KIRDI:	Kenya Industrial Research and Development Institute
KMnO4:	Potassium permanganate
M:	Molarity
MP:	Mid Parent
MPH:	Mid Parent Heterosis
MSE:	Mean Square of Error
OPV:	Open Pollinated Variety
QTL:	Quantitative Trait Locus
UK:	United Kingdom
USAID:	United State Agency for International Development
UV:	Ultraviolet

GENERAL ABSTRACT

World food security is greatly challenged by climate change effect. Sub Saharan Africa is adversely affected by drought with considerable yield losses. The solution to food insecurity in these areas depends on the breeding of crop genotypes with improved adaptation for yield, drought and nutrition. Thus, the study was undertaken to; a) investigate the performance of elite sorghum varieties for yield under moisture stress b) to evaluate the nutritional composition of International Centre for Research in Semi-Arid Tropics (ICRISAT) sorghum genotypes and, c) to assess the gene action for grain yield among the crosses generated between Kenya Agricultural and Livestock Organization (KALRO) and ICRISAT genotypes. The elite genotypes from KALRO were evaluated for grain yield under drought stress for three seasons at KALRO- Kiboko Substation during the 2014/2015 short and long rains. For nutrition analyses, grains from ten genotypes derived from ICRISAT were evaluated for nutritional composition at the University of Nairobi food science department. The data sets were subjected to analyses of variances (ANOVA). Results showed that two KALRO genotypes namely Red Swazi and Wheatland reported greater yield and two ICRISAT genotypes namely IESV23006DL and IESV23010DL scored highly in terms of total proteins and total phenols. The two selections from KALRO were then crossed to two selections from ICRISAT to generate population which combines both yield, drought tolerance and nutritionally rich genotypes using North Carolina mating design 11 (NCD11). The F_1 generations were advanced to F_2. Agronomic data was obtained from ten middle row plants randomly selected and subjected to ANOVA and mean squares obtained used to determine the combining ability of the traits. Analysis of variance revealed significant differences in plant height, panicle yield and days to

50% anthesis among the genotypes. These sorghum progenies are promising in ensuring food security and positively meet the challenges of malnutrition and lifestyle diseases affecting human health in view of climate change effects experienced in the semi-arid areas of Kenya.

Key words: Drought, nutritional composition, gene action

CHAPTER ONE

INTRODUCTION

1.1 Background information

Sorghum is the world 5th most preferred crop after wheat, rice corn and barley (FAOSTAT, 2012). Production of sorghum worldwide stands at about 15.27 tha^{-1} (FAOSTAT, 2015) of which Africa and Asia contributes about 90%. In terms of output per country, the USA is the world leading sorghum producer with about 10.9M tones followed by Nigeria (6.7 M tones), Sudan (6.2 M tones), India (5 M tones) and Ethiopia and Argentina at 4M tones respectively (USDA, 2015). In Africa, sorghum yields are low <1.1t/ha (Kumar *et al*., 2011) and this low production has been attributed to frequent drought, use of local landraces, among other constraints (Mangoma *et al*., 2014).

The arid and semi-arid areas of Kenya are characterized by low precipitation, frequent and prolonged drought and poor soils rendering agricultural production very low. Sorghum, which has been identified to guarantee yields under drought and poor soil conditions, is less preferred by the farmers as compared to more maize which is susceptible (Riziki *et al*., 2013). Despite the fact that sorghum can perform well under the above stated conditions, its productivity is still low and the low productivity has been attributed to drought stress, use of low yielding landraces, and poor adoption of improved sorghum genotypes amongst other constraint (Timu *et al*., 2014).

Drought in ASALs has always led to hunger, malnutrition among pregnant and school going children and often death of livestock. The Kenyan Government through the ministry of agriculture, livestock and fisheries in collaboration with ICRISAT bred

and released sorghum genotypes that are adaptable to these AEZ such as Gadam, KARI Mtama1 but this has been affected by poor technological transfer coupled with poor preference for sorghum by farmers who prefer local landraces which are poor in yields (Chamberlin *et al*., 2014, Timu *et al*., 2014). Comparatively, improved varieties have outperformed the local landraces in terms of yield, nutritional composition, and industrial applications since they are sweet, highly palatable, and low in tannin, protein and polyphenols for brewing purposes (Ratnavathi and Chavan, 2016).

Although sorghum has been extensively studied to contain enough nutrients to help manage malnutrition related illnesses, nutritional variations exist among different genotypes (Awika and Rooney, 2004). Studies have been carried out in sorghum genotypes to identify phenolic compounds that have been reported to control lifestyle diseases (Awika and Rooney, 2004). These phenols have also been reported to render protein non bioavailable.

Sorghum yield and nutritional composition are influenced by genetic factors as well as by G×E. Heritability studies on traits influencing grain yield could aid in the introgression of desirable traits into the locally adapted landraces and therefore improve sorghum production in the Eastern County.

1.2 Problem statement

Drought stress is responsible for poor crop production in the ASALs leading to rampant hunger and malnutrition (Knox *et al*., 2010). In the ASALs, farmers still prefer growing maize even with the critical low moisture levels leading to recurrent yield losses. KALRO and ICRISAT have bred and fast tracked the release of high

yielding sorghum hybrids which are capable to mitigate the effects of climate change (Olembo *et al.*, 2010).

1.3 Justification

Due to severity of drought and unreliable rainfall in the ASALs occasioned by climate change, a paradigm shift in agriculture has been initiated to promote agricultural technologies that are able to mitigate the current climate change effects. Among these technologies are the use of irrigated agriculture and the promotion of improved sorghum genotypes. Through a collaborative research approach, KALRO and ICRISAT have developed and released improved sorghum genotypes such as KARI mtama1, Seredo, Serena, and IS #76-23 which are high yielding under drought stress. Furthermore, breeding for improved nutritional content is currently being undertaken to develop sorghum genotypes of higher phenol and protein content to mitigate the problem of food insecurity and rampant malnutrition in these areas (ICRISAT, 2006).

Thus, this research aimed at identifying high yielding and nutritious sorghum genotypes suited for the ASALs coupled with elucidation of the gene action conditioning inheritance of these key traits. This will greatly enhance the sorghum breeding research in Kenya leading to development of superior sorghum varieties.

1.4 Study objective

The study was conducted so as to improve sorghum productivity in Kenya through identification of drought resilient, high yielding and nutritious sorghum genotypes.

1.4.1 Specific Objectives

1. To investigate selected elite sorghum genotypes from KALRO for grain yield under moisture stressed environment.

2. To evaluate improved ICRISAT sorghum genotypes for proximate composition.
3. To assess gene action associated with yield contributing traits in sorghum from crosses generated between KALRO and ICRISAT genotypes for sorghum improvement in Kenya.

1.5 Hypotheses

1. There is no variation in grain yield and drought tolerance among the elite sorghum genotypes.
2. There is no variation in nutritional composition among elite sorghum genotypes.
3. Grain yield is not influenced by additive gene effects.

CHAPTER TWO

LITERATURE REVIEW

2.1 Origin, classification and, races of sorghum

Sorghum is believed to have originated from Ethiopia-Sudan border of North Eastern Africa (Doggett, 1998; FAO, 1995) from which it spread to other parts of the world (FAO, 2007). Sorghum classification is based on maturity time and temperature. On maturity time, there are early, medium and late maturing genotypes (Smith, 1995, Gilchrest *et al*., 2017). The early maturing ones take about sixty days to mature whereas the late maturing ones take about one hundred and fifty days. Classification on the basis of temperature groups sorghum into three areas; tropical lowland, temperate, and cool-tolerant tropical high altitude (Doggett, 1988).

There are five races of sorghum which include Kafir, Bicolor, Durra, Guinea and Cauda tum to which the ongoing breeding advancement is credited (Karari, 2007). The distribution of sorghum from West Africa to the United States was facilitated by slave trade amidst other crop introductions such as guinea corn and chicken corn (Doggett, 1970; Smith and Frederiksen, 2000). In the Northern Africa, the brown and the white Durras were introduced in 1874, the Milo race in about 1880, feterita in 1996 and hegari in 1908 (Doggett, 1970; Dillon's *et al*., 2007). In the West and East Africa, India and China, the races guinea-caudatum, guinea kaffir is prevalent, where as in the Americas the kafir-cauda race dominates (Harlan and de Wet, 1972).

2.2 Potential role of sorghum in Kenya

The population density of East Africa is about 200 million and this is expected to rise two-fold by 2030 (World meter, www.worldometer.info). This population is

compromised by insufficient food security occasioned by continuous drought and pressure on arable land (Wassu and Simeret, 2013). Climate smart crops such as sorghum are highly recommended in addressing food security in the ASALs (Wassu and Simeret, 2013).

In Kenya, the non-arable lands constitute about 82% of the total land mass (Munyiri *et al*., 2010) and suffer from extreme poverty, poor rainfall, food insecurity and rampant malnutrition due to extreme temperatures, inadequate precipitation, soil erosion and low soil fertility (Munyiri *et al*., 2010). The use of local landraces, lack of farm inputs and lack of irrigation has further contributed to poor crop yields (Ryan and Spencer, 2001; Jens *et al*., 2007).

Sorghum has been reported to be drought resilient and produces even better yields with minimum precipitation and thus is the crop of choice in ensuring food security (Riziki and Mwangi, 2013). Furthermore, it requires little farm inputs such as fertilizers or sometimes does well in poor soils (Fetene *et al*., 2011; Riziki and Mwangi, 2013). Sorghum is rich in carbohydrates and the macro-elements such as magnesium, potassium, calcium and phosphorus; however, it has low protein content and other important minerals, for example, iron and zinc (Riziki and Mwangi, 2013). Sorghum is also used as a livestock feed in form of fodder and silage (Wambugu and Mburu, 2014); Motlhaodi *et al*., 2014). Sorghum is also rich in B-complex (Lloyd *et al*., 2010), iron and zinc (Mohammed *et al*., 2010), copper and pantothenate (Joseph and Lloyd, 2004) and gluten free (Ciacci *et al*., 2007). It has a crude protein content similar to wheat but lower than corn (Etuk *et al*., 2012) but lower in vitamin A (Carter *et al*., 1989). Sorghum therefore has the potential to be exploited in the management

of lifestyle diseases and since its drought tolerant it can quarantine adequate nutrition in view of climate change effects currently being experienced the world over. Therefore, the potential of sorghum to address food security, generate income and create jobs and manage life-style diseases has not been fully exploited in Kenya (Riziki and Mwangi, 2013).

2.3 Drought effects on plant growth

Inadequate water (drought) is the cause of major crop losses in the tropics (Blum, 1988). The ASALs experience intermittent and highly variable rainfall, high temperatures and poor soils. According to Prasad *et al*. (2008), drought stress is associated with high temperatures and moisture stress. The high temperatures increase transpiration rate and influence soil-water and temperature balance (Amelework, *et al*., 2015). Drought predictions were previously based on meteorological data (Blum, 2011) but currently drought is being assessed based on soil moisture balance and soil properties. Assessment of the soil properties remains paramount because inadequate soil moisture affects the plant ability to complete its growth period (Moussa and Abdel-Aziz, 2008).

Water stress occurs at different stages of plant development with considerable impact on grain yield (Tuinstra *et al*., 1997; Kabede *et al*., 2001). At germination stage, moisture deficit may lead to poor plant vigor (Baalbaki *et al*., 1999). At seed setting stage and at anthesis severe yield losses could be realized (Blum, 1996). Drought stress has been categorized into pre and post flowering drought stresses. Different varieties respond differently to moisture stress. Pre-flowering water stress negatively influences traits such as stand count, tillering ability, number of heads and seeds per

head whereas moisture deficit after flowering impacts on transpiration efficiency, photosynthetic rate and sugar translocation and results into poor yields early leaf senescence (Thomas and Howarth, 2000; Xin *et al*., 2008).

2.4 Grain yield selection under moisture stress in sorghum

Sorghum is a highly valued crop in the ASALs due to its ability to withstand drought and poor soil fertility (Kawano *et al*., 1983) hence the need to identify superior and adapted sorghum varieties. Several approaches have been utilized in evaluating the performance of sorghum for release in the ASALs. Evaluating a variable number of sorghum genotypes under optimal growing conditions of moisture levels for proper plant growth has been recommended as one of the treatment regimes. The use of optimal environmental conditions would be most preferred for most farmers since it is accompanied by minimal production cost (Atlin *et al*., 1989; Seetharama *et al*., 1984).

The extent of genetic gain from selection for broader adaptation from both optimal and non-optimal production environments depends on the growth conditions (Bramel-Cox *et al*., 1991). Thus, evaluation of the breeding materials should be carried out in both water stressed and poor soils to enhance the probability of selecting genotypes that are adaptable in both environments (Belete, 2018). The breeding scheme used in the management of segregating populations may influence the rate of genetic gain to be made under stress situations (Belete, 2018). Individual plants selected from early segregating populations under poor soil condition and inadequate moisture are unlikely to maintain similar expressions in subsequent generations. Thus, phenotypic evaluation under moisture stress environment should be done on genotypes that are pure and stable by deploying the most suitable breeding strategy (Belete, 2018).

2.5 Drought as a major sorghum production constraint in the semi-arid tropics

The greatest impact of drought stress depends on the stage of sorghum growth at which it occurs (Krupta *et al*., 2019). In sorghum production, drought stress is significant at the anthesis and seed filing phases of growth. Moisture stress at seedling stage affects crop establishment and the overall yields. Drought stress is categorized as either pre or post flowering drought stresses. Pre anthesis drought stress affects yield determining traits such as stand count, tillering capacity, number of heads and number of seeds per head whereas post-anthesis moisture stress affects transpiration efficiency, CO_2 fixation and carbohydrate translocation which leads to reduced yields and premature leaf senescence (Thomas *et al*., 2000)

2.5.1 Mechanisms of drought response in sorghum

Sorghum varieties adapted to the semi-arid tropics are equipped with several morphological, physiological and biochemical processes which confers drought tolerance ensuring crop survival and production (Krupta *et al*., 2017). Such responses include avoidance, recovery, survival and tolerance. Several mechanisms such as high stomatal conductance coupled with leaf rolling helps in maintaining water potential in the leaf thus lowering leaf temperature which in turn improves transpiration efficiency and carbon fixation. Tolerant sorghum genotypes are also equipped with dense, extensive and deep rooting system for water and nutrient absorption, proper osmotic adjustment, accumulation of proline and the ability to stay-green amidst moisture stress (Krupta *et al*., 2017).

2.5.2 Genetics of drought tolerance in sorghum

Different genotypes respond differently to drought stress and that drought response is influenced by several genes and by several phenotypic, physiological and biochemical factors (Belete, 2018). Previous studies by Ekanayake *et al*. (1985) reported polygenic inheritance in rooting traits. In other studies, Amento-Soto *et al*. (1983) drought tolerance was attributed to long and dense root network which was conditioned by additive-additive gene effect while the root tip thickness was influenced by minor gene effects. Leaf curling and fluid balance in drought tolerance has been associated with a single gene (Belete, 2018).

Genotypes which are tolerant to drought often remain green for a longer period and are known to exhibit a QTL responsible for greenness (Duncan *et al.,* 1981). However, the heritability of this QTL among most genotypes is not consistent. Heritability of the stay-green trait was reported to be controlled by dominant genes as in B35, recessive gene in R9188 and was also influenced by the environment (Belete, 2018). Heritability estimates of 80% and 60% among elite sorghum genotypes have been reported for broad and narrow sense for the stay-green trait respectively (Belete, 2018) enabling their introgression into sorghum improvement programs (Walulu *et al*., 1994). Osmotic adjustment reported in previous studies has been associated with the genes *oa1* and *OA2* (Tuinstra, *et al.,* 1997). The stay green trait has also been attributed to monogenic inheritance in sorghum (Belete, 2018).

2.5.3 Approaches towards breeding for moisture stress in Sorghum

Sorghum breeding programs have focused on the identification of sorghum genotypes with better yield and adaptation to drought (Amelework *et al*., 2015). This has been coupled with the mapping of novel genes like yield, plant itself, target environment and the economic environment which are key drought traits (Fernandez, 1992). Several methods have been deployed in breeding for moisture stress in sorghum for example pure line selection, pedigree, bulk selection and backcrossing.(Acquaah, 2007). Cytoplasmic male sterility and heterosis breeding have been exploited in sorghum improvement programs. Dogget (1988) reported an 86% heterosis on the seed weight per plant, an 82% increase in grain weight and 12% increase in stover weight in sorghum hybrids compared with parents.

Both direct and indirect approaches have been used in the development of sorghum varieties with tolerance to drought. The direct approach assumes that the growing conditions are optimal whereas the indirect approaches are done under moisture stress simulated conditions. Variations for stress tolerance among sorghum genotypes are also as a result of the interaction of genotype by environment rendering direct selection for a physiological trait in one environment challenging. Therefore, indirect selection is mostly preferred method since it takes into consideration yield per se, development traits and the response of the plant towards water stress (Ludlow and Muchow, 1990).

Screening for drought in the past has been done under near normal conditions since the maximum yield potential is only possible under these conditions. It has also been realized that there is a strong linkage between yield and environment (Tuinstra *et al*.,

1997; Habyarimana *et al*., 2004). Nevertheless, a significant genotype x environment interaction may hinder the realization of grain yield potential under poor growing conditions (Chapman *et al*., 2000a, b). Even though yield decline is realized under water stress conditions, Richards (1996) and Tuinstra *et al*. (1997) proposed that selection under these conditions is ideal for selection for yield and drought associated characters. Therefore, drought response is attributed to the tradeoff between osmotic adjustment within the plant and the plant physiological functions in combination with other biotic and abiotic stresses (Amelework *et al*., 2015).

2.6 Screening techniques for drought resistance

In an attempt to understand the balance between several drought tolerance traits and their importance for plant survival several screening methods have been employed. It is worth noting that drought screening trials should incorporate plant growth conditions and plant responses towards these stresses such as tissue water status, leaf area and stomatal conductance (Kidanemaryam, 2019). The screening methods used includes; the use of automated plant phenotyping platforms, automated rotating lysimeter systems, nondestructive measurement of plant water status over time, use of magnetic resonance equipment and other precision equipment's to quantify plant water, use of rain out shelter facilities. Of interest is the emerging field of phonemics which focuses on the characterization of the whole plant phenotypes by use of digital imaging tools (Kidanemaryam, 2019). However, the choice of screening method to be employed in the genetic improvement for sorghum should consider efficiency, reliability, sample size, and time (Johnson, 1980).

2.7 Combining ability studies in sorghum

The knowledge on gene action is a prerequisite tool for plant breeders since it helps them understand the degree of genetic variance from a breeding population and in the development of hybrids. The concept of gene action was first reported by Sprague and Tatum (1942) who described general combining ability (GCA) as the mean an arising from a line in a cross combination, whereas, specific combining ability (SCA) was applied depending on superiority or inferiority of a hybrid combination. GCA indicates the worth of an inbred as a parent of multiple hybrids. Estimates of GCA are useful for choosing a few key inbred to use as testers. SCA is as a result of genetic effects specific to a hybrid combination and not accounted for by GCA effects. SCA measures genetic effects that are specific to a hybrid combination. As a rule of thumb, GCA effects are additive whereas SCA is due non additive effects (Jinks, 1954), or assumed to be a deviation from additivity (Bernardo, 2014)

Performance of several crosses from a single parental line is a way of determining the worth of a genotype with all possible combination. When the average performances between the parents are subtracted from the average of all the crosses, the GCA of the line is derived. Every cross derivative provides a figure which is a summation of the GCA effects of the two parents. The extent of deviation may sometimes be smaller or bigger than the expected mean. The deviation is the SCA of the two lines in combination. The SCA is of interest because it indicates the degree of heterosis expressed in each cross while representing the dominance deviation value in the simplest case but ignoring epistatic deviation. Therefore, a cross between sorghums with greater combining ability, from diverse origin, is more likely to result in a hybrid

with a greater degree of heterosis which will also be manifested in a greater SCA for one of the lines in specific combination with the other.

Griffing (1956) reported that the inbreeding coefficient F=1 among inbred parents (homozygous), the genetic variance σ^2_G (variance among hybrids) could be termed as the combining ability where;

$\sigma^2G = \sigma^2_{GCA} + \sigma^2_{SCA}$

And,

σ^2_{GCA} and σ^2_{SCA} are the variances for general and specific combining ability effects respectively.

Partitioning of combining ability variance indicates both the major and minor gene effects and their interaction while SCA effects components reveals both dominance and epistasis (Rojas and Sprague, 1952). Kambal and Webster (1965) estimated the components of variance caused by GCA and SCA and their interaction with years for five traits in split-plot design and reported that both GCA and SCA were important in determining yield and other characters, but the GCA effects were prominent and stable over years. Beil and Atkins (1967) observed that variances for GCA were three times more than specific effects and found similar ratios with such traits as the number of kernels per panicle, number of panicles per plant, and weight of 100 kernels.

Indhubala (2010) reported the preponderance of non-dominant gene interaction in all traits observed in sweet sorghum. Makanda *et al*. (2010) reported combining ability for sorghum grain yield in different tropical and mid-altitude environments and

reported that GCA and SCA were significant for all the traits implying that both additive and non-additive gene effects. Similarly, Mahdy *et al*. (2011) revealed that GCA variance components for days taken to 50% anthesis, plant height, and 1000 seed weight were bigger than those of SCA in different environments whereas the SCA for grain yield was more than GCA effects. However, Tariq *et al.,* (2014) reported that the dominance variance was greater than the additive variance for all the parameters studied with a degree of dominance greater than one among sorghum genotypes.

2.8 Cytoplasmic male sterility in sorghum

The development of sorghum hybrids depends on the types of parents used. Sorghum is largely a self-pollinated plant and suffers from sterility issues. The sterility in sorghum is designated as cytoplasmic–genic male sterility on which hybrid production is dependent since it prevents self-pollination and eases emasculation by hand (Quinby and Martin, 1954; Stephens and Holland, 1954). Hybrid production has emanated from production of genotypes that are designated as male and female sterile parents depending on the presence or absence of fertility restoration genes. The R line (restorer line) contains the fertility-restoring genes and used as a male; sometimes it is designated a B line and can be sterilized by backcrossing with a male sterile designated as an A line.

2.9 Determinants of grain yield in sorghum

Yield is the ultimate product harvested in sorghum. Several characters within and without the plants contributes towards grain yield in crops. Researchers have pointed several QTLs involved in yield determination in sorghum (Madhusudhana, 2019).

Similarly, yield was also found to be associated with some phenotypic traits such as plant height and panicle characteristics.(Madhusudhana, 2019). However, the expression of yield is affected by the genotypic by environmental interactions.

Several researchers have reported the QTL responsible for grain yield in sorghum (S Hart *et al.*, 2001; Brown *et al.*, 2006; Srinivas *et al*., 2009; Reddy *et al*., 2013; Shehzad and Okuno, 2015;Sukumaran *et al*., 2016; Boyles *et al*., 2016;; Eight QTLs with diverse genetic origin were reported on linkage group (LG) 2, 3, 6, 9, and 10. Three of the QTL reported on linkage group 10 were meta-QTL indicating their consistent expression in diverse genetic backgrounds (Mace and Jordan, 2011). Six of the eight QTLs were major effect QTL controlling less than 10% of total phenotypic influence on grain yield. Shehzad and Okuno (2015) reported a major QTL for grain yield on linkage group 7 contributing about 22% of total variance. A robust and consistent QTL on linkage group 1 (*qYLD1.1*) was reported to influence grain yield both under stress and non-stress environments (Sukumaran *et al*., 2016). A major QTL on linkage group 6 (14.6%) was co-located with QTL for seven important grain yield determining traits (Srinivas *et al*., 2009). This QTL region on LG 6 harbored the major maturity gene, Ma_1, and major dwarfing gene, Dw_2. Such consistent and major QTLs are suitable for marker assisted selection (MAS) for grain improvement in sorghum.

2.10 Morphological characterization of sorghum

Sorghum landraces exhibit high morphological variations (Motlhaodi *et al*., 2014). Phenotypic traits have aided in selection of desirable genotypes in sorghum namely plant height, seed weight, panicle length and the days taken to reach 50% anthesis

(Kumar *et al*., 2011; Esperance, 2009). These morphological traits enhance the tolerance and survival of sorghum under intermittent drought conditions without compromising yields (N'guni *et al*., 2011). Morphological studies have been used to determine the genetic variation of sorghum and their ability to respond positively to environmental stresses. (Abdi *et al*.,2002; Motlhaodi *et al*., 2014).

Panicle characteristics and stalk juiciness are key morphological traits which contribute to altitudinal and ecological differentiation and reflect the patterns portrayed within their centers of diversity (Abdi *et al*., 2002; Deu *et al*., 2006). Some landraces are classified only by their glume color while others by panicle shape, which may also explain their weak genetic architectures (Claid and Chakauya, 2008). Further, Teshome *et al*. (1997) reported that leaf midrib color is the greatest morphological trait used in identifying specific sorghum landrace. Morphological traits such as prolific root system and ability to delay reproductive development have made sorghum to survive drought and yield higher produce (Alhassan, 2005).

Sorghum color is also a useful morphological trait (Adeline *et al*., 2007) with most land races exhibiting red grain color as the dominant color followed by brown color (Esperance, 2009). Panicle shape is easily identifiable by farmers in their fields (Claid and Chakauya, 2008; Abdi *et al*., 2002). The panicle shapes vary from compact elliptic panicle to very open panicle (Chantereau and Rattunde, 2006). Sorghum varieties with waxy leaves and stalks have shown drought tolerance (Reddy *et al*., 2007) while the shattering character associated with grain coverage and most preferred by farmers especially during threshing (Adeline *et al*., 2007).

2.11 Proximate composition of sorghum

Sorghum contains several nutritional components such as various phytochemicals like phenols that can be exploited in the management of malnutrition and modern lifestyle diseases such as cancers, hypertension, obesity and diabetes (Awika and Rooney, 2004; Ralph, 2000). These phytochemicals lower the risk of colon and skin cancers; promote cardiovascular health, and lower cholesterol levels due to their antioxidant characteristics (Sistino, 2003). Phenols in sorghum have also been known to hinder protein bioavailability by forming insoluble complexes however, this does not affect its antioxidant activity (Reid and Hagerman, 2001).

The phenolic compounds in sorghum are grouped into two categories; the phenolic acids and the flavonoids which also vary with the environment (Joseph and Lloyd, 2004). Phenols may influence the pigmentation of sorghum seed color like the red, brown and white sorghum grain types. However, sorghum grain color may not be accurate in determining the phenol levels.

2.12 Mating designs in sorghum

Breeding designs also referred to as mating designs have been used in the study of genetic traits among a set breeding population (Hallauer and Miranda, 1989). These mating designs give useful data on the extent of genetic variations and combining abilities for the different traits in the breeding population. Mating designs can be categorized into one, two, three or four factor designs based on the method of control brought by parents to be crossed. Simple and the commonly used designs are two factor designs namely diallel, the North Carolina Designs (NCD 1) and NCD 11). Other designs are triallel and quadrille. In any genetic study, a breeder should choose

a simple design but that will provide the required genetic estimates. According to Hallauer (2007), NCD11 mating scheme is a preferred cross-classification design because a larger number of a breeding population is used to generate fewer number of crosses than in a diallel design (Hill *et al*., 1998).

The North Carolina design 11 mating design was proposed by Comstock and Robinson (1948). Parents clustered as either males or females in this mating design (Hallauer and Miranda, 1989). The mating scheme results into progenies that is composed of male and female half sib families, and male x female full sib families. The genetic components can be determined from the mean squares obtained from the ANOVA of the North Carolina design 11 (Hallauer and Miranda, 1989). Gene effects and heritability can be calculated from the ANOVA (Henning and Townsend, 2005). The North Carolina design 11 mating scheme has been used to estimate genetic variances and heritability's in hop (Henning and Shaun Townsend, 2005), in beans (Elia, 2003) and in maize (Derera *et al*., 2001) but not widely used in sorghum.

CHAPTER THREE

PHENOTYPIC EVALUATION OF ELITE SORGHUM GENOTYPES FOR YIELD UNDER DROUGHT STRESS CONDITIONS

Abstract

Drought stress contributes to significant yield losses in sorghum especially in semi-arid areas of Kenya. The trial was conducted to investigate the grain yield of elite sorghum genotypes under moisture stressed environment. The genotypes in this study were evaluated during the short and long rains of 2014/2015 at KALRO Kiboko in a randomized complete block design (RCBD) with three replications for three seasons. Data was collected on plant vigor, days to 50% flowering, plant height, drought tolerance, grain yield, senescence and seed set based on ICRISAT 1993 sorghum descriptor. The collected data was subjected to analysis of variance (ANOVA) using GENSTAT software version 15 and means separated using Duncan's Multiple Range Test (DMRT). Results showed that the genotypes Red Swazi, Gadam, and Seredo significantly ($p<0.05$) gave the highest grain yield whereas Wheatland, IS #76-23, and Red Swazi were the earliest maturing varieties under water stress. All the varieties showed a moderate score on drought response. Grain yield was found to associate positively with all the agronomic traits studied signifying that selection for sorghum genotypes in the semi-arid areas of Kenya should be based on several agronomic parameters but more so on drought response and plant height.

Key words: Elite sorghum genotypes, drought stress, phenotypic evaluation

3.1 Introduction.

Sorghum is the fifth most important cereal crop. It occupies the second position among the stable food grains in the semi-arid tropics where it is a food security crop for more than 300 million people in Africa (Kadenemaryam *et al.*, 2019). In Africa, sorghum is ranked as the third most useful crop after maize and wheat while in Eastern Kenya it is ranked second after maize (Ngugi *et al*., 2013). Sorghum is relatively tolerant to low moisture potential than other cereals such as maize and wheat. Sorghum is projected to serve as a food security crop in view of the global climate change effect (Krupa *et al*., 2017). Despite Sorghum being endowed with suitable morphological, physiological and biochemical adaptation to drought, the production of the crop is still constrained by unpredictable rainfall and prolonged drought (Krupa *et al*., 2017).

Genetic variations exist among sorghum genotypes in terms of grain yield and drought tolerance, however, their degree of adaptation and mode of gene action on most of yield related traits have not been fully understood and applied in breeding programs (Ahmad *et al*., 2011). Heritability is a measure of the phenotypic variance due to genetic effect and plays a significant role in determining a breeding outcome (Tadesse *et al*., 2015). Heritability gives information as to which morpho-genic trait is to be transmitted to subsequent generations, breeding method to be employed, prediction of the genetic gain and the usefulness of gene effects (Waqar *et al*., 2008; Laghari *et al*., 2010). Both broad and narrow sense heritability have been exploited in breeding programs (Falconer and Mackay 1996). Rapid selection is accelerated by high heritability values. Nevertheless, it has been noted that heritability alone is not adequate if used without incorporating genetic advance (Najeeb *et al*., 2009). The degree of genetic gain

from a given trait in a given selection process is dictated by genetic advance. A bigger genetic advance with higher heritability estimates reduces selection intensity (Tadesse *et al*., 2015).

Several genotypes adaptable to semi-arid tropics have been bred and released to the farmers in drought prone regions. However, their adoption and utilization has been hindered by poor farmers' attitude towards sorghum. The current study sought to evaluate the elite sorghum genotypes under drought stress to determine their yield potential with regards to the current climate change.

3.2.1 Trial Station

The field experiment was conducted at KALRO-Kiboko Kenya for three seasons during the short and long rainy seasons of 2014/2015. KALRO-Kiboko lies at an altitude of 993 m above sea level (ASL) and is located on the latitudes $2^{o}15'$ S and longitude $37^{o}45'$E Rainfall pattern is bimodal with an annual mean of 600 mm. The region has annual mean maximum temperature of 30.6 ^{o}C, annual mean minimum.

3.2.2 Planting materials

The sorghum genotypes evaluated are marked by their local names, origin and pedigree as shown on Table 3.1.

Table 3. 1 Name, Origin and Pedigree of Genotypes Studied

Line no.	Name	Origin	Pedigree
1	Gadam	KALRO	Improved (OPV)
2	KARIMtama1	KALRO	Improved variety (OPV)
3	ICSVII	ICRISAT	Inbred line
4	IS76-23	ICRISAT	Inbred line
5	KAT487	KALRO	Improved variety (OPV)
6	KAT369	KALRO	Landrace (Makueni local)
7	Red Swazi	KALRO	Landrace
8	SDS5232	ICRISAT	Inbred line
9	Seredo	KALRO	Improved variety (OPV)
10	Serena	KALRO	Improved variety (OPV)
11	Wheatland	KALRO	Landrace

3.2.3 Experimental design

The genotypes were planted in three replications at spacing of 75cm by 25cm in a randomized complete block design (RCBD) at KALRO-Kiboko sub-station.

3.2.4 Scoring

The agronomic data was scored based on the sorghum descriptors developed by (IPGRI)/ICRISAT (1993) as reference for the observation.

3.2.5 Activities and data collected

Planting was done on 5m x 4m rows plots at a spacing of 75cm x 25cm. A compound fertilizer (NPK) applied during planting the rate of 50Kg ha^{-1}. Seed drilling was done followed by thinning at two weeks' time interval to provide a crop stand of 56,000 plants/ ha. Planting was done 15 days after the start of rains to stimulate drought stress with two subsequent sprinkler irrigations. Moisture stress was imposed by irrigating the plots after every 4 days for three hours per every day, from germination stage for one week (7 days) before anthesis when moisture stress was imposed. Two more irrigations were done as follows; the first one was applied, fourteen days after 50% of the plants had flowered while the second one was applied, twenty-six days after 80-100% of the plants had completed flowering.

Agronomic traits were scored as follows;

i. Seedling vigor measured 14 days after sowing was given a score of between 1-5, where 1 indicated the strongest vigor and 5, the weakest.
ii. Grain weight was measured from heads of two inner two rows in grams but excluded two border plants from each two rows.
iii. Days to flowering was recorded as the number of days from planting to when 50% of the plants in each plot flowered.
iv. Plant height was measured as the distance in centimeters from the base of the plant to the tip of the panicle from a mean of 5 plants at physiological maturity.
v. Senescence was measured in a score between 1-3, where Score 1, indicated

complete death of leaves and stalk,2 moderate and 3 indicated very slightly.

vi. Drought tolerance was measured using a score of between 1-3, where 1, indicated the most susceptible,2 moderate and 3 the most tolerant, 100 seed weight; was measured as the number of 100 seeds in each sample and weight expressed in grams.

3.2.6 Data analysis

The data collected were subjected to analysis of variance using General Statistics (GenStat) Discovery, 15th Edition. (Payne *et al*., 2011) to compute the means, variances among the agronomic traits. The mean separation was done using Duncan's multiple range Test (DMRT) at 5% significance level. Simple linear correlation coefficient (Pearson, 1985) was performed to understand the relationship among the agronomic traits studied. The correlation coefficient was defined by;

$r = cov.\ x1x2\ (var.\ x1)\ (cov.\ x2)$

Where: r = correlation coefficient cov.*x*1*x*2 = covariance between traits *x*1*x*2

var.*x*1= variance of trait *x*1 var.*x*2= variance of trait *x*2 to calculate simple linear correlation coefficients

Genetic variances were estimated by the formula given by Burton and Vane (1956) and Johnson *et al*. (1955) while genotypic and phenotypic covariances for different traits were calculated based on the formula given by Miller *et al*., (1958) as follows;

σ^2G (an estimate of genotypic variance) = (MSG −MSE)/r,

Where; MSG was the estimate of mean square of tested accession,

MSE was the estimate of mean square of error, r, refers to the number of replications; MSE is the estimate of σ^2E;

σ^2P (an estimate of phenotypic variance) = σ^2G (genotypic component of variance) +σ^2E;

PCV (phenotypic coefficient of variation) =$\sqrt{\sigma^2}$P/X×100,

Where; σ^2P was the phenotypic component of variance. X was the average mean of the trait

GCV (genotypic coefficient of variation) =$\sqrt{\sigma}$2G/X×100,

Where; σ^2G was the genotypic component of variance. X was the average mean of the trait;h^{2}B (broad sense heritability) =σ^2G/σ^2p,

Where;σ^2G is the genotypic component of variance and σ^2P was the phenotypic component of variance;

GA (genetic advance) was taken as a percent of the mean assuming selection of the superior 5% of the accessions;

(GA (as% of the mean) =K×$\sqrt{\sigma^2}$P/X×hB2×100,

Where; (the standardized selection intensity) = 2.06 (at 5%selection intensity), σ^2P was the phenotypic component of variance, h^{2}B was the heritability in broad sense, and X was referred to as the mean of the trait being evaluate

3.2 RESULTS

3.3.1 Weather data

Weather data for KALRO-Kiboko was obtained from Kenya Meteorological Department (KMD) (www.meteo.go.ke) in 2015 (Appendix 1). The temperatures during the experimental period ranged from a mean of 20.0 ^{0}C-18.0 ^{0}C for season one (2014 short rains) and from 19.0 ^{0}C-18.0 ^{0}C during second season, (2014 long rains). KALRO-Kiboko experienced a total of 271.35 mm and 440.65 mm during the 2014 short rains and 2015 long rains, respectively. Rainfall was lowest in January and highest in December in both the years.

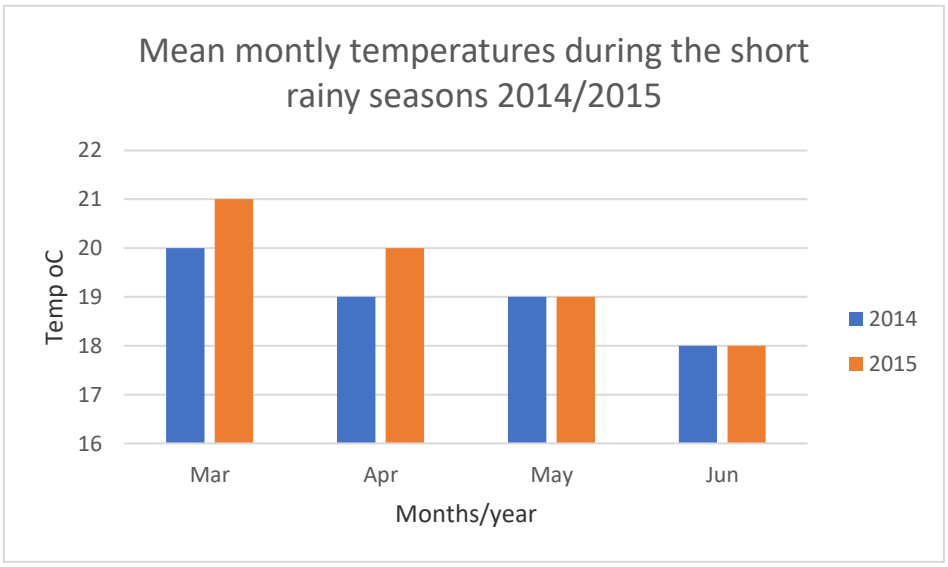

Figure 1. 1 Mean monthly temperatures during short rain seasons

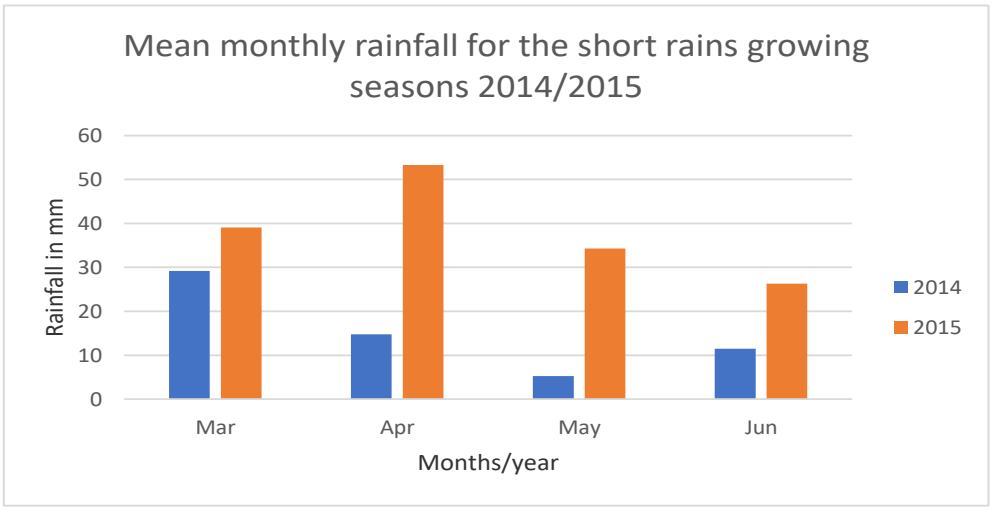

Figure 1. 2 Mean monthly rainfall during short rains growing season

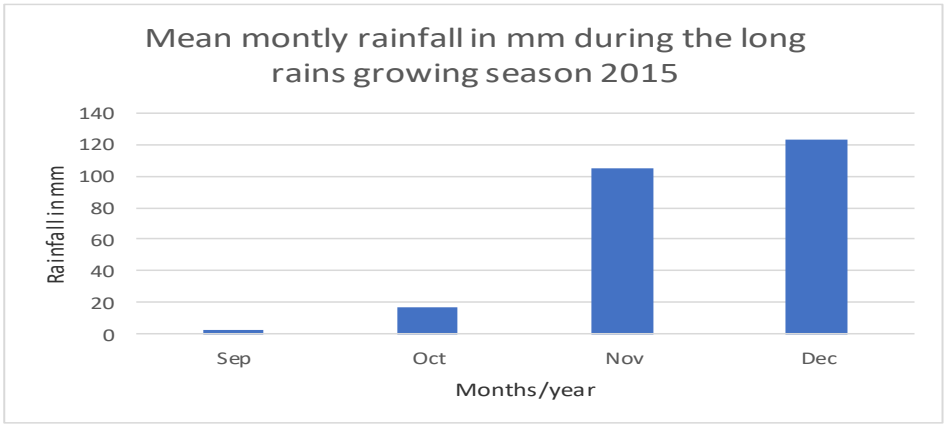

Figure 1. 3 Mean monthly rainfall

during the long rains growing season

3.3.2 Variation among the genotypes during the short rains March -May 2014

The analysis of variance (ANOVA) (Table. 3.2) revealed significant differences in terms of grain yield (p=0.525), plant height (p=0.042) among the genotypes.

Table 3. 2 Analysis of variance (ANOVA) among the genotypes studied during season 1 short rains (2014)

Source of variation	DF	SW	DTF	DT	YD	PH	PV	SS	SNS
Rep	2	0.1468	0.182	0.545	107989	114.7	16.545	1410.9	8.1565
Genotype	10	0.6538	161.6	2.303	612241**	3728.2**	146.788	2363.3	4.1818
Error	20	1.802	31.81	6.787	1312264	2994.5	196.182	2539.1	7.8182

Key: **=highly Significant at 95%, * = significant at 95%, DF=Degrees of freedom, SW=100 seed weight, DTF= days to 50%flowering, DT=drought score, YD=yield, PH=plant height, PV=plant vigor, SS=seed set%, SNS=senescence

3.3.3 Performance of the genotypes during the short rains

Significant differences (p=0.005) were reported for plant height (p=0.04) and grain yield (p=0.525) among the genotypes studied. The average plant height was 176.4cm, the shortest genotype was ICSV11 with the height of 155.0cm while the tallest was SDS5232 (194.3cm). Plant vigor was average among the genotypes. Seed set was all time high at an average78.6%. Seredo reporting the lowest seed set (71.70%) and Gadam the highest (90.00%). All the genotypes reported moderate drought tolerance score with an average score of 2.00. Senenceses was lowest among the genotypes with an average of 1.43. The average mean yield was 1418gms with SDS5232 reporting the highest (1643gms) while the lowest was ICSV11 (1137gms). The genotypes displayed significant differences in grain yield (p=0.525). The mean for 100 seed weight was 1. 8gms. Red Swazi reported the lowest seed weight (1.6gms) whereas ICSV11 (2.1gms) and Serena (2.1gms) reporting the highest respectively. The genotypes took an average of 74 days to flower. (Table 3.3)

Table3. 3 Mean performance for the agronomic traits evaluated during 2014 short rains at KALRO-KIBOKO

ENT. No	GENOTYPE	DTF	PH	PV	SS%	DT	SNS	YD	100SW
1	GADAMEL	74.8	174.2	14.67	90.00	267	1.00	1452	1.8
2	ICSV11	74.1	155.0	15.67	73.30	2.33	1.00	1137	2.1
3	IS#76-23	73.1	176.9	15.67	81.70	2.67	1.33	1495	1.9
4	KARIMTAMA1	73.9	178.3	17.33	93.30	2.67	1.33	1284	1.7
5	KAT369	75.4	182.9	16.33	73.30	2.33	1.67	1310	1.6
6	KAT487	73.4	184.8	16.33	88.30	2.33	1.00	1375	1.8
7	REDSWAZI	74.3	174.6	17.33	80.00	2.33	1.67	1501	1.6
8	SDS5232	76.7	194.3	17.67	73030	2.00	1.33	1643	1.8
9	SEREDO	73.8	186.9	16.33	71.70	2.33	1.33	1514	1.9
10	SERENA	74.8	172.6	16.33	73.30	2.00	1.33	1558	2.1
11	WHEATLAND	72.9	161.1	18.33	66.70	2.62	1.67	1463	1.8
	Grand mean	74.3	176.4	16.85	78.6	2.00	1.43	1418	1.8
	P<0.05	0.997	0.040**	0.904	0.089	0.732	0.427	0.525**	0.693
	LSD	16.058	20.84	4.614	18.10	0.436	1.065	436.3	0..511
	CV (%)	9.2	6.9	16.4	13.5	17.7	6.2	17.9	16.3

Key: **=highly Significant at P≤0.05, * = significant at P≤0.05, DF=degrees of freedom, SD=100 seed weight, DTF=Days to 50% flowering, DT=drought score,=YD-yield per plot, NPH= No. of plants harvested, PH=plant height, PV=plant vigor, SS=seed set%, SNS= senescence, LSD= Least significant difference of means (5% level); CV=Coefficient of variation

3.3.4 Variations among the agronomic traits evaluated genotypes during the long rains (October-December,2014)

The analysis of variance (ANOVA) revealed significant differences for drought tolerance (p=0.004), plant vigor (0.003) and senescence (p=0.023). (Table 3.4)

Table3. 4 Analysis of variance (ANOVA) among the genotypes for the agronomic traits evaluated during 2014 long rains

Source of variation	DF	SW	DTF	DT	YD	PH	PV	SS	SNS
Rep	2	0.2527	0.788	2.1818	94203	604.3	27.152	455	2.6061
Genotype	10	0.8751	24.242	3.6366*	415768	3666.8	36.582*	780.30	2.7273*
Error	20	1.3194	45.212	1.8818	1753952	3450.1	36.182	1325.79	4.7273

Key: **=highly Significant at 95%, * = significant at 95%, DF=Degrees of freedom, SW=100 seed weight, DTF= days to 50%flowering, DT=drought score, YD=yield, PH=plant height, PV=plant vigor, SS=seed set%, SNS=senescence

3.3.5 Mean performance of the genotypes during season 2 long rains 2014

Significant differences (P<0.05) was observed among the genotypes in terms of drought tolerance, plant vigor and senescence (Table3.5). The highest plant vigor was noted with Seredo and KAT487 recording 18.00 and 19.00 respectively. KARIMtama1 reported the lowest with 16.00. Drought score was moderate among

the genotypes however, significant differences (p=0.004) among the genotypes was observed. IS#76-23, KAT369 and Seredo were the most drought tolerant genotypes. Significant differences were noted in terms of senescence (p=0.023). SDS5232 was the least senescence (1.00) whereas KARIMtama1 and KAT369 the most senescence at 2.00 respectively. (Table 3.5)

Table 3.5 Mean Performance by the genotypes during Season 2 Long Rains 2014

ENTRY No.	GENOTYPE	DTF	PH	PV	SS%	DT	SNS	YD	100SW
1	GADAMEL	75.00	144.2	18.33	80.00	2.00	1.67	1668	1.9
2	ICSV11	73.67	177.9	18.67	85.00	2.66	1.67	1585	1.7
3	IS#76-23	73.33	171.7	18.00	81.70	3.00	1.33	1459	1.8
4	KARIMTAMA1	75.33	182.2	16.00	83.30	2.67	2.00	1708	2.0
5	KAT369	73.00	172.2	17.33	75.00	3.00	2.00	1502	1.8
6	KAT487	74.00	175.8	19.63	93.30	2.67	1.33	1462	1.9
7	REDSWAZI	74.33	185.2	18.67	75.00	2.67	1.67	1748	1.8
8	SDS5232	75.33	172.2	17.67	82.00	2.67	1.00	1367	2.3
9	SEREDO	73.00	176.1	19.00	80.00	3.00	1.67	1526	2.1
10	SERENA	75.00	174.4	16.33	83.30	2.67	1.33	1512	1.9
11	WHEATLAND	73.67	173.4	17.67	78.3	2.00	1.67	1479	2.0
	Grand mean	74.15	173.7	17.94	81.40	2.67	1.57	1531	1.9
	P-value	0.426	0.073	0.003**	0.362	0.004**	0.023**	0.888	0.280
	LSD	2.561	22.37	2.291	13.88	0.514	1.065	504.4	0.4365
	CV (%)	2.0	6.9	7.5	10.0	11.4	21.8	19.1	13.2

Key: **=highly Significant at P≤0.05, * = significant at P≤0.05, DF=degrees of freedom, SD=100 seed weight, DTF=Days to 50% flowering, DT=drought score,=YD-yield per plot, NPH= No. of plants harvested, PH=plant height, PV=plant vigor, SS=seed set%, SNS= senescence, LSD= Least significant difference of means (5% level); CV=Coefficient of variation

3.3.6 Variations observed during season 3 short rains 2015 (March -June)

The ANOVA revealed significant differences (p<0.05) in terms of days to 50% flowering, plant height (Table 3.6)

Table3. 5 Analysis of variance (ANOVA) among the genotypes between the agronomic traits during the short rains (2015).

Source of variation	DF	SW	DTF	DT	YD	PH	PV	SS	SNS
Rep	2	0.3224	0.182	0.2424	76289	26.47	0.727	28.79	0.4242
Genotype	10	0.1618	161.61**	1.5758	20588	791.07**	27.636	140.91	1.5151
Error	20	1.4351	31.81	2.4242	33727	257.24	29.273	354.33	1.5757

Key: **=highly Significant at 95%, * = significant at 95%, DF=Degrees of freedom, SW=100 seed weight, DTF= days to 50%flowering, DT=drought score, YD=yield, PH=plant height, PV=plant vigor, SS=seed set%, SNS=senescence

3.3.7 Mean performance among the genotypes for the agronomic traits evaluated during season 3 short rains (2015)

There were significant differences ($p<0.005$) among the genotypes for the agronomic traits such as days taken to 50% flowering ($p=0.001$) and plant height ($p=0.001$). Serena took the shortest time to flower (72 days) while SDS5232 took the longest time to flower (80 days) but averagely the genotypes took 74 days to flower. The average plant height was 176.0cm.). KAT369 was the tallest at (183.0cm) while Serena was the shortest at (165.8cm) (Table 3.7)

Table 3. 6 Mean Performance of Genotypes Short Rains 2015 Season 3

ENT. No	GENOTYPE	DTF	PH	PV	SS%	DT	SNS	YD	100SW
1	GADAMEL	75.67	174.4	17.00	83.33	2.67	1.00	1833.4	1.87
2	ICSV11	73.33	182.2	17.00	90.00	3.00	1.33	1920.1	1.96
3	IS#76-23	73.33	177.1	18.00	86.67	3.00	1.00	1689.5	2.00
4	KARIMTAMA1	75.33	181.3	19.33	90.00	3.00	1.00	1795.6	1.90
5	KAT369	76.00	183.3	18.00	88.33	3.00	1.33	1798.3	2.03
6	KAT487	73.33	175.0	18.33	90.00	3.00	1.00	1666.5	1.87
7	REDSWAZI	73.00	174.3	18.00	90.00	3.00	1.67	1819.5	1.97
8	SDS5232	80.33	170.4	19.33	88.33	2.33	1.00	1793.3	1.8
9	SEREDO	72.67	176.1	20.00	90.00	2.67	1.00	1826.0	1.87
10	SERENA	72.67	165.8	18.00	90.00	2.67	1.00	1682.8	1.93
11	WHEATLAND	73.00	175.5	20.00	82.82	3.00	1.00	1671.7	1.83
	Grand mean	74.36	176.0	18.64	88.45	2.48	1.12	1772.4	1.91
	P<0.05	0.001**	0.01**	0.109	0.635	0.285	0.089	0.327	0.958
	LSD	2.148	22.37	2.061	7.171	0.5930	0.428	221.18	0.371
	CV (%)	1.7	6.9	6.5	4.8	12.2	2.5	7.3	11.4

Key: **=highly Significant at P≤0.05, * = significant at P≤0.05, DF=degrees of freedom, SD=100 seed weight, DTF=Days to 50% flowering, DT=drought score,=YD-yield per plot, NPH= No. of plants harvested, PH=plant height, PV=plant vigor, SS=seed set%, SNS= senescence, LSD= Least significant difference of means (5% level); CV=Coefficient of variation

3.3.8 Variation among the genotypes across the three seasons 2014/2015

There were significant differences ($p<0.005$) among the genotypes for the agronomic traits evaluated such as days to 50%flowering, plant height and plant vigor. Season significantly influenced the genotypes in as far as drought tolerance, yield, seedling vigor, seed set% and, senescence was concerned. Significant genotype by season

(GXS) interaction was observed for the duration to achieve 50% flowering, plant vigor and plant height, yield and seed set% (Table 3.8).

Table 3. 7 Combined analysis of variance (ANOVA) among the genotypes across the three seasons during 2014/2015

Source of variation	DF	SW	DTF	DT	YD	PH	PV	SS	SNS
Rep	2	0.033	0.434	0.13	54620	167.4	10.5	53.28	1.04
Genotype	10	0.034	10.8**	0.25	28930	266.7**	3.3**	142.5	0.43
Season	2	0.091	0.5	1.9**	1002884**	72.5	37.4**	853.3**	1.82*
Genotype x season	20	0.067	8.1*	0.24	47215	275.9*	3.21	88	0.2
Error	64	0.064	2.9	0.21	55823	111.1	3.6	62.6	0.23

Key: **=highly Significant at 95%, * = significant at 95%, DF=Degrees of freedom, SW=100 seed weight, DTF= days to 50%flowering, DT=drought score, YD=yield, PH=plant height, PV=plant vigor, SS=seed set%, SNS=senescence

3.3.9. Mean performance of the genotypes across the three growing seasons during 2014/2015

All the genotypes displayed moderate to high scores in terms of drought tolerance across the three seasons. IS#76-23 was the most tolerant among the genotypes while Wheatland scored the least. Season significantly influenced all the drought related traits among the genotypes ($p<0.001$). High degree of senescence was observed for all the genotypes and this varied across the seasons however, not statistically significant. KAT 369, Red Swazi and, Seredo had a moderate score of 1.667 respectively (Table 3.9). The number of days taken to flower varied from 74-75 days; relatively the genotypes took about two and a half months to flower. Significant differences were noted among the genotypes as well as between genotype by seasons ($p<0.001$). The genotypes exhibited significant differences in plant height ($p=0.0017$) across the seasons. The average plant height was 175. 4cm. The tallest variety across the three seasons was KARI Mtama 1 at 182.3cm while the shortest one was Wheatland at 170cm. Generally, the varieties were medium in height. IS #76-23 having the highest number of plants harvested at 17.00, whereas ICSV11 had the lowest plant harvested at 16.00. Significant differences were noted among the genotypes as well as greater

interaction between genotype by season. There was a significance difference noted in seed set % (p= 0.024) among the genotypes. Red Swazi had the highest seed set at 90.56% whereas KAT487 had the lowest seed set% at 78.89% across the seasons. However, seed set was all time high among the genotypes across the three seasons. All the genotypes reported higher grain yields. Red Swazi had the highest grain yields with 1689.6 gms while KAT487 the lowest at 1501.3gms. The yields were stable across seasons (Table 3.9).

Table3. 9 Combined Means for Traits Evaluated During Short and Long Rains at KALRO-Kiboko during 2014/2015

ENTRY No	GENOTYPE	DTF	PH	PV	SS%	DT	SNS	YD	100SW
1	GADAMEL	74.8	164.3	16.2	83.33	2.444	1.222	1644	1.9
2	ICSV11	74.1	171.7	15.8	84.44	2.667	1.444	1547	1.9
3	IS#76-23	73.1	175.2	17.4	82.78	2.889	1.222	1548	1.9
4	KARIMTAMA1	73.9	182.3	17.1	83.33	2.778	1.444	1596	1.9
5	KAT369	75.4	179.5	16.3	88.89	2.778	1.667	1537	1.8
6	KAT487	73.4	178.4	16.4	78.89	2.667	1.111	1501	1.9
7	REDSWAZI	74.3	178	17.3	90.56	2.556	1.667	1690	1.8
8	SDS5232	76.7	178.9	17.3	81.67	2.444	1.111	1601	2
9	SEREDO	73.8	179.7	16.1	80.56	2.556	1.667	1639	2
10	SERENA	74.8	170.9	17.1	80.56	2.667	1.222	1584	2
11	WHEATLAND	72.9	170	16.4	82.22	2.333	1.444	1538	1.9
	Grand mean	74.3	175.4	16.7	77.22	2.616	1.384	1584	1.9
	P<0.05	0.39	0.017*	0.83	0.024*	0.323	0.077	0.871	0.86
	LSD	1.89	9.93	2.18	7.454	0.436	0.46	222.5	0.24
	CV (%)	2.7	6	13.9	9.6	17.7	35.3	14.9	13.4

Key: **=highly Significant at P≤0.05, * = significant at P≤0.05, DF=degrees of freedom, SD=100 seed weight, DTF=Days to 50% flowering, DT=drought score,=YD-yield per plot, PH=plant height, PV=plant vigor, SS=seed set%, SNS= senescence, LSD= Least significant difference of means (5% level); CV=Coefficient of variation

3.3.10 Association between phenotypic traits

Drought tolerance associated positively with seed set% (r=0.4781*) and seed weight (r=0.1979). Seedling vigor was positively correlated with senesces (r=0.2622), Plant height (r=0.0732), plant vigor (r=0.3471), 100 seed weight (r=0.099), yields (r=0.2889), and days to 50% flowering (r=0.1628). Days to 50 % flowering was positively correlated with senesces (r=0.3224), plant height (r=0.0722) and 100 seed weight (r=0.1655) (Table 3.10).

Grain yield was found to be correlated with all the agronomic traits evaluated but more significantly was noted with the plant vigor (r=0.5521**). The seed weight reported a positive association with plant height (r=0.0504). The plant vigor positively associated with senesces (r=0.0237), seed set % (r=0.0446), and plant height(r=0.1494). Plant height was positively associated with senesces (r=0.1055) and seed set % (r=0.1058) (Table 3.10).

Table3. 10 Phenotypic Relationship Between Grain Yield and Yield Related Traits for The Genotypes Evaluated at KARLO-Kiboko.

	YD	DT	PV	DTF	100SW	NPH	PH	SS%
YD								
DT	-0.213							
PV	-0.184	0.252						
DTF	-0.557*	0.007	-0.182					
100SW	-0.148	-0.325	-0.171	-0.129				
NPH	-0.251	-0.018	-0.394	0.33	0.069			
PH	-0.465	0.14	0.046	-0.077	-0.107	-0.154		
SS%	-0.211	-0.452	-0.006	-0.014	0.229	-0.053	-0.189	
SNS	0.011	0.244	-0.09	-0.269	0.019	-0.031	-0.071	0.117

Key: * = significant at P≤0.05, DF=degrees of freedom, SD=100 seed weight, DTF=Days to 50% flowering, DT=drought score, =YD-yield per plot, NPH= No. of plants harvested, PH=plant height, PV=plant vigor, SS=seed set%, SNS= senescence.

Yield was negatively correlated with all the traits studied (Table 3.11) except days to 50% flowering (r=-0.557). Drought tolerance score was negatively associated with seed set (r=-0.452) and with 100 seed weight (r=-0.325) but weakly positively correlated with senescence (r=0.244). Days to flower was weakly negatively correlated with senescence (r=-0.269) (Table.3.11**).**

Table 3. 11 Phenotypic Correlation Between Drought Tolerance and Yield Related Traits

	DT	PV	DTF	YD (gms)	100SDW	NPH	PH (cm)	SS%
DT								
PV	-0.02							
DTF	-0.65	-0.29						
YD (gms)	-0.40	-0.26	0.52					
100SDW	-0.16	-0.06	-0.19	-0.15				
NPH	-0.07	-0.26	0.06	-0.39	0.12			
PH (cm)	-0.37	0.04	-0.11	-0.10	-0.05	-0.10		
SS%	-0.29*	0.14	-0.05	-0.08	0.11	-0.03	-0.13	
SNS	0.12	-0.12	-0.31	-0.15	0.13	0.03	-0.09	0.27

*** = significant at P≤0.05, SD=100 seed weight, DTF=Days to 50% flowering, DT=drought score, =YD-yield per plot, NPH= No. of plants harvested, PH=plant height, PV=plant vigor, SS=seed set%, SNS= senescence.**

3.3.11. Phenotypic and genotypic associations

No significant variations were reported among the genotypes for the agronomic traits studied (Table3.12). Heritability estimates were low and ranged from 2%-15% except yield which had the highest heritability but negative (-95%). The GA as a mean varied from 0.118% in days to 50% flowering to 37% in yields. The GA was very low as well among these genotypes (Table 3.12).

Table3. 12 Phenotypic and Genotypic association between the Traits

TRAIT	S^2G	S^2P	GRMEAN	H^2%	GCV%	PCV%	GA%
100SDW	-0.0105	0.1218	1.9	8	5.4	18.37	3.02
DTF	0.183	12.847	74	1.2	0.537	4.805	0.118
DT	0.01326	0.4763	2.616	2	4.29	26.39	1.08
YD (gms)	-8964	94073	1584.1	-95	-6	19.36	37
NPH	-0.7703	1056.36	16.7	7	5.25	19.5	2.8
PH (cm)	51.86	438.86	175.4	11	4.105	11.94	2.9
PV	-0.1363	6.76	17.71	2	2.08	14.68	0.6
SS%	26.6	177.23	82.83	15	6	16.07	5
SNS	0.064	0.5084	1.384	12	18.28	51.52	12.73

Key: 100SDW=100 seed weight, DTF=Days to 50% flowering, DT=drought score, =YD-yield per plot, NPH= No. of plants harvested, PH=plant height, PV=plant vigor, SS=seed set%, SNS= senescence, GRMEAN=Grand mean S^2G=genotypic variance, S^2P=phenotypic variance, H^2%=broad sense heritability, GCV%=genotypic coefficient of variation, PCV%=phenotypic coefficient of variation, GA%=genetic advance

3.5 DISCUSSION

Variance analysis among the genotypes across the three season's revealed greater genetic variability among the sorghum genotypes evaluated. The observed variations could be explained by genotypic differences and also due to genotypic by season interaction. In season one or during the short rains (March -June), the plants experienced more water stress than during the long rains (October-December). The days taken to reach 50% flowering was averagely 74 days but this was reported across the seasons. Earliness is a form of genotypic adaptation to drought stress since plants that are able to flower early are capable of escaping terminal drought stress which often leads to reduced yield or complete crop failure (Tadesse *et al*., 2015).

Earliness is a key drought stress trait in breeding programs with the current study reporting early flowering genotypes which could utilize the available moisture leading

to high yields. Assefa *et al*., (2010) reported 36% yield reduction in sorghum due to moisture stress at the vegetative phase and 55% yield reduction attributed to moisture stress during the reproductive phase.

Plant heights across the seasons were significantly different and this was greatly influenced by the genotype and also by season. The average plant height across the season was 175. 4cm.The genotypes were tallest in season 1 and 3 (176.4cm) but shortest in season 2 (173.7cm). Adequate moisture levels in the soil are critical for proper growth and development of any plant. In moisture stress environment stunted growth, suppressed leaf number and elongation, reduced photosynthetic ability and low dry matter accumulation (Blum, 1996). In this study, the plants were shortest in season two which were the long rains (October-December 2014). During this season irrigation was applied just for four days in a week for three hours to facilitate germination and proper establishment, the rest of the growing season depended on natural precipitation which was scanty and sporadic as opposed to season 1 and 3 where supplementary irrigation was done. Genotypes that are able to escape drought are usually short in stature as a sort of genotypic adaptation to enable them utilize the little moisture available to complete their life cycle without compromising yields. Researchers have reported a strong association between plant height and grain yield (Ramasamy, 2013) where tall plants have been associated with longer maturity time with greater yield under optimal conditions but with poor yields under sub-optimal under unfavorable growing conditions (Karari, 2006).

Plant vigor influences growth rate and escape from growth stress. Crop that is able to establish fast may escape weeds, diseases, pest and even drought. In season 1, the crops were less vigorous as compared with season 2 and three respectively. These

genotypic differences could be attributed to moisture levels in the soil during germination phase. Senescence which is the ability of the plants to retain their leaf is an adaptation towards drought tolerance. Genotypes that are able to retain their green leaf for a longer period are able to convert radiant energy in sugars and translate the sugars into yields'. Seed set and seed weight differed across the seasons owing to the growing conditions and moisture levels throughout the growing seasons.

The negative correlation observed between days to 50% flowering and grain yield (r=-0.557) implies that delayed flowering was correlated with lowest grain yield. Under unfavorable environmental conditions, some plants are likely to delay flowering and anthesis till conditions become favorable, but may fail to flower completely if the conditions are unfavorable leading to no seed formation. Early flowering is a form of genotypic adaptation to current environment and highly correlated to drought (Kumar and Abbo, 2001; Tadesse *et al*., 2015). Earliness trait can protect the plant from most biotic and abiotic stresses like diseases and drought (Monpara and Dhameliya, 2013). The genotypes that flowered early also gave higher yields in both seasons since they were able to escape terminal drought.

Very little linear relationship was observed between the yield and drought revealing the role of genotype by season interactions. In this study, the genotypes Red Swazi, Gadam, and Seredo gave higher grain yields whereas Wheatland IS#76-23, and Red Swazi were the earliest maturing genotypes.

The variation observed between PCV and GCV for the traits evaluated were small signifying less environmental effect in the phenotypic traits studied. Similar reports had been cited by Sami *et al*., (2013) who observed small differences between PCV

and GCV on sweet sorghum genotypes .This implies that these genotypes have a narrow genetic base and will not therefore respond positively to selection further signifying that they have a common ancestry (Tadesse *et al*., 2015). However wider differences were noted for traits such as grain yield, plant height and seed set and therefore selection for improvement purposes could be based on these traits.

Heritability for most traits were low and ranged from 2%-15%. This means that most of the traits would not respond positively to selection and that are affected by environment. A report by Obilana and Fakorede (1996) also revealed that if a trait is affected by environment, then its heritability would be low in a population in which the environments differed widely. On the contrary, in controlled environment, these variations do not occur and the traits would portray higher heritability. However, the heritability for grain yield was highest among the traits studied though negative (-95%). This trait would therefore respond positively to selection. This is in agreement with findings by Ahmed *et al*., (2016) while working on local sorghum genotypes in Sudan.

The mean GA ranged from 0.118% in days to 50% flowering to 37% in grain yields. The low values for heritability and the low percentage of genetic advance suggest that the observed differences among the genotypes were due to non-additive gene effect. Rao and Patil (1996) suggested that selection should be based on traits with higher heritability and genetic advance.

3.6. Conclusion and Recommendations

This study identified four superior sorghum genotypes namely Red Swazi, Wheatland, IS#76-23 and Gadam which could be evaluated further for release within the ASALs.

It was also noted that the sorghum genotypes studied differed with respect to their yield and drought responses.

CHAPTER FOUR

PROXIMATE COMPOSITION OF ELITE SORGHUM GENOTYPES BRED FOR THE SEMI -ARID AREAS OF KENYA

Abstract

Hunger and malnutrition experienced in the semi-arid areas of Kenya is occasioned by continuous use of low yielding landraces with low nutritional composition coupled with drought stress. The study was undertaken to assess the nutritional composition of elite sorghum genotypes with an aim of identifying the ones with high protein and phenol content to help in the control of malnutrition and lifestyle diseases in the marginalized areas of Kenya. Ten grams of genotypes used in the study were oven dried to a moisture content of 12%. The samples were then grounded into flour using mortar and pestle. Each sample was then divided into three portions to represent three replications. Proximate components; ash, fat, moisture content, protein content, carbohydrates, total energy (kcal), total oxalates, and total phenols were determined following AOAC specification. Data was analyzed by ANOVA and means separation was conducted by Duncan's' Multiple Range Test (DMRT). The results showed a high significant difference ($p<0.005$) in energy, protein, ash and total phenolic. Genotype IESH2210 had the highest levels of energy 353.08 kcal in energy/cal while Gadam had the least at 334.30kcal. IESH2210RL had the highest protein content at 12.853% and the lowest was Gadam at 4.2%. Total phenolic contents were highest in ICV23006RL at 628.5mg/100g while they were lowest in IESV91104RL with 146.9mg/100g.Total phenols reported a positive significant association with crude fibre at (r=0.539**), Significant but negative association was recorded between phenols and CHO % (r=-0.929**) and with proteins(r=-0.596*). Genotypes IESV2210 and IESV23010DL scored highly in protein content and therefore can be

selected for sorghum improvement towards combating malnutrition in the semi-arid areas of Kenya.

Key words; Elite sorghum genotypes, proximate composition, Malnutrition

4.1 Introduction

The climate change effect has greatly hampered agricultural productivity in the tropics (Lobell *et al*., 2010). This has often resulted into frequent food shortages and rampant malnutrition especially in the ASALs of Kenya (Mohajan, 2014). Sorghum is considered as a poor man's crop due to its ability to perform well under drought stress, poor soils and requires less farm inputs (Riziki and Mwadalu, 2013). In SSA, sorghum is mainly grown by resource constraint farmers where it serves several purposes ranging from human to livestock feed (Tadesse *et al*., 2015). Due to climate change effects, most dependable and preferred cereals such as wheat and maize have become highly susceptible to moisture stress and as a result their yields are predicted to decline significantly by the year 2050 (Knox *et al.*,2010).With disastrous consequences on human livelihood in the semi-arid areas.

Breeding programs by the national agricultural research stations (NARS) focuses on breeding for drought tolerant crops and particularly high yielding and nutritious sorghum genotypes since improved/hybrids are known to yield better than landraces. However, their utilization has been hampered by poor uptake and preference on maize among the farmers in ASALs. These improved genotypes are rich in proteins; energy and micronutrients (Fe and Zn) providing the much-needed calories and protect the population from malnutrition and hidden hunger compared to the landraces (Muui *et al*., 2013)

Sorghum grains contain phenols which are important for the management of lifestyle diseases. These phenols have been reported to exhibit antioxidant property (Choi *et al*., 2007), anti-carcinogenic property (Kwak *et al*., 2004), lower cholesterol (Ha *et al*., 1998) and can reduce mortality associated with cardiovascular illnesses (Cho *et al*., 2000).

Despite the ability of sorghum to guarantee food security, control malnutrition and manage lifestyle diseases, its utilization is still very low due to overdependence on maize. This study sought to evaluate the proximate composition of elite sorghum genotypes bred for the semi-arid areas of Kenya so as to inform policy makers on the need to popularize sorghum technologies in Kenya.

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4.2 Materials and Methods

4.2.1 Materials

The Studies were conducted at the University of Nairobi, Department of food science and Nutrition based at the college of Agriculture and veterinary sciences (CAVs). In this study, grains of ten Sorghum genotypes obtained from ICRISAT were used (Table 4.1)

Table 4. 1 Name, Origin and, Pedigree of Grain Samples Used for the Study

Line no.	Name	Origin	Pedigree
1	ATX623XMACIA	ICRISAT	Inbred line
2	Gadam	ICRISAT	Improved line
3	ICSV111 IN	ICRISAT	Inbred line
4	ICSV23006DL	ICRISAT	Inbred line
5	IESH2210	ICRISAT	Inbred line
6	IESV22012	ICRISAT	Inbred line
7	IESV23010DL	ICRISAT	Inbred line
8	IESV91004RL	ICRISAT	Inbred line
9	KARI Mtama 1	ICRISAT	Inbred line
10	Macia	ICRISAT	Improved line

4.2.2 Sample preparation

Studied samples were manually cleaned from foreign materials and grounded into flour.

4.2.3 Methods of Analysis

4.2.3.1 Nutritional Analysis.

The representative samples of sorghum flour genotypes were divided into three portions and analyzed for proximate composition.

(1) Moisture Determination.

Moisture content was determined by AOAC 925; 10 (Horwirtz, 2000). Two grams (2 g) of powdered grains of each genotype was divided into three portions and placed into dry dishes of pre-determined mass. These were then oven for 1 h at 130° C/until a constant mass was observed. The samples were then removed from the oven and allowed to cool normally and reweighed.

Moisture % = W_1 - $W_2 * 100/ S_W$ Where; W_1 was the mast of the dish and fresh sample, W_2 is the mass of the dry sample and dish, and S_W is the sample weight.

(2) Ash% content

Four grams of the sample was placed into a crucible of known mass and heated in a muffle furnace set at 550° C. The samples were ignited until light grey color was observed. The sample was then removed and cooled at room temperature and reweighed.

Ash % = $W_1 - W_2 * 100/ S_W$, where; W_1 is the weight of the ash+crucible after ashing, W_2 is the weight of the empty crucible, and S_W is the weight of the sample taken.

(3) Determination of fat content.

Fat content was determined by Sox let extraction method. Two grams of the flour sample was placed into an already prepared extraction thimble. The sample containing thimble was fitted with fat-free absorbent cotton wool. The Sox let extraction apparatus was assembled and filled with petroleum ether spirit to a half capacity before the fat of the sample is extracted. Then, the extraction was allowed to run for 4 hours. Afterward, the extracted fat was removed, and then, oil/fat-containing flasks were placed onto the rotary evaporator to allow for solvent evaporate and oven drying at at 103° C for 30 min, followed by cooling in a desiccator and reweighing. Fat % = $W_f - W * 100 / S_W$,

Where; W_f is the mass of the receiver flask and fat deposit, W is the mass of the empty receiver flask only, and S_W is the mass of the sample used.

(4) Determination of crude fibre content

Two grams of preheated samples was placed into a one-liter (1 l) beaker, and then, digested in a hot plate for 1 h with a mixture of an equal volume of 2.5 M H_2SO_4 and 2.5 M NaOH. Then, filtration was done by moisturizing with small volumes of ethanol. The filtrate was dried in an oven at 100° C until a constant mass was obtained (W1). Then, the oven-dried samples were again incinerated at 600° C for 3 h in a muffle furnace followed by cooling and reweighed (W2).

Crude fiber % = $W1 - W2 * 100 / SW$,

Where; W1 is the mass of the porcelain crucible and sample before ashing, W2 is the mass of the porcelain crucible containing ash, and W is the mass of the sample.

(5) Protein Determination.

The test was performed by the Kjeldahl method of (W. Horwirtz, 2000). 0.5 g of sorghum flour sample was weighted into a 50 ml Kjeldahl flask, and 8 ml of concentrated H_2S0_4 was added with 2 grams of (copper and potassium sulfate) mixture catalyst. Samples were digested until pure colorless solution was observed. Then, digested samples were distilled by using Kjeldahl distiller, and the distilled steam gas (ammonia) was collected with 25 ml of the mixture of 2% boric acid mixed indicator of bromocresol green plus methyl red. The distilled sample was titrated by 0.1 N HCl until the first appearance of the pink color.

Crude protein % = $(a * b * 14 * 6.25 * 100) /W$,

Where; a represents the normality of the acid; b is the volume of standard acid used (ml), corrected for the blank (i.e., the sample minus the blank); W is the sample weight (g); and 6.25 is the conversion factor for protein from % nitrogen.

(6) Total Carbohydrate (CHO %)

It was determined as a total carbohydrate by subtracting measured protein, fat, ash, and moisture from 100%.

Total carbohydrate (%) = 100 − Moisture (%) + Protein (%) + Fat (%) + Ash (%).

(7) The Gross Food Energy.

The value was estimated by the following equation

Food energy kcal/ g = $(\%TC - \%CF) \times 4 + (\%TF \times 9) + (\%CP \times 4)$,

Where; TC is the total carbohydrate, CF is the crude fiber, TF is the total fat, and CP is the crude protein.

(8) Phenol Content determination.

Total phenols were determined by using vanillin-HCL assay methods using a UV spectrophotometer (Burns, 1971) as modified by (Rooney *et al*., 1972) cereal chemistry. One gram of the sample in a screw cap test tube was measured, and then, 10 ml of 1% HCl in methanol was added to the tube containing the sorghum sample. The sample-containing tube was placed on a mechanical shaker for 24 h at room temperature, and then, the tube was centrifuged at 1000g for 5 minutes. One milliliter (1 ml) of supernatant was taken and mixed with 5 ml of vanillin-HCl reagent in another test tube. Then, the sample was allowed to wait for 20 minutes to complete the reaction, and then, the absorbance of the colored intensity of the sample was measured using a UV-visible spectrophotometer at 500 nm.

Tannin (mg/g) = ($A_s - A_{b)}$ −intercept/ (Slope x *d* x *W)* x10,

Where;

A_s is the sample absorbance, A_b is the blank absorbance, *d* is the density of the solution (0.791 g/ml), *W* is the weight of the sample in gram, and 10 is the aliquot.

(9) Evaluation of total Oxalates

This was determined by the procedure outlined by Day and Underwood (1986) whereby 1g of the powdered composite sample was placed onto a 100ml conical flask followed by addition of 75ml $3MH_2SO_{4.\ The}$ mixture was centrifuged for one hour and filtered. The filtrate was titrated against hot 0.05 M $KMnO_4$ solution for 30s before decolonization was observed. $1cm^3$ of 0.05 M $KMnO_4$ was taken to represent 2.2 mg of oxalate.

4.2.4 Statistical analysis

GenStat Discovery, 15th Edition. Payne *et al*., (2011) was used for data analysis. The ANOVA obtained was used to compute the means. Mean separation was done using Duncan's multiple range Test (DMRT) and the probability level was allowed at 95% significance level (Snedecor and Cochran, 1987). Simple linear correlation coefficient (Pearson, 1985) was performed to understand the relationship among the agronomic traits studied. The correlation coefficient was defined by;

$$r = cov.\ x1x2\ (var.\ x1)\ \ (cov.\ x2)$$

Where: r = correlation coefficient cov.*x*1*x*2 = covariance between traits *x*1*x*2 var.*x*1= variance of trait *x*1 var.*x*2= variance of trait *x*2 to calculate simple linear correlation coefficients

4.3 Results

4.3.1 Analysis of variance

Analysis of variance (ANOVA) (Table 4.2) revealed significance differences ($p<0.005$) for ash%, Energy/cal, Protein content and total phenols.

Table4. 2Combined Analysis of Variances for the Proximate Composition on the Genotypes Studied

SOV	DF	MS	VR	Fpr
Ash%	2	1.60	4.79	<0.001**
Moisture content	2	2.53	0.14	0.998
Energy/cal	2	174.88	7.18	<0.001**
Fiber	2	0.63	0.00	0
Fat%	2	2.61	0.17	0.995
Oxalates	2	0.02	-	-
Proteins	2	20.70	2759.05	<0.001**
Total phenolics	2	79620.60	2600.49	<0.001**

Key: **= Significant at 5% level; V.R. = variance ratio; Fpr. =F probability, MS =mean sum of squares, - No data obtained

4.3.2 Proximate analysis

Proximate analysis results (Table 4.3) revealed that the mean moisture content was 8.53%. IESV23010DL had the highest moisture content of 10.350% and ICSV2300RL had the lowest moisture content of 7.513%. The average ash % was 1.623%. IESV91104RL had the highest ash % of 1.745% while KARI mtama1 had the lowest 1.520%. There was a great significant difference in ash content % ($p<0.001$). The mean for CHO% was 72.16%. Gadam had the highest CHO% of 76.47, followed by ATX623XMACIA which had 74.56%. The lowest was IES112210 which had a score of 69.84%. The range varied from 70-76%. There were significance differences in terms of energy in kilojoules among the accessions ($p<0.001$). The mean was 353.08. The highest was obtained by IESH2210 which had 361.5 and the lowest was obtained by Gadam (334.3) and ICSV1111N (349.0) respectively. The range varied from 351-359 for the rest of the genotypes.

The mean fibre % was 2.76%. ICSV23006RL had the highest (3.75%) whereas Gadam had the lowest (2.27%). The mean for protein % was 9.509%. IESH2210 had the highest protein % of 12.853, this was followed by IESV23010DL (12.082), IESV91104RL (11.820) and IESV22012 (10.813). Gadam had the lowest protein content of 4.200%. There was great significant difference noted between accessions ($p<0.001$). The mean fat % was 5.25. IES112210 had the highest fat content (6.560%) whereas Gadam had the least (2.27). The mean for oxalates was 0.35%. ATX623XMACIA had the highest (0.45%) whereas ICSV1111N had the least (0.21%). The mean for total phenols was 301.5mg/100g.ICV23006RL had the highest

(628.5mg/100g) whereas IESV91104RL had the least (146.9mg/100g). There was great significant difference among the accessions ($p<0.001$).

Table4. 3 Proximate Composition of Elite Sorghum Genotypes Studied

GENOTYPE	Ash %	Moisture %	Energy/cal	Fat %	Fibre %	Oxalates %	Proteins %	Total phenols	CHO %
ATX623XMacia	1.62	8.1	353.31	4.24	3.06	0.45	6.83	257.2	74.56
Gadam	1.59	9.68	334.31	3.6	2.27	0.41	4.2	194.9	76.47
ICSV111 IN	1.61	9.15	349	5.37	2.74	0.21	9.77	154.8	70.56
ICSV23006RL	1.71	7.51	352.89	5.03	3.75	0.3	9.564	628.5	72.27
IESH2210	1.675	7.73	361.53	6.56	2.38	0.33	12.85	222.2	69.84
IESV22012	1.65	8.41	358.77	5.98	2.41	0.41	10.81	227.9	70.8
IESV23010DL	1.58	10.35	356.09	6	2.5	0.31	12.09	542.9	70.3
IESV91104RL	1.745	7.81	358.98	6.14	2.71	0.41	11.82	146.9	70.42
KARIMtama1	1.52	8.41	350.97	4.74	3.22	0.28	8.39	354.9	72.81
Macia	1.53	8.1	354.99	4.83	2.6	0.42	8.767	284.4	73.54
Grand mean	1.624	8.53	353.08	5.25	2.76	0.35	9.509	301.5	7216
P value (95%)	<0.001	0.998	<0.001	0.995	0	0	<0.001	<0.001	0
LSD (95%)	0	7.288	8.406	6.671	0	0	0.148	9.33	0
CV	0	50.2	1.4	74.6	0	0	0.9	1.8	0

Key: LSD= Least significant difference of means, (5% level); CV=Coefficient of variation

4.3.3. Correlation between proximate components

The total phenols were significantly correlated with total CHO% and proteins but negatively (r=-0.929 and r=-0.596 respectively) the only positive correlation was with the fibre content % (r=-0.539) (Table 4.4).

Table4. 4 Correlation Coefficients between Total Phenols and Nutritional Traits Measured in Elite Genotypes

	Totphn	CHO%	Ash%	Energy	Fat%	Fibre%	M.C%	Oxal%
Totphn								
CHO_%	-0.929**							
Ash_%	-0.629	0.48						
Energy	-0.61	0.29	0.46					
Fat_%	-0.355	0.15	0.27	0.55				
Fibre_%	0.539**	-0.47	-0.54	-0.45	-0.09			
M.C%	-0.446	0.22	0.33	0.65	0.87	-0.14		
Oxal%	0.836	-0.76	-0.65	-0.58	-0.26	0.68	-0.33	
Prtn%	-0.596*	0.84	0.13	-0.23	-0.18	-0.17	-0.14	-0.39

Key: **highly significant at p<0.0I, *significant at p<0.05, Totphn=total phenols, m.c=moisture content, oxal%=oxalate %, prtn%=protein%

4.4 Discussion

Sorghum is a critical crop in the provision of vitamins, proteins and micronutrients necessary for maintenance of proper health, growth and development in view of climate change effects (Salgueiro *et al*., 2002, Chan *et al*., 2007, Masresha Minuye Tasie and Belay Gezahegn Gebreyes.2020). Determination of proximate composition of sorghum would improve sorghum utilization and product development in Kenya. (Masresha Minuye Tasie and Belay Gezahegn Gebreyes. 2020)

The ash % content of sorghum is related to mineral content. The mean for ash % was 1.60% and ranged from 1.52%-1.74%. This range agrees with those reported by various researchers for various sorghum genotypes evaluated for example 1.30 to 3.40 (Moharram and Youssef, 1995), 0.77 to 1.39 (Chung *et al*., 2011) 1.43 to 1.92% (Pontieri *et al*., 2012), and 1.51 to 2.06% (R. M. E. Hamad, 2006). IESV91104RL reported the highest ash content of 1.74% and this could be attributed to variations arising from soil, water, altitude and climatic differences in which the sorghum was grown (Tasie and Gebreyes. 2020).

The mean for energy content was 353.08Kcal/100g and ranged from 334.3 to 361.5 Kcal. These findings concur with those reported by S.O. Onyango *et al*. (2020). The total energy is related with the total carbohydrates (CHO) since it's the carbohydrates that are oxidized to release energy in the body for vital body functions. IESV2210 reported the highest energy /cal values of 361.53Kcal. Much of this energy is contributed by the carbohydrates, fats and to some extent proteins. The genotype

IESV2210 with the highest energy value also had the highest fat content (6.56%) and the highest protein content (12.85%) in this study.

Sorghum is considered a cheaper source of proteins for the poor people residing in the semi-arid tropics however; its bioavailability is affected by tannins which complexes with the proteins hence influencing its digestibility after cooking as compared to other cereals like maize and wheat (Duodu *et al*., 2002). IESV2210 reported the highest protein content (12.85%). The range for the protein content among the genotypes was 4.2%-12.85%. Gadam reported the lowest protein content (4.2%) and significant variations reported among the genotypes. These results agree with findings by Dicko *et al*., (2006), Johnson *et al*., (2010) and Badigannar et al. (2016). The observed variations in protein contents could be attributed to genotype by environmental interaction (Deosthole *et al*., 1972). The genotypes IESV2210, IESV22012, IESV23010DL and IESV91104RL reported highest protein content as compared to the rest and as such should be considered for sorghum improvement towards control of malnutrition in the ASALs.

The total phenols content ranged from 334.3-628.5mg/100g with a mean of 301.5mg/100g. IESV23006RL reported the highest phenol content of 628.5mg/100g. Variations in phenolic content in sorghum have been documented. Sedghi *et al*. (2010) reported a range of 10mg/100g to 351mg/100g and 0.021 to 0.681%. Kaijage *et al*., (2014) reported a range of 2.18%-5.76% on twelve sorghum genotypes in Tanzania. Food materials containing high phenol content are not favored for consumption because phenols impact negatively on nutrient availability and digestibility unless processed adequately (Tasie and Gebreyes, 2020). Phenols also influences sensory taste of the food by making them bitter hence reducing their

consumption. The genotypes Gadam, ISCSV111N, and IESV91104RL reported very low phenol content and are therefore recommended for food product development and consumption particularly in the developing countries characterized with rapid population growth and hidden hunger. Phenols have been reported to protect the sorghum plant against bird attack, fungal infections, insects and parasitic weeds (Beta *et al*., 2000). It has also been reported that the polyphenols in the seeds also prevent losses due to premature germination and damage from mold (Harris and Burns, 1970).

The association between the total phenols with crude fibre content (r=0.539**) implies though, fibre content did not show significant variation among cultivars, phenolic contents are indicators of high level of crude fibre and therefore phenols can be used as a secondary selection criterion for fibre content. Crude fibre encompasses a complex of indigestible sugars, (Awika and Rooney, 2004). The significant positive correlation observed between total phenols and crude fibers suggest complexes with phenols in grain sorghum (Dykes and Rooney, 2006). As reported in the present study, the genotypes that had the highest crude fibre content also had the highest total phenols and one can therefore safely conclude that these genotypes also had the highest tannin levels.

Positive correlation observed between total phenols and total oxalates (r=0.836) suggests that oxalates are associated with phenols and together they form complexes that renders oxalates non bio-available or low as reported in this study (Awika and Rooney, 2004). The negative and significant correlation between total phenols and CHO% (r=-0.929*) and proteins(r=-0.596*) is due to the fact that phenolic acid forms complexes with proteins, minerals and carbohydrates making them unavailable (Bryden *et al*.,2007).

In the studied sorghum genotypes, there was a tremendous variation that can be exploited in breeding cultivars high in polyphenols, low in oxalate content, high in energy and protein content to mitigate the effect of rising modern life-style diseases, hidden hunger and malnutrition.

4.5 Conclusion and recommendation

This study found that the sorghum genotypes differed in most of the parameters evaluated. These variations were attributed to genotypic effects, environmental and soil type. This study recommends that the genotypes IESV23010DL and IESV2210 are high in protein content and thus should be considered for sorghum improvement in the ASALs. The genotypes ATX623XMacia and Gadam revealed very low protein and phenol content and are therefore suited for baking and brewing purposes.

These selected genotypes should be considered by food industries, consumers and breeders for sorghum improvement for the control of malnutrition and job creation in the country. It can be concluded from this study that determination of nutritional components of various sorghum genotypes is important in designing and developing highly nutritious food products of good quality and also assist breeders in executing a suitable breeding program for sorghum improvement as well as in improving sorghum value chain.

This study further recommends that the selected genotypes could be introduced to the farmers in the semi-arid areas to control rampant malnutrition among school going children and pregnant women since severe drought is associated with household food

insecurity and malnutrition. Consequently, these genotypes should be introgressed into the locally adapted landraces to improve on yield and protein content.

CHAPTER FIVE

GENE ACTION FOR YIELD RELATED TRAITS IN ELITE SORGHUM GENOTYPES BRED FOR SEMI-ARID AREAS OF KENYA

Abstract

Sorghum is a promising cereal crop in SSA in view of climate change effect. This study was undertaken to assess gene action on yield contributing traits on elite sorghum genotypes bred for the semi-arid areas of Kenya. Four elite genotypes were selected for the study; 'IESV23006DL and IESV23010DL were used as males whereas Red Swazi and Wheatland as females. The mating design employed was North Carolina Mating Design 11. The F_1 progenies were evaluated under field conditions at ICRISAT (Kiboko) field station in 2015/2016 and advanced to F_2. Seven agronomic parameters namely; Days to 50% flowering, plant height, grain yield, ear exertion, panicle length, panicle width and seed set. Grain yield was reported to associate positively with panicle length, panicle width and plant height. Comparisons on genetic variances (additive and dominance variance) and dominance ratio in this study revealed the significance of non-additive gene effect on plant height and panicle length while the additive effect was found to control grain yield. Day's to50% flowering, plant height, grain yields revealed the influence by GCA and SCA effects. The male parents were better combiners as depicted by their relatively higher GCA effects and therefore most suited for sorghum nutritional improvement in the ASALs of Kenya.

Key words: Gene Action, elite sorghum genotypes, GCA, SCA

5.1 Introduction

Climate change poses the biggest threat to world food security. Most cereals except sorghum remains very vulnerable to drought effects and may even become extinct by the year 2050 (Knox *et al*., 2010). In spite of this, the world population is increasing rapidly putting a lot of stress on agricultural land and governments on food security. Sorghum is the only crop projected to withstand climate change and guarantee world food security (Lobbel *et al*., 2012). However, sorghum productivity is hampered by the use of low yielding and low nutritious landraces. The semi-arid areas of Kenya constitute about 80% of the Kenyan population (Muui *et al*., 2013). Most of these people are extremely poor and are not technically and financially equipped to mitigate the effect of drought. As a result, food insecurity and malnutrition are frequent in these areas (Riziki and Mwadalu, 2013). Furthermore, sorghum is less preferred compared to the more vulnerable maize.

Climate change has been associated with genetic erosion. Understanding the variations on the morphological traits determining grain yield with respect to sorghum is crucial for breeders in guaranteeing the world future food crisis. The information on the mode of inheritance on these traits will assist in designing breeding strategies which will deliver genotypes that are adaptable, high yielding and nutritious. This study sought to investigate the mode of inheritance of grain yield associated traits from crosses generated from high yielding and nutritious sorghum genotypes so as to inform the breeders and policy makers on the need to improve and popularize sorghum towards realization of food security in view of climate change effect.

5.2 Materials and Methods

5.2.1 Plant materials

The parental sorghum genotypes that were used are represented in table 5.1.

Table5. 1 Name, Origin, Pedigree, and Role df Parental Materials Used in the Study

Line no	Name	Origin	Pedigree	Role in the cross	Desirable traits
1	IESV23006DL	ICRISAT	Inbred line	Male	High yielding, moderate drought tolerance moderate height, high in protein content
2	IESV23010DL	ICRISAT	Inbred line	Male	High yielding, moderate drought tolerance moderate height, high in protein content
3	Red Swazi	KALRO	Landrace	Female	Average yield, tolerant to drought, low in protein content, average plant height
4	Wheatland	KALRO	Landrace	Female	Dwarf, highly tolerant to drought, Average yields, low in protein content

5.2.2 Field trial

Crossing and field evaluation activities were conducted at KALRO-Kiboko, a sub center used for dry land research in Makueni County, Eastern Province, Kenya. It is located about 187 km east of Nairobi. It lies at an altitude 993m above sea level (ASL) and latitude of 2^{o}15'south and longitude 37^{o}45'E. It is classified under agro-ecological zone 5. The mean annual rainfall is 615mm with a bimodal distribution. The short rain is more reliable and falls in October to January with a seasonal mean of 328mm. The long rain falls from March to June with seasonal mean of 233mm.It has mean annual maximum temperature of 30.6^{o}C, and mean annual minimum temperature of 17.4^{o}C and overall means temperatures of 24^{o}C. The soils are sandy clay.

5.2.3 Generation of the crosses

The parental genotypes IESV23006DL and IESV23010DL were used as males whereas Red Swazi and Wheatland were used as females. The mating design North

Carolina mating design 11(NCD11) as proposed by Mather and Jinks (1982) was used to generate the progenies used in the study. At the start of anthesis, the females were emasculated by hand to kill the pollens grains whereas the males were bagged to collect the pollens. When the female florets were completely opened the panicle were reduced to a few florets and pollen transferred to the panicle while shaking gently followed by bagging to prevent outcrossing. Fertilization were done early in the morning on receptive stigmas

5.2.4 Field management and evaluation

The F_1 seeds were harvested and drilled in four-meter rows alongside their parents as checks in randomized block designs with three replications in short rains 2015/2016. Spacing used was 0.75m between rows. Thinning was done three weeks after germination at 0.2m between plants leaving one plant per hill. DAP and CAN fertilizers were applied at recommended rate of 46 kg P_20_5/ha and 54kg/ha, respectively. Weed control was done three times. Off types were removed regularly and the true to type F_1s were tagged, harvested and seeds processed. During the long rains, October-November 2015/2016, the F_1 seeds were advanced to F_2 in randomized plots in three replications.

5.2.5 Data collection and analysis

Data was collected on the F_2 population from middle rows with a net plot area of $6m^2$ for the major the phenotypic characters as; Days to 50% flowering, plant height, drought score, panicle yield, panicle length, panicle width, ear exsertion using sorghum descriptors (IPGRI, 1993) on 40plants that were randomly selected .and bagged. Analysis of data was done to analysis using Gens tat version 15^{th} Edition Payne *et al*., (2011). The ANOVA obtained was used to determine the GCA effects

for the parents as outlined by Kearsey and Pooni (1996) as follows; GCAf= X_f-μ and GCA_m=Xm-μ

Where;

GCA_m and GCA_f=GCA of male and female parents respectively

X_f –mean of female parent, Xm-mean of male parent, μ-overall mean of all crosses

The SCA effects of the crosses were computed according to (Kearsey and Pooni, 1996) as follows; SCAx =X_x-E (X_x) =X_x - [GCA_f+GCA_m+ μ]

Where;

SCA_x=SCA effects of the two parents in the cross, Xx =observed mean value of the cross, E (X_x) =GCAf and GCAm of female and male parents respectively

The standard error (SE) and the standard error of the difference (SED) for the SCA effects were calculated according to (Dabhokar, 1992 as follows;

SEmale = √ (MSE/s*r*f), SEfemale = √ (MSE/s*r*m) and SED male = √ (2MSE/s*r*f), SED female= √ (2MSE/s*r*m),

Where:

MSE = mean square error; r = number of replications; f and m = number of female and male parents, respectively.

5.2 Results

5.2.1Analysis of variance

ANOVA (Table5.2) reported significant difference in terms of plant height, days to 50% flowering and panicle yield among the genotypes signifying greater genetic variability among the genotypes studied.

Table 5. 2 Analysis of Variance (ANOVA) for the Genotypes Studied

SOV	DF	DTF	PH	SS%	PL	PW	GY	EST
Rep	2	1766.86	49357.00	285.68	63.00	6.22	18979.00	11871.00
Gen	3	748.615***	23851.5***	51.28	347.00	12.92	57732**	913.00
Error	6	352.82	4884.60	102.56	65.00	15.19	66370.00	507.00
CV%		0.00	7.80	0.00	6.30	10.20	-	30.70
LSD 95%		4.99	18.55	2.69	2.14	1.03	75.50	5.96

Key: DF=degrees of freedom, DTF=days to 50% flowering, PH=plant height, SS%=seed set, PL=panicle length, PW=panicle width, GY =grain yield, EST=ear exsertion, LSD=least significant differences, CV=coefficient of variation. **p < 5% and *<p1% levels of probability respectively**

When the treatments were partitioned into parents, crosses and their interaction (Table 5.3.), it was found that the crosses differed greatly in days to 50% anthesis and the panicle characteristics. Both the female and male parents revealed significant differences in plant height, panicle length panicle width and grain yield. The interaction between Females X Males displayed significantly for panicle width and grain yield. The variance estimate (σ^2GCA) and (σ^2ca) were significant for days to 50% flowering, plant height and panicle length. Similarly, the variance estimates for GCA were equally significant for days to 50% flowering, plant height and panicle length. The GCA / SCA ratio was greater than one for traits such as panicle length, panicle width and grain yield and less than one for number of days taken to achieve 50% flowering, and plant height. Highest dominance was reported for days taken to reach 50% anthesis, plant height, and the panicle attributes such as length and width.

Table 5. 3 Combined Analysis of Variance for Parents and Crosses

SOV	DF	DTF	PH	PL	PW	PY	EXS	SS%
Crosses	3	62.5*	144.421	20.42**	6.042	2103.7**	12.38	90.00
Female	1	144	122.84***	121.3**	13.1**	1901.3**	9.31	90.00
Males	1	25.8**	146.033	38.5**	5.9**	1692.3**	10.82	88.33
FemalesxMales	3	10.3	132.42	13.9	5.2**	1520.6**	9.11	88.0
σ^2Females	-	3.01**	2031.20**	8.21**	6.22	160.14	11.73	-
σ^2Males	-	20.63**	1010.44**	6.45**	5.900	120.6	11.73	-1.67
$\sigma^2$2GCA	-	5.23**	1031.14**	7.91**	0.177	130.5	-	-
σ^2SCA	-	8.20**	1310.12**	7.52**	0.144	120.6	-	-
σ^2GCA/σ^2SCA	-	0.63	0.787	1.05	1.229	1.08	-	-
σ^2A	-	0.023	534.1	0.006	0.006	-496.6	-	-
σ^2D	-	1.087	659.78	0.002	0.010	2915.6	-	-
σ2A/σ2 D		0.021	0.809	3.05	0.6	-0.170	-	-

Key; *=highly Significant at P≤0.01, ** = significant at P≤0.05, SOV=source of variation DF=degrees of freedom, SD=100 seed weight, DTF=Days to 50% flowering, GY-grain yield, PL= panicle length, PH=plant height, SS=seed set%, EXS=ear exsertion**

The estimates for general combing ability (GCA) (Table5.4) revealed that the male parents IESV23006DL and IESV23010DL reported negative but highly significant values for days to 50% anthesis and plant height a marked GCA effect for panicle weight whereas the female parents (Red Swazi and Wheatland) reported negative significant GCA for days to 50%Flowering. Red Swazi displayed a marked GCA effects for plant tallness whereas Wheatland had a bigger negative GCA for plant height. The GCA for panicle length was negative though not significant in Red Swazi which also reported positive significant GCA for panicle weight. Among the crosses, ICSV23006DLX Red Swazi, ICSV23006DL X Wheatland and ICSV23010DL X Red Swazi reported no significant GCA for days to 50% flowering, ICSV23010XWheatland reported positive GCA values. No significant GCA was reported for plant height, panicle length, panicle width, panicle yield, ear exsertion and seed set% among the crosses.

Table 5. 4 General Combining Ability Effects for the Parents and Crosses According to NCD11 Mating Design

Male Parents	DTF	PH	PL	PW	GY	EXS	SS%
ICSV23006DL	1.62**	40.182**	-1.34	8.15**	11.2	-3.37	0.0
ICSV23010DL	-1.86***	-43.02**	0.772	8.85**	12.5	-3.58	0.812
Female Parents							
Red Swazi	-0.76**	16.50**	-1.566	9.20**	9.25	-	-
Wheatland	-2.02**	-20.12	3.478	6.92	10.74	-	-
Crosses							
ICSV23006DLXRedswazi	-0.26	-21.6	-0.66	3.98	0.17	-	-
ICSV23006DLXWheatland	-0.23	16	-0.49	3.56	0.19	-	-
ICSV23010DLXRedswazi	-0.36	15.63	-0.52	4.23	0.18	-	-
ICSV23010DLXWheatland	0.21	18.36	-0.12	3.68	-0.14	-	-

Key; *=highly Significant at P≤0.01, ** = significant at P≤0.05, DF=degrees of freedom, SD=100 seed weight, DTF=Days to 50% flowering, GY-grain yield, PL= panicle length, PH=plant height, SS=seed set%, EXS=ear exsertion.**

The analysis of specific combining ability (Table 5.5) reveals that the cross IESV23006DL X Red Swazi reported positive and significant SCA for days to 50% flowering but negative GCA for panicle weight and ear exsertion. Similarly, the cross

ICSV23010 X Red Swazi reported positive significant SCA for days to 50% flowering and a non-significant negative ear exsertion. IESV23006DL x Wheatland reported no significant negative SCA for plant height, panicle length and panicle weight whereas the cross IESV23010DL X Wheatland gave negative non-significant SCA for days to 50% flowering and panicle weight but reported positive significant SCA for panicle length.

Table 5. 5 SCA Effects of the Progenies Tested

CROSSES	DTF	PH (cm)	PL (cm)	PW (cm)	GY (gms)	EXS	SS%
ICSV23006DLXRedswazi	1.9*	-3.10	0.65	-0.5	52.0	-1.5	-
ICSV23006DLXWheatland	0.2	-6.1	-1.2	-0.7	49.2	0.1	-
ICSV23010DLXRedswazi	3.5**	9.8	2.9	0.5	46.8	-3.5	-
ICSV23010XWheatland	-0.29	10.30	2.75*	-1.7	46.8	-0.7	-

****=highly Significant at P≤0.005, * = significant at P≤0.05, DF=degrees of freedom, SD=100 seed weight DTF=Days to 50% flowering, GY-panicle yield, PL= panicle length, PH=plant height, SS=seed set%, EXS=ear exsertion, -No data**

5.3. Discussion

The ANOVA obtained for parents revealed significant differences for number of days taken to obtain 50% flowering, plant height and grain yield. This implies that greater genetic variability exists among these parents with their crosses which could be exploited for a breeding target. These further demands the need to analyze the SCA from the populations derived from the crosses. When the treatments were partitioned into parents, crosses and their interaction, it was found that the crosses showed significant differences in days to 50%flowering, panicle length and yield. The male and female parents revealed significant differences in plant height, panicle length, panicle width and grain yield. The Females × Males interaction displayed significant scores for panicle width and grain yield. The male parents displayed remarkable variances in as far as days to 50% flowering, panicle length, panicle width and grain yield are concerned better than the females implying that that they are better

combiners and can produce progenies with desired traits. This is in agreement with Kale (2016) who found similar results while working on gene action in sorghum on different environment.

GCA represents the fixable parts of the genetic variance present and is useful in the breeding of high yielding genotypes. The estimates for general combing ability (GCA) in this study revealed that the male parents IESV23006DL and IESV23010DL reported highly negative significant values for days to attain 50% anthesis and plant height. Similarly, the male parents reported positive and significant GCA values for panicle weight. The female parents (Red Swazi and Wheatland) also reported significant but negative GCA for days to 50% anthesis. Red Swazi (parent) gave positive significant GCA for plant height whereas Wheatland had a bigger negative GCA for the same trait. The GCA for panicle length was negative though not significant in Red Swazi which also reported positive significant GCA for panicle weight. These results conform to those reported by Gilchrest *et al*., (2017). Parents reporting significant but positive GCA values for plant height also yielded better signifying a strong relationship between GCA and performance per se and can be considered good parents in agreements with those reported by Iyamar *et al*. (2001) and Chaundry *et al*. (2006). Negative GCA for plant height is desirable in sorghum improvement programs since it's highly correlated to dwarfness and hence making plants to resist lodging and facilitates easier harvesting using combine harvesters (Fellahi *et al*., 2013). Consequently, negative combining ability effect in sorghum is desirable since it is correlated with earliness (Makanda, 2017).

Plant height modification is probable using these lines since it has been shown to be controlled to a bigger extent by additive genes effects as portrayed in their remarkable

GCA effects (Justine *et al*., 2015). Negative GCA for panicle exsertion is undesirable since leaf sheath encourages the development of fungal infections and insect larvae at the base of the panicle and the whole panicle (Dogget, 1988). Crosses reporting positively significant general combining ability effects for plant height also reported good yield performance pointing a correlation between the two traits and thus can be regarded as good combiners. This concurs with reports by Kulakarni *et al*. (2006).

The specific combining ability (SCA) reveals that the cross IESV23006DL X Red Swazi reported significant SCA for days to 50% flowering but negative GCA for panicle weight and ear exsertion. Similarly, the cross ICSV23010 X Red Swazi reported positive SCA for days to 50% flowering. IESV23006DL X Wheatland reported no significant negative SCA for plant height, panicle length and panicle weight whereas, the cross IESV23010DL X Wheatland gave negative non-significant SCA for days to 50% flowering and panicle weight but reported positive significant SCA for panicle length. A large positive significant SCA implies that the parents are good combiners and that they provided adequate ground for the expression of the desirable alleles influencing the trait even though the parents did not express any trait superiority (Gilchrest, 2017).

The variance estimate σ^2GCA and σ^2SCA were positive for days to 50% flowering, plant height and panicle length. The variance due to SCA was higher than GCA suggesting the role of non-additive gene action in the inheritance of the trait and this could be attributed to complementarily between the parents (Gilchrest, 2017). The GCA / SCA ratio was greater than one for panicle traits implied the role of additive gene action. This corroborates those reported by Aruna *et al*., (2010). The ratio

GCA/SCA for days to 50% flowering and plant height was less than unity suggesting that gene control is non-additive. Mohammed (2009) reported that additive gene action was noted to control days to 50% flowering and forage yield while non-additive gene effects influenced plant height where σ^2GCA/σ^2SCA ratio was less than one. Mahdy *et al*. (2011) found that both additive and non-additive gene action were important for inheritance of plant height and grain yield, and they found the additive effect-controlled days to anthesis. Several researchers indicated the preponderance of additive and non-additive gene action in heritance of grain yield and some agronomic traits (Kenga *et al*., 2004; Abdel-Mottaleb, 2009; Mohammed, 2009; Mahday *et al*., 2011).

The variances due to dominance effect (σ^2 D) were bigger compared to additive variances (σ^2A) in most traits studied with the exemption of panicle length. This agrees with those reported by Fellahi *et al*., (2013) and Rani *et al*., (2015). The variations noted in additive variance with GCA and dominance variance with SCA variance followed by subsequent estimation of the ratio σ^2A/σ^2 D which was more than unitary for the panicle length, panicle width and panicle yield revealed the preponderance gene influence on the traits. For characters such as days to 50% flowering, plant height, ear exsertion, seed set, additive gene action was predominant. Similar findings were reported by Kenga *et al*., (2005) and Tadesse *et al*. (2008).

5.4 Conclusion and Recommendations

There is need for exploitation of genetic variability for crop improvement purposes. The genotypes that exhibit higher GCA could be exploited for sorghum improvement programs through accumulation of desirable alleles using a suitable breeding method.

In this study, the male parents IESV23006DL and IESV23010DL reported higher GCA for panicle yield and yield determining traits and thus could be utilized for advancing sorghum hybridization programs in the semi-arid areas. Similarly, the crosses exhibited higher SCA for panicle yield and plant height. Comparisons on genetic components (additive and dominance variance) and dominance ration in this study revealed the preponderance of dominant gene influence for yield associated characters while major gene effects were significant for panicle yield. Thus, superior genotypes should be selected from the segregating F2 population and advanced further.

CHAPTER SIX

GENERAL DISCUSSION, CONCLUSION AND RECOMMENDATIONS

6.1 Introduction and Conclusion

The use of sorghum is becoming popular over the world due to its ability to tolerate drought stress. In Kenya ASALs, drought stress continues to lower agricultural productivity especially on the most preferred maize crop resulting to rampant food insecurity and malnutrition. Farmers in the ASALs regions of Kenya still insist on growing the less tolerant maize and, in a few cases, sorghum land races which take longer time to mature and are low yielding. In an attempt to address the agricultural production constraints, the NARS has developed and released new improved sorghum genotypes with better adaptation to water stress and nutrition while guaranteeing good yields. Therefore, the study was conducted under the following objectives (1) to evaluate elite sorghum genotypes from KALRO for grain yield under drought stress, (2) to evaluate the elite sorghum genotypes from ICRISAT for proximate composition and (3) to investigate gene action on grain yield determining traits.

To evaluate the sorghum genotypes for grain yield and drought, seven sorghum genotypes were grown at KALRO Kiboko for two seasons. Significant genotype by season interaction was reported among the traits studied. During season 1, early flowering was noted. The genotypes Red Swazi, Gadam, and Seredo gave the highest grain yields whereas Wheatland IS#76-23 and Red Swazi were the earliest maturing genotypes. The positive correlation between drought and seed set confirmed that the genotypes studied were also drought tolerant.

For proximate composition determination, larger genotypic differences were observed among the sorghum genotypes. High phenol content was associated with high crude fibre content which constitutes complex carbon derivatives. Therefore, selection for crude fibre should be considered alongside phenols. This study revealed that the genotypes that reported highest crude fibre also had the highest total phenols implying that these genotypes also had the highest tannin levels (Awika and Rooney, 2004). The levels of oxalates reported were very low and varied from 0.3-0.45% and this therefore makes sorghum one of the few cereal crops with favorable levels of oxalates. A diet having high oxalates more than 50mg per day is not recommended since it results into a condition known as oxalosis (Helen Comer *et al*., 2017). The positive correlation between total phenols and total oxalates (r=0.836) suggested that oxalates are associated with phenols and together they form complexes that renders oxalates unavailable, or low. These make sorghum diets ideal as high oxalate diets are not recommended for human diet as reported (Awika and Rooney, 2004). Genotypes assessed me this study showed great variation in terms of proteins that could be exploited in breeding cultivars with high proteins to mitigate the effect of malnutrition in the ASALs.

The genotypes that exhibited higher GCA should be exploited for sorghum improvement programs through accumulation of desirable alleles using a suitable breeding method. In this study, the male parents IESV23006DL and IESV23010DL showed good GCA for grain yield and other yield contributing traits and thus can be utilized to develop superior sorghum varieties for release in the ASALs. The differences noted from additive and dominance variances with dominance ratios points to the preponderance of dominant gene effect on yield contributing traits while

major gene influence was found significant for panicle yield. The male parents displayed significant differences in days to 50% flowering, panicle length, width and yield than the females implying that that they are better combiners and can produce progenies with desired traits.

6.3 Recommendations

The following recommendations have therefore been made from the study;

1. The genetic information on gene action, genetic variability, and heritability on the sorghum genotypes under study concerning grain yield should be exploited for sorghum improvement purposes.
2. Information on correlation among traits should be exploited in the selection of quantitative traits for future sorghum improvement with emphasis on the strength and direction of the trait association.
3. Molecular techniques should be employed in the validation of genes responsible for drought response and total phenol content.
4. The segregating populations from the crosses should be evaluated further to identify the best performing once for possible release to the farmer

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APPENDICES

Appendix 1: Mean monthly temperatures (^{o}C) for 2014/2015 growing seasons in Kiboko

Year/ Month	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
2014	17	20	20	19	19	18	18	19	19	20	19	18
2015	19	20	21	20	19	18	18	19	20	22	20	19

Appendix 2: Mean monthly rainfall (mm) for 2014/2015 growing season in Kiboko (Makueni County)

Year/ Month	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
2014	3.45	73.64	29.21	14.78	5.26	11.48	1.48	5.24	17.99	17.2	36.15	55.47
2015	13.13	16.78	39.04	53.29	34.3	26.28	6.06	4.08	2.97	17.21	104.61	122.9