BREEDING WITH WILD RELATIVES: SCREENING SORGHUM PRE-BREEDING MATERIAL FOR PERFORMANCE AND ADAPTATION IN WESTERN KENYA

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A THESIS SUBMITTED TO THE SCHOOL OF AGRICULTURE AND BIOTECHNOLOGY IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE AWARD OF DEGREE OF MASTER OF SCIENCE IN PLANT BREEDING AND BIOTECHNOLOGY, UNIVERSITY OF ELDORET, KENYA

2025

DECLARATION

Declaration by the Candidate

This thesis is my original work and has never been presented for the award of an academic degree in any other university and should not be copied, or reproduced in any format without written authority from the author and/or University of Eldoret.

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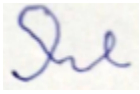
Approval by the Supervisors

This thesis is submitted with our approval as the university supervisors.



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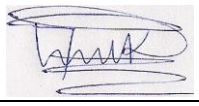

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DEDICATION

This thesis is dedicated to my beloved Parents Dickson Ligeyo and Pamela Nachibwede for their encouragement and financial support which ensured that I carried out my MSc. Studies. Special dedication also goes to my siblings and friends for their encouragement and emotional support and during my studies.

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ABSTRACT

Sorghum (*Sorghum bicolor* L. Moench) is an essential cereal for food security and resilience to climate change in Kenya. Continuous utilization of traditional landraces coupled with biotic and abiotic stresses have led to low sorghum yields in western Kenya. Further, the limited amount of genetic variation within the cultivated sorghum gene pool has constrained breeding efforts to overcome major production constraints. The development of new sorghum diversity through the use of wild and weedy species to enrich cultivated sorghum germplasm offers a novel and promising opportunity. The objectives of this study were to: (i) determine agronomic performance of sorghum wild relatives (SWR) in western Kenya (ii) determine genotype by environment interaction and stability of SWR in selected sites in western Kenya. (iii) Introgress genes from sorghum wild relatives into selected cultivated Kenyan Lines and determine the amount of heterosis in the sorghum crosses for selected traits. Twenty-one (21) SWR plus 4 checks were evaluated for performance in a 5 X 5 alpha lattice replicated thrice at Kibos, Nyabisawa, Sega and Godkwer agro-ecologies. Genotype by Environment interaction (GEI) and yield stability was determined using the Additive Main Effect and Multiplicative Interaction (AMMI) model across 4 environments. A total of 9 crosses were developed and evaluated at Kibos site using RCBD replicated thrice. Results showed significant variation at $p < 0.05$ among sorghum tested for majority of traits studied at the four sites which indicated the existing genetic, difference among the entries tested. The mean grain yield was higher in Kibos (2.1t/ha) in comparison to the other 3 sites mainly because of higher soil fertility levels while Nyabisawa site had the least mean yield of 1.6 t/ha. Entries 466 and 588 were the most promising for grain yield. The AMMI ANOVA for grain yield showed significant effects for genotype (G), environment (E) and GEI. For grain yield, the differences among the (E) accounted for 8.7% of the total variation while the G and GEI accounted for 42.1% and 15.4% respectively of the variation. About 20% of SWR Genotypes were more stable than the checks. A total of 9 crosses were developed and 85% of them exhibited high mid-parent heterosis on majority of the phenotypic traits tested which showed transgressive inheritance and hence possibility for further breeding using the SWRs. The best grain yield per plant heterotic cross combination identified was (RUC26 X 586) which expressed high positive heterosis over both mid and better parent (194.27% and 137.89%, respectively). This cross also showed significant positive average heterosis and heterobeltiosis for yield-contributing components. This study has identified and developed potentially diverse new sorghum germplasm which can be useful in further breeding and yields improvement in western Kenya.

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LIST OF ABBREVIATIONS

AMMI – Additive main effect and multiplicative interactions

ANOVA – Analysis of Variance

CGIAR – Consultative Group for International Agricultural Research

CWR – Crop wild relative

DAP – Diammonium phosphate

EMS – Error mean square

FAOSTAT - Food and Agriculture Organization of the United Nations Statistics Division

ICRISAT- International Crops Research Institute for the Semi-Arid Tropics

FAO – Food and Agriculture Organization of the United Nations

GEI – Genotype Environment Interaction

GP1– Genepool 1

GP2– Genepool 2

GP3– Genepool 3

KALRO – Kenya Agriculture and Livestock Research Organization

KNBS –Kenya national bureau of statistics

PCA – Principal component Analysis

RCBD – Randomized complete block design

SWR – Sorghum wild relative

USDA – United States Department of Agriculture

CHAPTER ONE

INTRODUCTION

1.1 Background information

Sorghum (*Sorghum bicolor* L. Moench) is one of the world's top cereal crops which ranks fifth in terms of production and area sown after wheat, rice, maize and barley (Tonapi *et al.*, 2020). It is especially important in semi-arid regions of Africa due to its resilience to environmental stress and is a staple food for over half a billion people in over 30 countries in Africa (Wani, 2018). It is genetically suited to hot and dry agro-ecologies which are frequently drought-prone and therefore fragile making them difficult to support the growth of other food grains (Reddy and Reddy, 2019). Sorghum originated and was first domesticated in Ethiopia, in Eastern Africa, from where it was introduced to other regions of the world with wide agro-ecology (Li *et al.*, 2010). It is primarily used as animal feed, human food and for industrial purposes (Dahlberg *et al.*, 2011). However sorghum is gaining more popularity in food products due to increase in demand for specialty grains, especially those that are free of gluten by developed countries (Taylor *et al.*, 2006). Demand for sorghum is quickly rising with if being valued as a gluten-free replacement for wheat. Sorghum is a nutrient-rich grain that is high in soluble fibre and antioxidants and may reduce the risk of diseases such as type II diabetes and celiac disease which is an inherited auto-immune condition whereby consumption of gluten from wheat and related prolamins from barley and rye causes damage to the villi of the small intestine resulting in malabsorption of nutrients (Jones, 2017; McGinnis and Painter, 2020). Sorghum has high economic demand in Kenya because it's a major ingredient in the process of sorghum beer

production (Njagi *et al.*, 2019). This important role has led to increased demand for white sorghum for malting and this is projected to utilise more than half of the national sorghum production (KNBS, 2017). Other industries that utilize a lot of sorghum are the animal feed industry to produce feeds and in the production of ethanol and syrup. In order to cater for the increasing demand, the country maximize sorghum potential through commercial production and trade of sorghum (Njagi *et al.*, 2019).

Globally, sorghum is grown in 40 million hectares accounting for an annual production of 58 million tonnes. Top world producers as of 2022 were the USA with a total production of 9.6 million tonnes annually, followed by Nigeria 6.6 million tonnes, Mexico 5.9 million tonnes, India 5.3 million tonnes, Ethiopia 4.5 million tonnes, Sudan 4.45 million tonnes, South Sudan 3.6 million tonnes, and Argentina 3.1 million tonnes, China 2.6 million tonnes and Brazil 2 million tonnes annually (FAOSTAT, 2023).

In Kenya, the area under sorghum production has been on the rise due to the promotion of the crop by the government agencies as one of the climate smart resilient crops to boost food and nutritional security and increase rural income (FAOSTAT, 2023; Ogeto *et al.*, 2013). However, despite the increase in area under production due to these efforts of promotion of the crop, sorghum yields have continued to be poor (Egesa *et al.*, 2016). The poor yields are due to both biotic and abiotic factors which include: drought brought about by climate change among other factors, low soil fertility, increased soil acidity, bird damage, Striga weed infestation, use of cultivars with low yield potentials, pests like Sorghum shoot fly *(Antherigona varia),* Stem borers *(Busseola fusca),* boll worm and Aphids, and diseases (Karanja *et al.*, 2014). Therefore, developing new sorghum breeding

materials with useful diversity for adaptation to climate change is needed to improve resilience and productivity.

Additionally, because of the foreseen impact of climate change, increased population, and the changing production and consumption trend on the agricultural production systems, crops will require to produce good yields in more challenging growth conditions. The wild plant species are considered to become useful resources of diversity containing more allelic diversity (Breithaupt, 2008; Jha *et al.*, 2014; Reynolds *et al.*, 2007). Therefore, this study screened some sorghum pre-breeding material and developed some crosses to increase the diversity of the cultivated sorghum gene pool in order to improve sorghum productivity in western Kenya.

1.2 Statement of the problem

Sorghum production in western Kenya is still low due to many constrains including biotic and abiotic stresses, lack of high-yielding and good quality sorghum varieties, inadequate adoption of improved varieties, inadequate post-harvest management practices among others. These production challenges have led to about 90% yield losses (Koech *et al.*, 2019). Sorghum improvement worldwide has largely focused on using genetic variations within cultivated sorghum gene pools which over time has reduced significantly (Dweikat, 2005; Wooten, 2001). This has resulted in partial genetic uniformity within cultivated species which has slowed down development of multiple stress tolerant varieties with wide adaptation.

Wild plant species together with weedy crop relatives are valuable sources of novel genetic variation and have the capacity to enhance yield improvement and many stress-adaptation

traits(G. Ananda *et al.*, 2020). Normally, transferring important chacteristics from wild relatives into ergonomically acceptable forms and new varieties is challenging and therefore these gene pools remain unexploited in sorghum. Although sorghum breeders in Kenya have over the years made good progress in the development of new crop varieties to overcome some of these production constraints along with improvement in sorghum yield to feed the increasing Kenyan population, some of the constraints such as drought, bird damage, and Striga weed among others are still persistent. Further breeding effort is still necessary so as to completely overcome these constraints. Therefore, exploiting valuable genetic potential in the wild and weedy relatives of sorghum to enhance the diversity of the cultivated sorghum gene pool can further contribute to enhancing resilience in sorghum.

1.3 Justification

Sorghum is an essential cereal crop in western Kenya which is largely grown at the subsistence level and by smallholder farmers. The crop is a dietary staple for most of the rural poor who live in fragile semi-arid lands. The emergence of industrial utilization of sorghum products has created new market demands for the sorghum grain for use in brewing, baking, and ethanol industries. Additionally, health consciousness and blood sugar-related complications demand the consumption of high fibre and low-calorie foods which has further boosted the demand for sorghum and other related grains which have been associated with low-income earners. However potential utilization of sorghum is hindered by continued low production due to lack of diverse varieties with wide adaptation which could grow in major regions of sorghum production in Kenya. This has led to importation from neighbouring countries despite the country’s production potential.

Climate change in the recent years has led to increased drought and unpredictable rainfall patterns which has caused low sorghum yields due to severe moisture stress, increased occurrence of sorghum crop pests and diseases. Low soil fertility and increased mineral toxicity in the sorghum growing areas of western Kenya have further contributed to low yields since fertilizer and other input use by farmers is limited (Ouma and Gudu, 2016). The major source of seed for these farmers is saved seed from the previous crop which are landraces that are low yielding and susceptible to biotic and abiotic stresses (Gesare *et al.*, 2014) hence the need to diversify sorghum sources. Use of pesticides, and other cultural control methods to control major sorghum constraints have yielded less results due to high labour and pesticide costs. Further genetic diversity within cultivated gene pool is almost exhausted and hence the need to look at other potentially available gene pools.

Therefore, the development of new sorghum genetic diversity through tapping genes from wild and weedy sorghums offers a novel and promising approach to enhance sorghum genetic diversity for adaptive traits and provide the foundation for breeding better, more resilient and widely adapted varieties. This endeavour, although little explored to date, offers significant promise for creating new options for improved resilience and productivity in the face of climate change, increased vulnerability and variability. The differential response of genotypes across different testing environment is considered as a hindrance in selecting and recommending genotypes due to yield fluctuations obtained across locations (Fasahat *et al.*, 2014) . Modelling genotype by environment interaction (GXE) offers opportunity for selection and recommendations of adapted genotypes that show positive interaction with the specific location which helps in improving performance across location (Ceccarelli and Grando, 2007).

1.4 Study objectives

1.4.1 General objective

The general objective of this study was to contribute to improved sorghum productivity in western Kenya through the use of new diverse genetic materials obtained by selection from sorghum wild relatives.

1.4.2 Specific objectives

1. To determine agronomic performance of sorghum wild relatives plant introductions in selected sites of western Kenya
2. To determine genotype by environment interaction and stability of sorghum introductions in western Kenya
3. To introgress genes from sorghum wild relatives into selected cultivated Kenyan Lines and determine the amount of heterosis in the sorghum crosses

1.5 Null hypothesis

H_1: The agronomic performance will not differ significantly among the sorghum wild relatives tested

H_2: Genotype by Environment interactions have no influence on the performance and stability of sorghum wild relatives' introductions

H_3: There will be no significant amount of heterosis among the sorghum crosses derived between sorghum wild relatives and Kenyan lines

CHAPTER TWO

LITERATURE REVIEW

2.1 Sorghum origin and domestication

Sorghum is believed to have originated in north-eastern Africa (Ethiopia, Sudan, East Africa), where the greatest diversity of both wild and cultivated species occurs (Acquaah, 2007). Ethiopia is the primary centre of origin and diversity for this crop as shown by the presence of wild and cultivated sorghums there (Dillon *et al.*, 2007; Firew, 2006). It is suggested that wild sorghum was domesticated to cultivated sorghum by selections from subspecies *verticilliflorum*, a wild progenitor, about 5000-7000 years ago (G. K. S. Ananda *et al.*, 2020). The three sorghum types (Cultivated, wild and intermediate) developed from farmer selection for cultivated traits and natural selection for wild characteristics (Olembo *et al.*, 2010). Disruptive selection has been important in the evolution of the species resulting in several levels of a particular character being maintained in the population (Rueffler *et al.*, 2006). It is also suggested that domestication of sorghum happened in Ethiopia and some areas of Congo and with secondary centres of origin in India, Sudan and Nigeria (Acquaah, 2007; Fetene *et al.*, 2011).

2.2 Sorghum Taxonomy and Botanical description

Sorghum is a diploid (2n=2x=20) crop classified into two groups; the wild and the cultivated sorghums. The genus *Sorghum* belongs to the grass family *Poaceae*, subfamily *Panicoideae*, tribe *Andropogoneae*, and sub tribe *Sorghinae* (Venkateswaran *et al.*, 2019). The genus is a very diverse group which has made the classification of domesticated and wild sorghums difficult (Wiersema and Dahlberg, 2007). The genus consists of twenty five recognized species which are classified morphologically into five subgenera:

Chaetosorghum, *Heterosorghum*, *Parasorghum*, *Stiposorghum* and *Eusorghum* (Price *et al.*, 2005; USDA ARS).

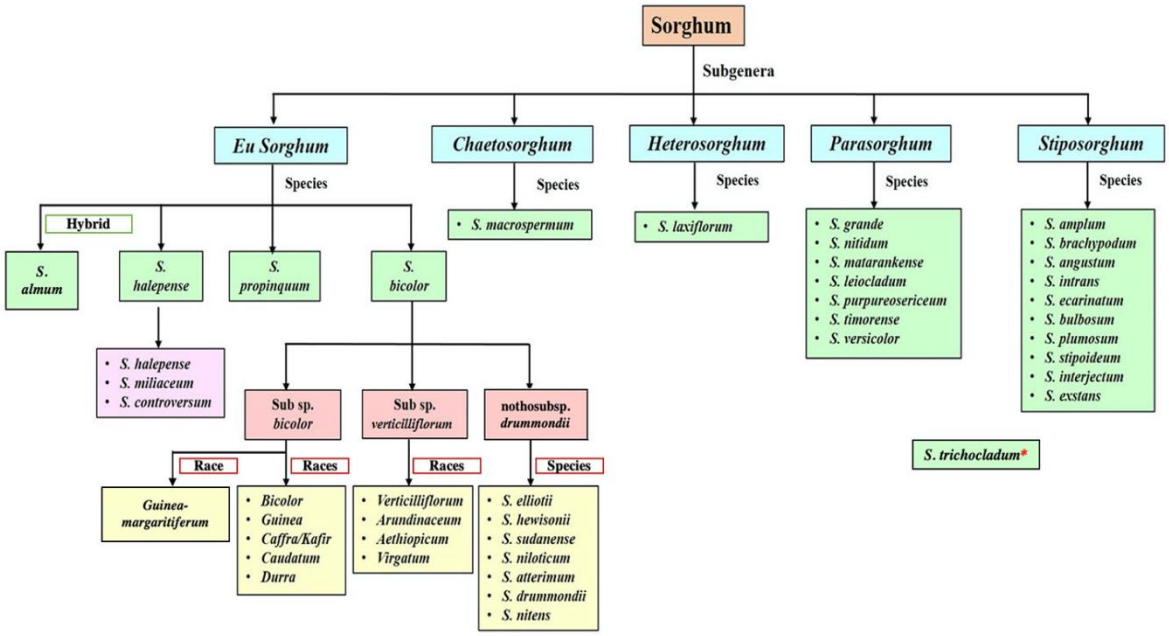

Figure 1: Classification of Sorghum (De Wet, 1978; Dillon *et al.*, 2007; Venkateswaran *et al.*, 2019a; Wiersema and Dahlberg, 2007). **'***The exact Position within the phylogeny is still unknown'.

Cultivated sorghum belongs to the subgenus *Eusorghum*. *Eusorghum* is composed of three species; *S. bicolor*, *S. propinquum*, and *S. halepense*, which are native to Africa and Southern Asia (De Wet, 1978). *Chaetosorghum* and *Heterosorghum* consist of species *Sorghum macrospermum* and *Sorghum laxiflorum*. *Sorghum macrospermum* is found in a single region in the Northern Territory of Australia, North West of Katherine. *Sorghum laxiflorum* is more broadly dispersed and is found in Australia, Papua New Guinea, and the

Philippine Island. Ten species compose the subgenus *Stiposorghum*: *S. amplum, S. angustum,* S. *brachypodum,* S. *bulbosum,* S. *escarinatum*, S. *extans, S. interjectum, S. intrans,* S. *plumosum* and *S. stipoideum* which are all indigenous to Australia. The seven species of *Parasorghum* include: *S. grande,* S. *leiocladum,* S. *matarankense,* S. *nitidum*, S. *purpureo-sericeum*, S. *timorense* and *S. versicolor.* These species occur in Asia, Australia, Africa, and Central America (Garber, 1950; Lazarides *et al.*, 1991).

The species *S. bicolor* contains three subspecies, subsp. *bicolor*, which contains 5 morphologically distinct cultivated sorghum races, subsp. *arundinaceum* a widely distributed wild African complex, and subsp. *drummondii*, a complex of stabilized derivatives between cultivated sorghum and weedy relatives (De Wet, 1978). There are five basic cultivated sorghum botanical races in subsp. *Bicolor.* These include; bicolor, caudatum, durra, kafir and guinea.

Durra race originated from Ethiopia and the Horn of Africa, and later spread to Nigeria and the savanna region of West Africa They have a very compact panicle with curved penducle, and the tiny glumes are attached to globular grain. This race is mostly grown in East Africa, the Middle East and India. The *kafir* race are small sorghums with relatively compact and cylindrical panicles consisting of symmetrical grain flattened on the ventral surface and convex on the dorsal. This race is grown mostly in eastern Africa and southern Africa. The *caudatum* race is characterized by asymmetric grain, flattened on the ventral surface and convex on the dorsal. The panicle morphological structure varies with shape. This race is mainly found in Central and East Africa and originated in Kenya or Ethiopia (Acquaah, 2007).

The *bicolor* race is characterized by loose panicles with grains covered by large closed glumes and is mostly distributed in Asia and Africa. The *guinea* sorghums are tall with loose panicles, spikelets with open glumes enclosing an elliptical grain and photoperiod sensitive. These sorghums are mainly grown in the west and central Africa.

The *Sorghum* genus has 3 gene pools based on the degree of cross-compatibility (Harlan and De Wet, 1971).

The primary gene pool of sorghum contains members of the subgenus *Eusorghum* that are sexually compatible. It includes all subspecies of *Sorghum bicolor* and *S. propinquum*. These species are fully inter-fertile and the high level of compatibility permits spontaneous hybridization, out crossing and introgression (Dillon *et al.*, 2007b; Ejeta and Grenier, 2005). For this reason, they have provided the base for breeding efforts until recent times. Sexual Compatibility between domesticated and wild taxa in areas with sympatric occurrence has often resulted in wild relative/weedy/domesticated hybrid complexes, including intraspecific and interspecific crosses (Ellstrand *et al.*, 1999).

The secondary gene pool is comprised of the tetraploid relatives including *S. x almum* and *S. halepense.* Members of GP2 and GP1 including cultivated sorghum have the potential to hybridize with each other despite ploidy level differences, to produce either sterile triploids or partially fertile tetraploids (Arriola and Ellstrand, 1996; Arriola and Ellstrand, 1997).

The most widely recognized weed amongst the *Sorghum* species is *S. halepense* (Johnson grass) which is a serious problem in many areas (Arriola and Ellstrand, 1996). Studies on the introgression of crop genes between cultivated sorghum and *S. halepense* based on the

number of alleles and timing of exposure suggested a lasting impact of cultivated sorghum on the genetic composition of *S. halepense* populations (Morrell *et al.*, 2005).

The tertiary gene pool (GP3) consists of the wild sorghum relatives from other subgenera of *Sorghum – Chaetosorghum, Heterosorghum, Parasorghum and Stiposorghum.* Members of GP3 in nature do not out-cross or introgress with those of GP1 and GP2. Wild Australian species form the majority of the tertiary gene pool, comprised of 19 divergent *Sorghum* species (Lazarides *et al.*, 1991). The species in GP3 constitute an untapped gene pool for breeding. However, outcrossing cultivated sorghum with this group is difficult even under laboratory conditions.

Cultivated sorghum does not hybridize naturally with the wild species of *Sorghum* due to pollen-pistil incompatibility (Hodnett *et al.*, 2005). The pollen of undomesticated species behaves abnormally in the pistils of *S. bicolor* and pollen rarely grows beyond the stigma, thus embryo formation does not occur. However, incompatibility may be overcome for breeding purposes under laboratory conditions. A sorghum accession homozygous for a recessive allele that permits exogenous pollen growth in its pistils has been identified (Laurie & Bennett 1989). This overrides pollen-pistil incompatibility, making possible hybridization between *S. bicolor* and undomesticated *Sorghum* species. Hybrids between *S. bicolor x S. macrospermum*, *S. bicolor* x *S. angustum* and *S. bicolor* x *S. nitidim* have been produced, although hybrids had to be recovered by embryo rescue and tissue culture in some instances. Thus, genomic introgression from wild germplasm into sorghum can occur and it is now technically possible to accelerate the incorporation of novel genes into future cultivars (Kuhlman *et al.*, 2010; Price *et al.*, 2005; Price *et al.*, 2006).

Sorghum belongs to the Poaceae family and is a herbaceous annual grass of tropical origin propagated from seed with modest water requirements. It is predominantly a self-pollinated cereal with the degree of spontaneous cross-pollination, of about 3-10% depending on panicle types (Dje *et al.*, 2004; Poehlman and Sleper, 1995). Secondary roots emerge from the first node and develop into an extensive system which can penetrates 1.5 to 2.5 meters into the soil and extend one meter away from the stem. A large amount of root material contributes to the build-up of soil organic carbon after removal of the aerial parts of the plant and can help add soil organic matter even with the removal of Stover (Wilhelm *et al.*, 2004). The root system supports the development of secondary growth from an adventitious bud from the stem making ratoon cropping a success (F. Kazungu *et al.*, 2023). Sorghum stalk height varies between 0.6-4.5 meters, depending on the type and variety. Tillers produced may be two or more with the number of nodes ranging between 7-18 or more (Acquaah, 2007). Axillary tillers can develop to compensate for the damage done on the stem, may arise from any bud from any node except the lowest node of the stem, where roots develop and provide support to tall varieties.

The leaves can either be alternate or arranged at an angle to each other and can be 7-24 in number depending on type. Trichomes can be found on the upper surface and leaf sheath and provide resistance against shoot fly.

The sorghum panicle has a central rachis bearing primary, secondary and tertiary branches with racemes of spikelets which usually occur in pairs. The sessile spikelet is bisexual and ovoid whereas the other spikelet is sterile and only contains stamens. (Doggett, 1988). Flowers usually open at night and early morning starting with those at the upper part of the

panicle and the entire panicle takes 6 to 9 days to flower. A mature panicle usually contains about two thousand grains partly covered by glumes (Acquaah, 2007).

2.3 Ecological requirement for production of sorghum

Sorghum has a wide adaptability to a range of environmental conditions and will produce significant yields under conditions that are unfavourable for most other cereals. It tolerates water logging and thus grows also in areas of high rainfall despite being primarily a plant of hot, semi-arid tropical environments. It requires an average annual rainfall of between 250-900 mm that is well distributed but optimal performance is with more than 900 mm annually (Muindi and Esilaba, 2021; Young and Long, 2000). It grows widely and grows well in altitudes of between 800-2000 meters above sea level.

Sorghum can tolerate a wide range of soil conditions, from heavy clay to light sand. Sorghum is tolerant to saline growing conditions. Due to its adaptability to poor soils, it is mainly grown on low potential, shallow soils with high clay content but usually performs poorly on sandy soils. A pH of between 5.5 and 8.5 is optimal for its growth and shows tolerance to alkaline conditions. The crop tolerates small durations of water logging with soils having clay percentage of between 10% and 30 % are optimal for growth (F. K. Kazungu *et al.*, 2023; Muindi and Esilaba, 2021).

Sorghum requires ideal temperatures for perfect germination and growth. Optimal temperature for germination is 15 °C while 27-30 °C is the optimal temperature for good growth and development. Very high temperatures decrease yield and delay flowering. (F. Kazungu *et al.*, 2023; Prasad *et al.*, 2021).

Sorghum is a short-day plant meaning it requires long uninterrupted nights to flower. The optimum photoperiod for flowering in sorghum is between 10 and 11 hours (F. Kazungu *et al.*, 2023; Muindi and Esilaba, 2021).

2.4 Sorghum Utilization

The primary use of sorghum is for food in Africa, especially in the dry land regions where it's a principal crop (FAOSTAT, 2022). The crop is utilized in different forms, where the grain is used for human food and homemade beverages. Sorghum grains are prepared for a variety of food products. This includes use as a boiled food similar to rice, roasting or popping like maize, threshing and grinding into flour to make bread, fermented and non-fermented porridges, pancake, muffins, dumplings, sorghum stew, sorghum *pilau,* breakfast cereals or couscous, as well as preparation of alcoholic and non-alcoholic beverage (ICRISAT, 2010; Taylor, 2010; Tiimu, 2014). Sorghum grain and other parts are also milled for animal feed and fodder, fencing materials, wood fuel, construction material, industrial starch, fuel, and the natural dye or food colour (Mekbib, 2009; Ratnavathi and Patil, 2013). According to Taylor (2010), sorghum has been proven to be the best alternative to barley crop in beer brewing thus making it an important crop in food and beverage industry and is also an important source of industrial starch. Plant residues can be used as fuel and building material (stalks). The stalks of sweet sorghum varieties with high sugar content are used to make sugar and syrup (CGIAR). Sorghum as a biofuel crop occupies 2nd position (after maize) in grain-based ethanol production in the United States of America, and offers novel learning opportunities relevant to weed biology as well as to the improvement of a wide range of other forage, turf and biomass crops (Kresovich *et al.*, 2005).

2.5 Sorghum Production and Yield statistics

Sorghum has a wide geographical distribution, being cultivated in the Americas and Asia, as well as its native Africa. Globally, the Average Land under sorghum cultivation worldwide between 2011 and 2022 was 42 million hectares accounting for an average annual production of 61 million tonnes. Production ranged between 56.7 million tonnes (2019) and 68.3 million tonnes (2014). This was a fluctuating trend in global production. Top world producers between 2011 and 2022 were the USA with a production average of 9.4 million tonnes annually, followed by Nigeria 6.6 million tonnes, Mexico 5.5 million tonnes, India 5.0 million tonnes, Sudan 4.6 million tonnes, Ethiopia 4.5 million tonnes, , South Sudan 4.3 million tonnes, and Argentina 3.0 million tonnes, China 2.8 million tonnes and Brazil 2.3 million tonnes annually (FAOSTAT, 2023).

Over the African continent as a whole, sorghum is the second most important cereal after maize occupying 22% of the total area planted to cereals. The average area under sorghum production in Africa between 2011 and 2022 was 27.64 million Hectares and total production and the average yield was 27.31 million tonnes and 0.98 t/ha, respectively. Annual production in the continent within those years has been fluctuating with highest production being 30.2 million tonnes (2016) and lowest production of 23.5 million tonnes (2012) (FAOSTAT, 2023).

In the Eastern Africa region, the average total area under production was 5.1 million hectares while the total production and average yields were 7.2 million tonnes and 1.4 t/ha, respectively. Highest annual production was 8.0 million tonnes (2020) while lowest annual production was 6.3 million tonnes (2011) (FAOSTAT, 2023).

In Kenya, it is mainly grown in Western, Eastern, Northern Rift valley and some parts of Central region. The annual production average was 188,998 tonnes between 2011 and 2022. The lowest production was 117,000 tonnes recorded in 2016 and 2022 while the highest was in 2020 at 315,000 tonnes. National average annual production between 2011 and 2022 has been fluctuating. The average area under sorghum cultivation between 2011 and 2022 was 220,485 ha, ranging from 184,654 ha in 2016 to 254,125 ha in 2011. The country's average yield per hectare between 2011 and 2022 was 0.86 t/ha. This yield is low compared to the potential yield of 3-4 t/ha (FAOSTAT, 2023).

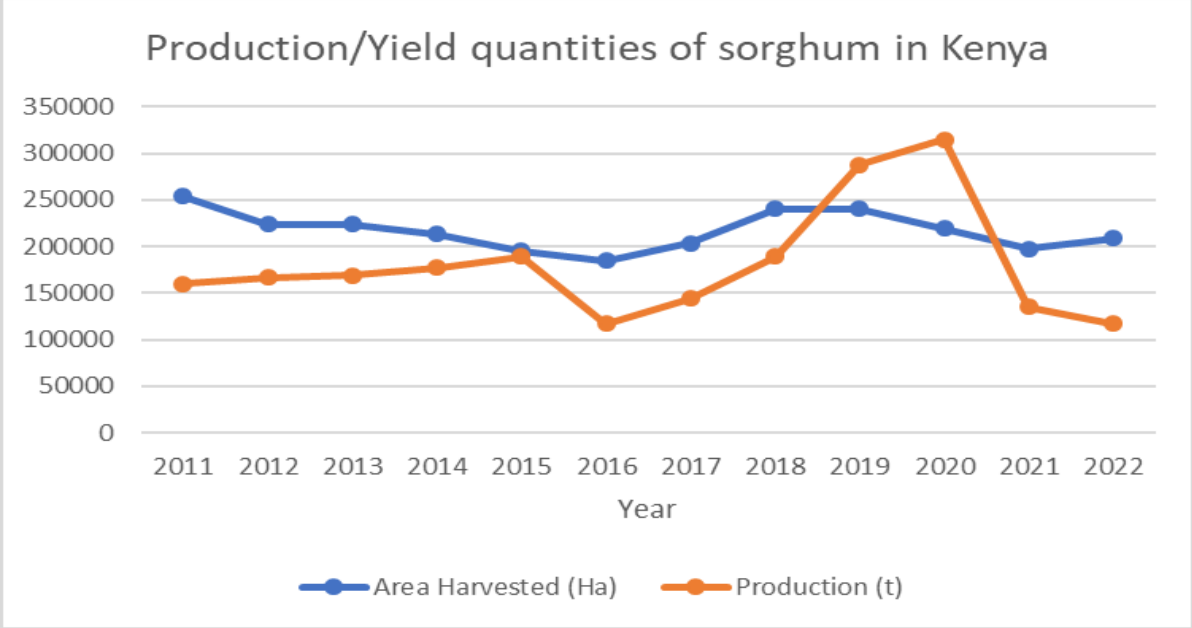

Figure 2: Yield quantities of Sorghum in Kenya (FAOSTAT, 2023)

2.6 Sorghum Production Constraints

Sorghum production and productivity is constrained by several biotic and abiotic stresses. Soil water deficit is the major abiotic constraint of sorghum production in Kenya. This deficit affects the sorghum crop severely during crop establishment, early growth,

flowering and during grain fill and causes significant yield reduction (Charles *et al.*, 2006). Kenya has experienced diminishing rainfall amounts over the years, probably due to the effects of global climate change. This has led to decreased sorghum production making her a food deficit country with most areas receiving relief food supplies in many of the years (Ogeto *et al.*, 2013).

Another abiotic stress affecting Sorghum production is Soil acidity and soil nutrient deficiency. Acid soils (pH of ≤5.5) are among the limitations to agricultural production worldwide especially the production of grain crops. They limit crop yields in many developing countries where food production is critical owing to high Al toxicity and P deficiency. Studies have shown Al toxicity interferers with a wide range of cellular processes resulting in the inhibition of root cell division and elongation, thus reducing water and nutrient uptake consequently resulting in poor plant growth and yield (Pineros et al., 2005). Gallardo et al. (1999) Carver and Ownby (1995) reported that Al toxicity decreases drought tolerance and use of subsoil nutrients restricting the full expression of the genetic potential of the plant.

Phosphorus is a macro nutrient essential for the growth of crops and is the 2nd most limiting macro-nutrient required for growth of crops in the tropics after nitrogen (Lynch, 2011; Parentoni *et al.*, 2010). The available soil phosphorus in western Kenyan ranges between 2 to 5 mg P/kg which is low as compared to the optimal range required for high crop production of between 10 to 15 mg P/kg soil (Kisinyo *et al.*, 2014; Obura, 2008). Although phosphorus deficiency has been found to reduce growth and delay maturity, sorghum is commonly cultivated with little or no fertilization due to inaccessibility and high prices of P-fertilizer and liming elements, often unaffordable to resource-poor subsistence farmers

(Ouma *et al.*, 2012). The use of inorganic phosphorus fertilizer has negative effects on the environment in that the fertilizer is washed into water bodies by surface runoff thereby causing eutrophication of lakes and other surface water bodies (Malakouti *et al.*, 2008).

Biotic constraints to sorghum production include; diseases, insect pests and weeds. These factors play a greater role in yield reduction reaching approximately 40% in susceptible varieties (Repellin *et al.*, 2001). The major diseases of sorghum include anthracnose, leaf blight, rust, smut, mould and downy mildew. Anthracnose is caused by *Colletotrichum sublineolum* Hann. Kabát et Bub. (syn. C. *graminicola* (Ces.) G.W. Wils.) and causes major loss in the crop of upto 67% on susceptible cultivars (Sharma *et al.*, 2012; Thomas *et al.*, 1996) The disease is observed in all sorghum growing areas worldwide (Costa *et al.*, 2015; Patil *et al.*, 2017) and the effects are more pronounced in warmer areas where temperatures and relative humidity are the highest (Burrell *et al.*, 2015; Crouch and Beirn, 2009; Patil *et al.*, 2017). Leaf blight disease is caused by *Exserohilum turcicum* (Pass) Leonard and Suggs and leads to yield loss of up to 50% (Ngugi *et al.*, 2000). Sorghum rust (*Puccinia purpurea Cooke*) is prevalent in most sorghum-producing areas affecting grain yield and forage quality (Hulluka and Esele, 1992). Other important diseases of sorghum are head smut (*Sporisorium reilianum*) and downy mildew (*Peronosclerospora sorghi*) (Gowda *et al.*, 1995; Gwary *et al.*, 2007).

Some important insect pests affecting sorghum crop are sorghum shoot fly, sorghum midge, stem borers, *Chilo partellus*, *Busseola fusca* and termites (Wortmann *et al.*, 2009). The sorghum midge is the most damaging insect pest of sorghum worldwide (Teetes and Pendleton, 2000). The female sorghum midges oviposit eggs in flowering sorghum spikelets in which the developing larvae feed and abort the development of the kernel and

this can lead to 100% grain destruction. Originating in Africa, sorghum midge is unique among sorghum insect pests by being specific to *Sorghum,* and all members of the genus *Sorghum* are potential hosts. Genetic resistance to the sorghum midge exists within the genus *Sorghum* (Johnson *et al.*, 1972; Jotwani *et al.*, 1971; Peterson *et al.*, 1989; Wuensche *et al.*, 1981). Inheritance of the resistance is quantitative and recessive (Boozaya-Angoon *et al.*, 1984; Teetes and Johnson, 1978). Resistance mechanisms have been studied and the effect of resistance on sorghum midge larvae determined (Waquil *et al.*, 1986a; Waquil *et al.*, 1986b; Waquil *et al.*, 1986c). Resistance is quantitative and recessive, with the number of resistant plants dependent on pest abundance. Also spikelet flowering time and morphology influence the level of resistance (Diarisso *et al.*, 1998a; Diarisso *et al.*, 1998b).

Bird damage leads to the major constraints of sorghum production in most SSA countries which can lead to 60% yield loss even when human scares are present in the field (Hiron *et al.*, 2014; Masters *et al.*, 1998; Orr *et al.*, 2013). In Kenya, Quelea quelea is the most destructive bird species although doves and other species are reported by farmers in different regions (Brooks *et al.*, 2009).

Striga (*Striga hermonthica*) is a parasitic weed of sorghum and other cereal crops that significantly affects sorghum production in Kenya and globally especially in areas where soil fertility and moisture stress are limiting factors(Gebretsadik *et al.*, 2014; Haussmann *et al.*, 2000). Gebisa and Butler (1993) reported 65-100 % yield loss due to its infestation. Besides withdrawal of water, nutrients and assimilates, *Striga* damages its host by inducing enzyme and plant hormone changes, disrupting host water relations and carbon fixation (Press *et al.*, 1996). *Striga* is extremely difficult to control because unlike other weed species that do much harm to the crop after they emerge from the ground, much of the

impairment of host growth and productivity is complete before *Striga* emerges above ground. Moreover, the number of seeds produced by each *Striga* plant varies between 30,000 and 50,000 and sometimes it may produce up to 100,000-minute seeds of 0.2 mm diameter that may remain viable up to ten or more years (Gebisa, 2007a). Among the control measures recommended for Striga the use of crop cultivars with improved levels of resistance and tolerance against the parasite is the most economic, feasible and environmentally friendly method of control (Ananda *et al.*, 2020).

2.7 Crop wild relatives and Plant breeding

2.7.1 Crop wild relatives

A crop wild relative is a wild species related to a cultivated crop. The demand for increased crop productivity and uniformity in the field and the market place has led to crop domestication and improvement process which entails successive rounds of selection that results in the isolation of genetic diversity valuable to agriculture from ancestral wild species.

This selection process has led to the development of the crop cultivars grown today which have reduced their genetic variation, making them to have less allelic diversity than their wild progenitors and other crop wild relatives (Van Heerwaarden *et al.*, 2011). Although potentially valuable genetic variation has been filtered out of crop gene pools, many of these traits, such as disease resistance, drought tolerance and yield-related traits, are still preserved in the crop wild relatives. (Abbasher *et al.*, 1998; Hufford *et al.*, 2013; Sawler *et al.*, 2013). Plant breeders have also worked to recover some of the beneficial genetic diversity by crossing cultivated varieties with wild species. They have employed the use of genetic diversity which previously was inaccessible either due to genetic incompatibilities

or large geographic distance which was non-overlapping (Dwivedi *et al.*, 2008; Ogbonnaya *et al.*, 2013).

2.7.2. Potential and prospects of breeding from the wild

The use of wild species to introduce beneficial traits to crops started at the beginning of the 18th century, with their use in developing commercial cultivars beginning in the 19th century. The use of crop wild relatives in crop improvement programs for most crops gained pace in the 1970s and 1980s (Ananda *et al.*, 2020).

There has been significant successes in introducing traits from wild species into cultivated crops especially those for overcoming biotic stresses. Some examples are the introduction of late blight resistance from the wild potato. and stem rust resistances from the wild wheat (Kilian *et al.*, 2010).

Plant breeders are progressively looking to wild species to widen the genetic bases of crops so as to ensure improved crop yields in more challenging conditions (Cooper *et al.*, 2001; Moore, 2015).

Rice, tomato and wheat, in particular, have large and well-established prebreeding programs that focus specifically on CWR, applying advanced genomic tools and diverse characterization and evaluation data (Kilian *et al.*, 2011; Nemeth *et al.*, 2015). Crops such as cowpea, cassava, sorghum, sweet potato, pearl and finger millets have yet to benefit from large-scale investment in prebreeding programs and are therefore in the earlier stages of developing varieties using CWR. For some of these crops, progress has been made in identifying wild species as sources of traits of interest, but the release of varieties that contain wild material in their pedigrees remains rare (Dempewolf *et al.*, 2017) .

2.7.3 Sorghum crop wild relatives and their potential use in plant breeding

The adaptability of these wild *Sorghum* species to colonize a wide range of soil and moisture conditions across a wide range of micro-environments is shown through their ability to survive very hot, dry, nutrient-limited environments. Many of the wild *Sorghum* species have developed resistances to the many pests and diseases that affect sorghum grain production globally (Komolong *et al.*, 2002). Cultivated sorghum harbour a lower amount of genetic diversity than wild sorghum due to the genetic bottleneck it undergoes during the domestication process (Ananda *et al.*, 2020; Muraya *et al.*, 2011; Mutegi *et al.*, 2011). The potential use of wild sorghum relatives in sorghum improvement programs has been documented by various researchers., most existing hybrids have been developed through crosses of S. bicolor with members of gene pools 1 and 2 due to the incompatibility of crossing S. bicolor with species in GP-3 (Dempewolf *et al.*, 2017). These include *S. bicolor subsp. verticilliflorum* (Cox *et al.*, 1984; Jordan *et al.*, 2004) and *S. propinquum* (Wooten, 2001) being used to increase yield; S. halepense being used to introduce perennialism (Cox *et al.*, 2002; Dweikat, 2005); and S. propinquum being used to increase height and earliness of development (Wooten, 2001).

Striga-resistance mechanisms such as low germination stimulant production, germination inhibition, and low haustorial initiation activity have been found in wild sorghum (Ananda *et al.*, 2020). *S. bicolor subsp. drummondii's* has allelopathic properties, which reduce the growth of weeds in the cultivated field, has resistance to ergot disease and also nematode tolerance(Tsukiboshi *et al.*, 1998; Viaene and Abawi, 1998) *S.halepense* has shown resistance to pests such as green bug, chinch bug, and sorghum shoot fly (Ananda *et al.*, 2020; Dweikat, 2005).

Furthermore, wild sorghum has novel grain starch properties that could be used to improve the digestibility of crop-sorghum for intensive livestock industries (Dillon *et al.*, 2007a). Thirty-two accessions from wild sorghum showed total resistance to shoot fly (*Atherigona soccata*) damage under field conditions. Similarly, 15 species of wild sorghum species showed high levels of resistance to *Chilo partellus* under artificial infestation in the field while the accession of *Chaetosorghum* was highly susceptible (Ananda *et al.*, 2020) . Sharma and Franzmann (2001) observed that wild species from Australia possess high levels of resistance to the sorghum midge, *Stenodiplosis sorghicola*.

Another example of the use of sorghum CWRs is the CROP TRUST-Sorghum project. This is a CWR project titled Adapting Agriculture to Climate Change: "Collecting, Protecting and Preparing Crop Wild Relatives" which aims to collect important species of crop wild relatives, ensure their long-term conservation, and facilitate their use in breeding new improved crops. This research is part of the project phase that sought to participatorily evaluate pre-breeding sorghum materials with farmers in Kenya (CROPTRUST, 2021).

2.8 Heterosis in Sorghum

Heterosis refers to the superiority in performance of a hybrid relative to its parents. The superior performance can be in form of increased biomass, size, yield, growth rate, tolerance to biotic and abiotic stresses and fertility.

In sorghum, their hybrid potential is estimated by heterobeltiosis (percent increase over better parent) and average heterosis (percent increase over average of the parents) (Hochholdinger and Hoeckenger, 2007). The degree of heterosis varies with respect to the genetic distance of the parents, their reproductive mode, the traits investigated (Zhou *et al.*,

2012), the developmental stage of the plants (Groszmann *et al.*, 2013) and the environment. Concerning environmental variation, biotic and abiotic conditions shown to affect heterosis include soil type, topography, climate, solar energy, temperature and water availability (Blum, 2013; Munaro *et al.*, 2011).

Heterosis for grain yield is principally due to an increased number of grains per branch, mostly at the lower branches of the panicle (Blum, 2013), and a larger panicle itself. The average high-parent heterosis for grain yield is estimated at 20-60%. Further, heterosis is also expressed for plant height, maturity and abiotic stress tolerance like chilling stress (Windpassinger *et al.*, 2016).

Heterosis on several quantitative characters in sorghum has been studied by various researchers. (Salini *et al.*, 2008) reported that high significant mean performance of hybrids with that of parents suggested the existence of heterosis for all the traits and the importance of non-additive gene effects in determining these traits. (Makanda *et al.*, 2010) observed that hybrids were predominant for grain yield and expressed up to 285% standard heterosis and overall mean yield was significantly higher for hybrids as compared to parents and standard check varieties, and this was attributed to high levels of average heterosis and standard heterosis respectively. (El-Dardeer *et al.*, 2011) studied heterosis under normal and water stress conditions and reported the better parent heterosis was generally manifested for plant height, panicle length, panicle width and grain yield per plant and crosses *viz.*, ICSA-364 x ICSR- 66, ICSA-364 x ICSR-102 and ICSA-490 x ICSR-66 had exhibited significant standard heterosis for grain yield over check, Shandaweel-1. Mahdy *et al.* (2011) reported positive heterosis for grain yield and 1000-grain weight and negative heterosis for days to 50% blooming over different environments.

2.9 Genotype by Environment interactions

The exploitation of genetic variability is the most important tool in plant breeding and this has to be inferred by phenotypic expressions. Genotypic expression of the phenotype depends on the environment (Kang, 1998) and genotypes do not react in a similar way to change in the environment. Genotype by Environment interaction (GEI) becomes a major challenge to crop improvement when the relative performance of genotypes is dissimilar in different environments. Generating broadly adapted varieties with superior yield performance is a major challenge affecting plant breeders (Adugna, 2007). In plant breeding variety selection experiments plant breeders evaluate many genotypes over a wide range of environments before a specific genotype is released for production (Rahmatollah *et al.,* 2013). GEI is commonly evaluated in these experiments (Yan *et al.*, 2007). GEI effects are of special interest for identifying the most stable genotypes, mega-environments and adaptation targets in most plant breeding programs (Sabaghnia *et al.*, 2013). The performance of every variety in a location is determined by the environment main effect (E), genotype main effect (G), and the genotype by environment interaction (GEI) effect (Yan and Tinker, 2005).

Several statistical methods have been developed to characterize the effect of GEI of genotypes and to predict phenotypic responses to environmental changes. These include; coefficient of variability (Francis and Kannenberg, 1978), mean variance component for pairwise GEI (Plaisted and Peterson, 1959), ecovalence (Wricke, 1962), stability variance (Shukla, 1972), and regression coefficient and the sum of squared deviations from regression (Eberhart and Russel, 1966; Finley and Wilkinson, 1963; Perkins and Jinks, 1968). However, statistical methods for characterizing stability are generally not able to

provide an accurate and complete response model for this interaction (Holhs, 1995), as the genotypic response to environmental variation is multivariate, while most stability indices have a univariate response (Crossa, 1990). Therefore, graphical methods have been developed to resolve the response of various genotypes across different environments (Yan *et al.*, 2001). The two commonly used graphical methods are the Genotype plus Genotype by Environment Interaction (GGE) biplot model and the Additive Main effect and Multiplicative Interaction (AMMI) model.

The Genotype plus Genotype by Environment Interaction (GGE) biplot model is an important model to analyse multi-environment trial data and to interpret complex GEI (Yan, 2001). It can effectively differentiate and display the interaction pattern graphically and also identify ″which-win-where″ and delineation of mega-environments among the testing sites (Yan and Tinker, 2006). GGE biplot analysis partitions G + GEI into principal components through singular value decomposition of environmentally centred yield data(Yan, 2001).

Additive Main effect and Multiplicative Interaction (AMMI) model is also used to quantify the stability of the genotypes across locations using the Interaction Principal Component Analysis (IPCAs). The AMMI model proved to be a powerful tool in analysing GEI patterns. (Crossa *et al.*, 1990). This method combines an analysis of variance (ANOVA) and a principal component analysis (PCA) in a unified approach that can be used to analyse multi-location trials(Crossa *et al.*, 1990; Gauch and Zobel, 1996; Zobel *et al.*, 1988). The ANOVA studies the main effects of genotypes and environments and the principal component analysis (PCA) then focuses on the non-additive part of the model representing

GEI. AMMI provides the GEI sum of squares with a minimum number of degrees of freedom. In addition, AMMI concurrently quantifies the contribution of each genotype and environment to GEI and provides an easy graphical interpretation of the results using a biplot technique to classify genotypes and environments together (Kempton, 1984; Zobel *et al.*, 1988). This model is therefore used to identify high performing genotypes that have wide adaptability and mega-environments, and identify the environments in which genotypes have specific adaptability (Ferreira *et al.*, 2006; Gauch and Zobel, 1996; Kempton, 1984).

2.10 Stability Analysis

Stability usually refers to consistency of performance of genotypes in a range of conditions/environments(Annicchiarico, 2002). The major cause for different stability among genotypes and different performance from various test environments is non-repeatable GEI (Yan and Hunt, 2002). The Stability model that was initially commonly used by plant breeders is based on linear regression and was first proposed by Finley and Wilkinson (1963). This was later modified by Eberhart and Russel (1966) who suggested a different selection measure of the stability of a genotype based on high mean yield, unit linear regression and low deviation from regression. The success of a plant breeding program relies on the development and identification of genotypes with good and stable performance across target environments for harnessing maximum gains from the selection. The stability of yield performance is one of the most desirable characteristics of a genotype to be released as a variety, which allows the developed varieties to be adopted in a large area or targeting varieties to their best growing environments (Falconer and Mackey,1996). Superior genotypes selected using stability analysis rather than average performance is that

they have the advantage of improved productivity across the environments which reduces GEI. Stability is grouped into 3 types: Type-1, Type-2 and Type-3 Lin *et al.* (1986).

i. Type 1 (static/biological stability)

This stability type recognizes that a stable genotype is the one having small variance across the tested environments. It is useful in estimating stability in a limited range of environments, and for selection of genotypes for specific adaptation (Becker and Leon, 1988). When the sample estimate is not significantly different from zero, environmental changes will not influence the genotype performance and hence the genotype is stable (Norden *et al.*, 1986).

ii. Type 2 (Dynamic/Agronomic stability)

Dynamic stability is whereby a genotype response to changes environmental changes has no deviation from the general response of all genotypes in the environment. This stability is useful for traits such as yield which are quantitative in nature (Norden *et al.*, 1986).

iii. Type 3 (Eberhart – Russell)

A genotype is considered to have type-3 stability if the error mean square from the regression model on the environmental index is small. This type of stability depends on the measurements of unpredictable irregularities in the response to the environment as provided by the deviation from regression because the regression part is predictable (Eberhart and Russel, 1966).

Several stability parameters were developed which can identify stable genotypes across environments. These parameters are grouped as either univariate or multivariate. The

univariate is further grouped into parametric and non-parametric. The most used parametric approaches are Wricke's ecovalence (Wi 2), Shukla's stability variance (i2), deviation from regression (S2d), and linear regression slope (bi). Nonparametric technique such as Kang's stability statistic (YSi) is based on a genotypes' ranking in each environment, and genotypes with constant performance across environments are stable genotypes. These types of stability are all univariate as opposed to the GEI which is multivariate. Therefore, the GEI provides a more robust inference based on multivariate stability approaches

Multivariate approaches for stability analysis

The most commonly used multivariate models for stability analysis are the additive main effects and multiplicative interaction (AMMI) method and the biplot technique (GGE biplot). The additive main effects and multiplicative interaction (AMMI) method gives information on main and interaction effects in addition to a biplot. It is specifically efficient for illustrating adaptive responses (Annicchiarico, 1997a; Fasahat *et al.*, 2014) and is recently suggested as a replacement to the joint regression analysis for most of the breeding programs (Annicchiarico, 1997b). The GGE biplot was developed by (Yan *et al.*, 2000) to represent genotype main effects and GEI graphically. It is the best predictor of genotype stability for a small number of genotypes (Rose *et al.*, 2008).

Although AMMI and GGE are equivalent in achieving predictive accuracy, the AMMI method is considered superior to GGE for evaluating yield trial data, (Gauch, 2006) because it shows genotype main effects, environment main effects and interaction effects, whilst the GGE biplot only displays G and G × E effects (Gauch *et al.*, 2008).

This study therefore adopted the AMMI method because of its superiority over GGE for evaluating yield trial data showing genotype main effects, environment main effects and interaction effects. In addition, it has ability to identify productive genotypes with wide adaptability and mega-environments, and to delimit environments in which genotypes have specific adaptability.

CHAPTER THREE

METHODOLOGY

3.1 Site Description

Determination of performance and adaptation, Genotype by Environment interaction and stability studies of sorghum wild relatives from West Africa was carried out at the four sites namely, Nyabisawa, Godkwer, Kibos and Sega. Development of the crosses between wild relatives and cultivated sorghum as well as determination of heterosis was carried out at KALRO Centre located in Kibos Kisumu County. The site characteristics are described below.

Kibos site is located at 0^0 53'S, and 34^0 52'E in Kisumu County. The area has an altitude of 1679 metres above sea level (m. A.s.l). It receives a mean annual rainfall of between 1200 – 1300 mm with a mean minimum temperature range of between 16^0C – 19^0C while the mean maximum range is between 27^0C – 30^0C. The soils are classified as vertisols with dark greyish brown to dark brown sandy clay loam, texture underlain by brownish to greyish brown clay loam to light clay (Ouma and Gudu, 2016).

Sega is located at 0^o 15'N and 34^o 20'E in Siaya County in western Kenya. It has an elevation of between 1140 – 1400 metres above sea level (m.a.s.l) with a bimodal annual average rainfall pattern of between 800 – 1200 mm. The mean minimum temperature range is 15 – 17^0C while the mean maximum range is between 27 – 30 ^{0}C. The soils are orthic Acrisols characterized by low pH (4.5) (Jaetzold and Schmidt, 1983; Kisinyo, 2011).

Nyabisawa site is located at 1^o 03'S and 34^o 24'E in Migori county in western Kenya. It has an elevation of between 1281 m.a.s.l with an average annual rainfall of between 1000

– 1400 mm. The mean annual temperature range is 22 – 24^{o}C. The soils are humic ferralsols dominantly sandy loam with a pH of 5.75, (Jaetzold and Schmidt, 1983; OUMA, 2014). Godkwer site is located at 1^{o} 07'S and 34^{o} 33'E. The altitude is 1220 m a.s.l. with average annual rainfall of 1020 mm. The temperature range is between 23^{0}C and 25^{0}C. Soils are mainly gravely sandy clay Humic Cambisols with a pH of 5.5 (Jaetzold *et al.*, 1985).

3.2 Determination of Agronomic Performance of selected sorghum plant introductions from West Africa in Western Kenya

3.2.1 Plant materials

Twenty-one sorghum wild relatives used in this study were obtained from the Rongo University CWR sorghum breeding program. These materials were introductions from ICRISAT Mali-West Africa which were a pre-breeding population that was developed between an early maturing local variety from the Guinea race (CSM 63E) and unadapted wild donor parents (BBISS-08 and BBISS-09) from subspecies *Verticilliflorum* and were in their fifth backcross generation. The others were Kenyan locally adapted released varieties and landraces commonly grown and maintained by farmers in western Kenya. Materials used and their phenotypes are shown in Table 1.

Table 1: Plant materials consisting of twenty-one SWR and four checks used for the study at Kibos, Nyabisawa, Godkwer and Sega

ENTRY_NO	PEDIGREE	CROSS
466	BCJD194F6-10-1-1-1-1-1	BBISS-08//CSM63E
509	BCJD194F6-53-1-1-1-1-1	BBISS-08//CSM63E
468	BCJD194F6-11-1-1-1-1-1	BBISS-08//CSM63E
550	BCJD224F6-9-1-1-1-1-1	BBISS-09//CSM63E
512	BCJD194F6-56-1-1-1-1-1	BBISS-08//CSM63E
555	BCJD224F6-14-1-1-1-1-1	BBISS-09//CSM63E
590	BCJD224F6-49-1-1-1-1-1	BBISS-09//CSM63E
542	BCJD224F6-1-1-1-1-1-1	BBISS-09//CSM63E
503	BCJD194F6-47-1-1-1-1-1	BBISS-08//CSM63E
501	BCJD194F6-45-1-1-1-1-1	BBISS-08//CSM63E
586	BCJD224F6-45-1-1-1-1-1	BBISS-09//CSM63E
585	BCJD224F6-44-1-1-1-1-1	BBISS-09//CSM63E
582	BCJD224F6-41-1-1-1-1-1	BBISS-09//CSM63E
514	BCJD194F6-58-1-1-1-1-1	BBISS-08//CSM63E
536	BCJD194F6-80-1-1-1-1-1	BBISS-08//CSM63E
529	BCJD194F6-73-1-1-1-1-1	BBISS-08//CSM63E
588	BCJD224F6-47-1-1-1-1-1	BBISS-09//CSM63E
504	BCJD194F6-47-1-1-1-1-1	BBISS-08//CSM63E
556	BCJD224F6-15-1-1-1-1-1	BBISS-09//CSM63E
605	BCJD224F6-64-1-1-1-1-1	BBISS-09//CSM63E
560	BCJD224F6-19-1-1-1-1-1	BBISS-09//CSM63E
Ochuti	Local check	
Gadam	Commercial check	
MUK 60	Improved variety check-short	
T 53 b	Improved variety check-tall	

3.2.2 Experimental Design

The experiment was set up in a 5 X 5 α lattice incomplete block design with three replicates. There were 5 blocks with each block having 5 entries each planted in 2 rows of 4m long. The spacing was 75cm between rows and 20cm between hills. The spacing between replicates and also between the blocks was 1M.

Planting was done at the onset of the long rains of 2019 (March). DAP fertilizer was used as a source of fertilizer at planting and was applied at a rate of 26kgP per hectare. Five seeds were planted in each hole and later the plants were be thinned to two per hole. Agronomic practices to raise a healthy crop were carried out as recommended.

3.2.3 Data collection

Data was collected on the following attributes which were used to determine performance based on sorghum descriptors by the International Board for Plant Genetic Resources (IBPGR, 1993).

a) Early vigour

This was observed and recorded three weeks after sowing on plot basis. It was scored on a scale of 1 – 5, where 1 = low vigour (plants showing minimum growth, less leaf expansion and poor adaptation; 3 = moderate vigour; 5 = high vigour (tall plants with expanded leaves and robustness) (Kishore *et al.*, 2007).

b) Days to 50 percent Flowering

The number of days from the date of sowing till 50 percent of the population reached mid anthesis in each treatment was observed and recorded.

c) Plant Height

Plant height was measured and recorded in centimetres from ground level to the tip of the matured panicle of the plant using a measuring tape.

d) Panicle Length and breadth

The length of the panicles was measured in centimetres from the base of the panicle to the tip of the panicle. Panicle breadth was measured at the middle of the panicle where it is widest. This was done using a measuring tape.

e) Grain yield

Grain yield was measured from each plot at harvest. Whole-Plot Harvest was done then sun drying and threshing then weights were taken when the grains had obtained 13% moisture content and expressed in tonnes per hectare.

Statistical Analysis

The grain yield and yield components data for each individual location was analysed using R statistical software version 4.1.1 agricolae package and means separated by Tukey's test at $p \geq 0.05$ significance level (R, 2021).

Linear Model;

$Y_{ijk} = \mu + \tau_i + \Upsilon_j + \rho_{k(j)} + \Sigma_{ijk}$

Where:

Y_{ijk} ----- Plot observation

μ - overall mean

τ_i----treatment effect

Υ_j ---- replicate effect

$\rho_{k(j)}$—block within replicate effect

Σ_{ijk} --- Random error effect

3.3 Determination of Genotype x Environment Interaction and Stability

GEI was analysed using the Additive Main effect and Multiplicative interaction model (AMMI). Stability analysis was conducted based on Additive Main effect and Multiplicative interaction model (Gauch and Zobel, 1996).

Additive Main effect and Multiplicative interaction model

The sum of squares for GEI was divided into *n* singular axes or main components of interaction (IPCA), which described the standard portion (ANOVA), with each axis corresponding to an AMMI model. AMMI models with one or two main axes (AMMI1 and AMMI2 models respectively) are the most commonly used because of their simplicity in biplot graph representations. Biplot graph interpretation is based on the variation of the additive main effects (genotype and environment) and the multiplicative effects of GEI. According to Zobel *et al.* (1988), for the AMMI2 graph, genotypes that have low scores on IPCA1 (first interaction principal component axis) or IPCA2 (second interaction principal component axis) or both, contribute little to the interaction indicated by a general adaptation. On the other hand, those with high scores, be it positive or negative, have strong interactions and are specifically adapted to the environment that has the same sign score.

The following statistical model was fitted

$$y_{ij} = \mu + Gi + Ej + \sum \lambda_k \gamma_{ki} \eta_{kj} + \delta ij$$

Where;

- y_{ij} is the measured mean of the ith genotype in the jth environment, μ is the overall mean
- G_i the genotypic effect,
- Ej, environmental effect
- $\sum \lambda_k \gamma_{ki} \eta_{kj}$ a sum of multiplicative terms accounting for environmental effects,
- δij the residual variance

3.4 Development of crosses between Kenyan sorghum varieties and wild relatives

3.4.1 Genetic materials used in the study

The plant genetic materials used in the study which were Seven adapted Kenyan sorghum lines and seven selected SWRs are presented in Table 2.

Table 2: Materials used in Crossing consisting of seven adapted Kenyan sorghum lines and seven selected SWRs

Recurrent Parents				Donor Parents		
No.	**Entry**	**Source**		**No.**	**Entry**	**Source**
1	RUT53B	Rongo University		1	466	ICRISAT-Mali
2	RUMUK 154	Rongo University		2	586	ICRISAT-Mali
3	RUE32	Rongo University		3	514	ICRISAT-Mali
4	RUC26	Rongo University		4	588	ICRISAT-Mali
5	RUT30B	Rongo University		5	504	ICRISAT-Mali
6	KENSORG 5	Rongo University		6	565	ICRISAT-Mali
7	RUMUK 60	Rongo University		7	560	ICRISAT-Mali

3.4.2 Field set up and Planting

Seven adapted Kenyan sorghum lines and seven selected SWRs were crossed in a North Carolina II design (Comstock and Robinson, 1952) mating design during the short rains of 2022 (September) at KALRO center in Kibos for the development of experimental material for estimation of heterosis. Nine successful crosses were developed. The small number of crosses produced was mainly due to self-pollination of the recurrent parents and to some extent partial self-incompatibilities between the SWR genotypes and the recurrent

parents (Kashyap *et al* 2022). Nine F1 hybrids developed were evaluated during the long rain season of 2023 along with parents. Each entry was sown in a single row of 4 m long with a uniform spacing of 60 x 15 cm in a Randomized Complete Block Design (RCBD), replicated three times. Planting was carried out at the onset of long rains and standard agronomic practices were carried out as recommended.

Data collection

The data was collected on fifteen randomly selected plants in each plot and mean observations were taken. A total of eight agronomic traits were evaluated in this experiment as per the IPGRI, (1993) descriptors for sorghum. These included;

1) **Days to 50 percent Flowering**

The number of days from the date of sowing till 50 percent of the population reached mid anthesis for both F1s and parents was recorded.

2) **Plant Height**

Plant height was measured using a measuring tape and recorded in centimetres from ground level to the tip of the matured panicle of the plant.

3) **Panicle Length**

This was measured using a measuring tape and recorded in centimetres from the base of the panicle to the tip of the panicle.

4) **Number of Primary Branches per Panicle**

The total number of primary branches were counted and recorded in each panicle in both F1s and parents.

5) **Panicle breadth**

The Panicle breadth was measured at the middle of the panicle where it is widest using a measuring tape.

6) **100-Seed Weight**

One hundred seeds were taken randomly from each panicle and their weight was measured using an electronic scale and expressed in grams.

7) **Panicle exertion**

Distance from the base of the panicle to the flag leaf was measured using a measuring tape and recorded in cm for both F1 plants and parents.

8) **Grain Yield per Plant**

The grain yield from the F1 plants and parents was weighed separately and expressed in grams.

Statistical Analysis

The mean performance of parents, as well as hybrids, were subjected to statistical analysis using R statistical software. Heterobeltiosis (Better parent heterosis), Average heterosis, and significance of heterosis were calculated according to Prasuna (2012).

Estimation of Heterosis

Heterosis over Average Parent: Heterosis was expressed as the percentage increase or decrease observed in the F1 over the mid-parent using the following formula (Prasuna, 2012; Ramesh *et al.*, 2018).

'Average heterosis (%);

$$H1 = \frac{\overline{F1} - \overline{MP}}{\overline{MP}} X\ 100$$

Where;

$\overline{F1}$= Mean of F1

$\overline{MP}$ = Mean of parents

Heterosis over Better Parent: This was expressed as a percentage increase or decrease observed in F1 over the better parent according to the following formula.

Heterobeltiosis (%) (H2);

$$H2 = \frac{\overline{F1} - \overline{BP}}{\overline{BP}} X\ 100$$

Where;

$\overline{F1}$= Mean of F1

$\overline{BP}$ = Mean of better parent

For the characters like days to 50% flowering, earliness is desirable so the early parents were taken as better parents.

Test of Significance of Heterosis: To test the significance for different types of heterosis computation of standard error (SEm) for average heterosis and heterobeltiosis were calculated based on error mean squares (EMS) from the ANOVA tables consisting of parents and crosses. The significance of heterosis *i.e.* average heterosis, and heterobeltiosis was then tested by comparing the calculated 't'- value with the tabulated student's 't'-value for appropriate error degrees of freedom at 5 percent and 1 percent level of significance (0.05 and 0.01 level of probability), respectively (Prasuna, 2012; Ramesh *et al.*, 2018)

t_{calc} for BP and MP= $\frac{\overline{F1} - \overline{BP}/\overline{MP}}{SEm}$

Where $SEm = \sqrt{\frac{2EMS}{r}}$

EMS = Error mean of squares

r = Number of replications'

CHAPTER FOUR

RESULTS

4.1 Performance of selected SWR Genotypes in Western Kenya

The analysis of variance for the various agronomic traits and yield components for each of the four sites showed significant mean sum of squares ($P \leq 0.05$) due to genotypes for most of the traits tested except for panicle breadth at Nyabisawa.

Grain yield

There was differential performance of the genotypes for grain yield across the four sites. There were significant differences ($P \leq 0.05$) observed for this trait in all the four locations.

At Kibos differential performance for grain yield was observed among the genotypes. Most SWR genotypes showed good performance for this trait which compared well with those of checks. Some of them (466, 588 and 504) outperformed commercial and local checks (Table 3). The highest yielding genotype at this site was T53b (2.79 t/ha) followed by 466 (2.78 t/ha) then 504 (2.77 t/ha). From the bottom, Obamo had the least yield (1.43 t/ha) followed by 605 with 1.57 t/ha. In Nyabisawa the SWR genotypes performance compared well with the checks with some of them (560, 588 and 565) exceeding commercial and local checks (Table 3).

MUK 60 was the highest yielder (2.77 t/ha) followed by T53b (2.67 t/ha). Among the SWR genotypes, 588 was the highest yielding (2.0 t/ha) followed by 565 with 1.9 t/ha. Genotype 605 had the lowest yield (0.83 t/ha) followed by Obamo with 0.93 t/ha. Performance of SWR genotypes in Godkwer site was also good and they compared well with the checks.

MUK 60 was the best performing at this site (3.2 t/ha) followed by T53b (3.0t/ha). Genotype 560 was the highest yielding among the SWR at this site with 2.6 t/ha. Genotype 503 had the least performance for this trait (0.93t/ha) followed by Obamo (1.0t/ha) then entry 605 with 1.1t/ha. At Sega, T53B exhibited the best yield performance of 3.0t/ha followed by MUK 60 with a mean yield of 2.23t/ha. Genotypes 504, 514 and 588 were the best performers at this site and outperformed the local and commercial checks. Obamo had the least mean grain yield of 1.18t/ha. (Table 3).

Table 3: Means for Grain yield of sorghum Genotypes evaluated at four sites in western Kenya during the long rains of 2019

Genotype	Grain yield (t/Ha)				
	Kibos	**Nyabisawa**	**Godkwer**	**Sega**	**Means**
466	2.78ab	1.90a-c	2.37a-f	2.22ab	2.32
468	1.61ab	1.73a-c	1.40e-i	1.72ab	1.62
501	2.08ab	1.33bc	1.53d-i	1.97ab	1.68
503	1.87ab	1.17bc	0.93i	2.06ab	1.57
504	2.77ab	1.53bc	1.43e-i	2.39ab	2.02
509	1.71ab	1.33bc	1.60c-i	1.72ab	1.6
512	1.57ab	0.93bc	1.80c-i	1.73ab	1.51
514	2.34ab	1.77a-c	2.53a-d	2.31ab	2.14
529	2.09ab	1.53bc	2.03b-h	1.98ab	1.97
536	1.76ab	1.53bc	1.33f-i	1.51b	1.53
542	1.73ab	1.30bc	1.67c-i	2.04ab	1.66
550	1.59ab	1.87a-c	1.37e-i	1.58b	1.54
555	2.11ab	1.57bc	1.83c-i	1.71ab	1.8
565	2.63ab	1.90a-c	1.80c-i	1.87ab	2.02
560	1.84ab	1.97ab	2.6a-c	1.79ab	2.03
582	2.20ab	1.07bc	2.33a-g	1.65ab	1.86
585	2.41ab	1.90a-c	1.83c-i	1.71ab	1.97
586	2.38ab	1.77a-c	2.53a-d	1.65ab	2.01
588	2.59ab	2.00ab	2.40a-e	2.08ab	2.28
590	2.30ab	1.43bc	1.30g-i	1.57b	1.58
605	1.57ab	0.83c	1.10hi	1.44b	1.3
Gadam	1.82ab	1.23bc	1.77c-i	1.7ab	1.62
MUK 60	2.51ab	2.77a	3.20a	2.23ab	2.64
Obamo	1.43b	0.93bc	1.00hi	1.18b	1.13
T53B	2.79a	2.67a	3.00ab	3.00a	2.95
CV %	14.50	15.47	12.62	15.70	
SE	0.30	0.25	0.24	0.27	
Grand mean	2.10	1.60	1.67	1.87	

Note: Means in the same column followed by the same letter are not significantly different at $P \leq 0.05$ according to Tukeys range test.

Early Vigour

There were significant differences ($P \leq 0.05$) observed for this trait in all the four locations (Table 4). In Kibos differential performance of the genotypes for early vigour was observed. Most SWR genotypes showed good performance for this trait with all of the having a score of >3 and their performance compared well with those of checks with some of them (genotype 501 and 529) exceeding commercial and local checks (Table 4). The highest vigour score was recorded in genotype 501 (5.03) followed by T53b (5.02) a check then 529 (5.01). Genotype 468 had the least score of 3.02.

In Nyabisawa the SWR genotypes compared well with the checks with some exceeding the checks. Genotype 514 had the highest score (4.0) followed by 560 (3.63) while Gadam had the lowest score (2.62) (Table 4). In Godkwer, genotype 565 was the best performer (5.04) followed by 536 (5.02) then MUK 60 (4.95) while genotype 605 had the least performance for this trait (2.95) with all the other entries having a score >3 at this site. The overall mean vigour score for Sega was 3.7 with genotype 509 having the highest score of 4.67 followed by 555 (4.5) while Obamo had the least score of 2.33, which was the least vigour score across the 4 locations (Table 4).

Table 4: Means for Early vigour for sorghum Genotypes evaluated at four sites in western Kenya during the long rains of 2019

Genotype	Early vigour				
	Kibos	**Nyabisawa**	**Godkwer**	**Sega**	**Means**
466	4.85ab	3.30a	4.55a-c	3.67a	3.75
468	3.02b	3.00a	4.65ab	3.00a	3.08
501	5.03a	3.00a	4.06a-c	2.67a	3.50
503	4.04ab	3.00a	3.61a-c	4.00a	3.33
504	3.41ab	2.62a	4.31a-c	3.67a	3.38
509	3.45ab	3.00a	4.32a-c	4.67a	3.46
512	3.49ab	3.30a	4.25a-c	3.67a	3.46
514	4.52ab	4.00a	4.62ab	4.67a	4.46
529	5.01ab	3.00a	4.4a-c	3.33a	3.83
536	3.50ab	3.30a	5.02a	4.33a	3.96
542	3.41ab	3.00a	4.22a-c	4.33a	3.46
550	4.55ab	3.00a	3.08bc	4.00a	3.42
555	4.49ab	3.30a	4.62ab	4.50a	4.00
565	4.56ab	2.62a	5.04a	3.67a	3.92
560	3.61ab	3.63a	4.61a-c	3.67a	3.46
582	3.34ab	3.30a	3.99a-c	3.33a	3.50
585	4.47ab	3.00a	3.97a-c	3.67a	3.62
586	4.57ab	3.30a	4.96a	4.33a	4.21
588	3.36ab	3.00a	4.97a	3.67a	3.83
590	3.45ab	3.30a	3.73a-c	4.33a	3.62
605	3.91ab	3.00a	2.95c	4.33a	3.25
Gadam	4.53ab	2.62a	4.07a-c	2.67a	3.54
MUK 60	4.45ab	3.30a	4.95a	3.33a	4.04
Obamo	4.98ab	3.00a	4.65ab	2.33a	3.5
T53B	5.02ab	3.30a	4.30a-c	3.67a	3.92
CV %	7.53	11.04	6.29	16.80	
SE	0.05	0.05	0.04	0.05	
Grand mean	4.07	3.11	4.32	3.74	

Note: Means in the same column followed by the same letter are not significantly different at $P \leq 0.05$ according to Tukeys range test.

Days to 50 percent flowering

The performance of the genotypes differed significantly for Days to 50% flowering across the four sites. Most of the SWR genotypes showed good performance for this trait which compared well with those of checks (Table 5). In Kibos, performance of the SWR genotypes compared well with that of the checks. Genotype 504 and 588 took the longest time to reach 50% flowering (87.6), this were followed by genotype 582 (86.7). Gadam took the shortest time to reach 50% flowering (67.3) and was followed by genotype 605 (70.9). In sega, genotype 536 took the longest time to reach 50% flowering (79.4) followed by 586 (79.0). Genotype 466 had the shortest time to reach 50% flowering (62.7) and was followed by genotype 590 (66.6). In Nyabisawa, genotype 468 took the longest time to reach 50% flowering (73.3) followed by Obamo (73.2). Gadam took the shortest time to reach 50% flowering (60.3 days) and was followed by genotype 512 (62.2). In Godkwer genotype 504 took the longest time to reach 50% flowering (82) followed by 503 (81.2). Gadam had the shortest time to reach 50% flowering (62.7) and was followed by genotype 514 (65.3) (Table 5).

Plant Height

For plant height, the performance of the genotypes differed significantly across the four sites. Highest grand mean for this trait was recorded in Kibos (303.62 cm) followed by Sega (267.84) then Godkwer (241.23) and lowest (232.47 cm) in Nyabisawa. The tallest genotype 588 exhibited the tallest mean height (324.0 cm) while Gadam was the shortest (125 cm). The SWR genotypes were much taller than most of the checks except for Obamo (Table 5). In Kibos the checks exhibited better performance for this trait compared to the

SWR genotypes (Table 5). Genotype 565 had the highest mean height (392.81 cm) followed by genotype 588 (376.37 cm). MUK 60 had the least mean height (110.12 cm) followed by Gadam (126.71cm). In Nyabisawa genotype 536 recorded the tallest mean height (295.14cm) followed by 586 (292.23 cm) while Muk 60 recorded the least mean height (134.87 cm). The checks had a height less than the average of all genotypes (232.47cm) (Table 5). Similarly, at Godkwer the checks attained mean heights that were shorter than the average height of all genotypes. Highest mean at this location was observed in genotype 501 (314.41cm) followed by genotype 586 (295.81 cm) while the least mean height was observed in Gadam (116.75 cm) followed by Muk 60 (139.00 cm). The Highest mean height for Sega was recorded in genotype 588 (344.63 cm) followed by 605 (327.55cm) while Gadam had the least height of (129.28 cm) (Table 5).

Table 5: Means for Days to 50% Flowering and Plant Height for sorghum Genotypes evaluated at four sites in western Kenya during the long rains of 2019

Genotype	Days to 50 % Flowering					Plant Height				
	Kibos	Nyabisawa	Godkwer	Sega	Means	Kibos	Nyabisawa	Godkwer	Sega	Means
466	85.89ab	65.99a	79.36ab	62.68g	77.20	240.87de	218.21a-d	183.20e-h	222.37fg	216.00
468	84.30ab	73.32a	81.33a	69.85d-f	79.50	274.30c-e	222.18a-d	211.46c-g	249.55d-g	242.00
501	80.37a-c	65.09a	77.99a-c	67.97e-g	73.50	330.12a-d	282.48ab	314.41a	253.11c-g	300.00
503	85.31ab	72.91a	81.23a	73.64a-f	79.70	343.04a-c	231.56a-d	244.43a-e	282.66b-f	276.00
504	87.56a	70.52a	82.01a	72.73a-f	78.50	263.72c-e	213.18a-d	225.71b-f	268.54b-f	241.00
509	75.60b-d	66.61a	67.32c-e	74.3a-e	69.00	302.17a-d	223.19a-d	266.36a-d	273.31b-f	264.00
512	78.09a-d	62.15a	76.76a-c	75.45a-d	71.70	209.05ef	160.48cd	154.99f-h	201.39g	182.00
514	81.41a-c	63.10a	65.31de	74.35a-e	70.00	295.78b-e	194.91a-d	201.02d-g	287.59a-e	243.00
529	80.75a-c	67.64a	74.29a-d	74.03a-e	74.10	346.15a-c	256.01a-c	275.70a-d	292.75a-e	291.00
536	82.54a-c	68.99a	75.65a-d	79.38a	75.40	347.29a-c	295.14a	291.39a-c	302.76a-d	302.00
542	83.88ab	70.59a	76.02a-d	70.31c-f	76.90	347.73a-c	229.42a-d	284.81a-c	300.52a-d	290.00
550	82.54a-c	64.19a	78.36a-c	77.34ab	74.80	305.09a-d	205.98a-d	263.83a-d	303.25a-d	264.00
555	82.61a-c	72.89a	72.97a-e	70.36b-f	75.70	349.02a-c	249.78a-c	265.88a-d	294.91a-e	289.00
565	85.35ab	67.66a	75.25a-d	78.61a	74.80	392.81a	279.64ab	282.29a-c	254.32c-g	299.00
560	84.96ab	64.82a	75.53a-d	76.01a-d	74.50	325.67a-d	259.78a-c	284.24a-c	313.98ab	301.00
582	86.68ab	70.66a	75.54a-d	77.24a-c	77.00	353.19a-c	269.09ab	288.81a-c	310.92a-c	308.00
585	84.33ab	72.79a	73.98a-d	73.97a-e	77.50	347.33a-c	271.14ab	268.63a-d	254.2c-g	288.00
586	83.35ab	67.97a	76.48a-c	79.02a	76.60	372.34ab	292.23a	295.89ab	292.62a-e	318.00
588	87.58a	67.50a	75.42a-d	74.34a-e	77.00	376.37ab	273.49ab	295.00ab	344.63a	324.00
590	81.88a-c	66.19a	73.69a-e	66.64fg	74.00	332.98a-c	288.42a	260.25a-e	291.22a-e	291.00
605	70.86cd	71.87a	69.71b-e	77.36a	70.10	293.59b-e	180.14b-d	196.69d-h	327.55ab	250.00
Gadam	67.32d	60.33a	62.70e	69.67d-g	63.20	126.71fg	142.63d	116.75h	129.28h	125.00
MUK 60	75.39b-d	73.03a	72.68a-e	79.04a	74.30	110.12g	134.87d	139.00gh	138.11h	140.00
Obamo	82.83ab	73.19a	76.31a-c	74.01a-e	77.60	334.20a-c	223.82a-d	211.67c-g	234.37e-g	248.00
T53B	81.11a-c	68.38a	75.78a-d	77.38a	74.40	270.78c-e	213.89a-d	208.43c-g	271.99b-f	240.00
CV %	2.95	7.41	3.05	2.10		6.10	8.35	6.41	4.50	
SE	2.41	5.07	2.28	2.37		18.53	19.41	15.46	17.32	
G mean	81.70	68.33	74.87	73.83		303.62	232.47	241.23	267.84	

Note: Means in the same column followed by the same letter are not significantly different at $p \leq$ 0.05 according to Tukeys range test.

Panicle Length

Results for performance of the genotypes for Panicle Length was observed to differ significantly at Kibos, Godkwer, Sega and Nyabisawa (p>0.05) (Table 6

In Kibos all SWR genotypes showed good performance for this trait and their performance compared well with those of checks with all exceeding the checks (Table 6). The longest panicle at this site was 34.48cm and was observed in genotype 605 followed by genotype 509 with 33.53cm. The shortest length observed was 16.65cm in Obamo. In Nyabisawa the longest panicle length 36.78cm was observed in genotype 586 which was followed by 34.38cm observed in genotype 582 while shortest panicle length was observed in Obamo (16.4cm). In Godkwer the longest panicle being observed in genotype 509 (38.58cm) followed by genotype 605 (36.25cm) and the shortest in Obamo (16.0cm). Genotype 605 had the longest panicle length (39.67cm) in Sega followed by genotype 588 (38.83cm) while Obamo had the shortest length of 15.33 cm (Table 6).

Panicle Breadth

Generally, for panicle breadth, the checks had a wider panicle compared to the SWR Genotypes at all the sites. Panicle Breadth varied significantly at Kibos, Godkwer and Sega while Nyabisawa did not show significant differences (p>0.05) (Table 6).

Best performance (5.62 cm) for this trait was recorded in Sega. This was followed by Kibos site (4.81cm) then Godkwer (4.65cm) while least performance (4.08 cm) was recorded in Nyabisawa (Table 6). The highest panicle breadth was recorded in genotype T53b (7.12 cm) followed MUK 60 (5.21cm) while among the SWR genotype 536 had the largest breadth of 4.93cm. Entry 605 had the least breadth of 3.85cm. All the checks

performed better than the SWR genotypes for this trait. genotype T53b had the widest mean panicle breadth at all the four locations. Genotype 605 had the least mean breadth at Kibos, Godkwer and Sega while genotype 514 and 560 had the least mean panicle breadth (3.98) at Godkwer (Table 6).

Table 6: Means for Panicle Length and Panicle Breadth for sorghum Genotypes evaluated at four sites in western Kenya during the long rains of 2019

Genotype	Panicle length (cm)					Panicle Breadth (cm)				
	Kibos	Nyabisawa	Godkwer	Sega	Means	Kibos	Nyabisawa	Godkwer	Sega	Means
466	22.27e-h	31.62ab	28.50a-e	33.33ab	28.7	4.74cd	4.33a	4.50bc	5.27bc	4.73
468	22.81e-g	26.61a-f	25.33b-f	27.17bc	25.6	4.50d	4.00a	4.50bc	4.67bc	4.42
501	29.64a-d	33.42ab	34.17ab	38.17a	34.8	4.88b-d	4.00a	4.50bc	5.81bc	4.8
503	28.01cd	30.52ab	29.75a-d	35.67ab	30.9	4.63cd	4.02a	4.42bc	5.22bc	4.55
504	26.64d-f	29.85abc	31.50a-c	27.17bc	28.8	4.72cd	4.00a	4.50bc	4.84bc	4.52
509	33.53ab	31.70ab	38.58a	33.83ab	34.3	4.63cd	4.00a	4.50bc	5.29bc	4.62
512	21.57f-i	24.70b-f	23.08c-f	32.17ab	25.4	4.61cd	3.99a	4.58bc	4.97bc	4.55
514	28.97b-d	29.81a-d	29.33a-d	33.17ab	30.2	4.66cd	3.98a	4.42bc	5.57bc	4.64
529	26.41d-f	30.15ab	28.75a-e	38.00a	31.9	4.73cd	4.00a	4.42bc	5.84bc	4.75
536	30.13a-d	34.32ab	31.00a-c	35.83ab	33	4.89b-d	4.83a	4.83bc	5.20bc	4.93
542	28.13cd	28.98a-e	34.08ab	32.5ab	30.8	4.87b-d	3.99a	4.42bc	5.29bc	4.66
550	32.07a-c	30.25ab	34.25ab	34.17ab	33.1	4.71cd	4.02a	4.50bc	5.82bc	4.77
555	31.25a-d	32.15ab	33.33a-c	35.5ab	33	4.62cd	4.01a	4.50bc	5.21bc	4.57
565	29.05b-d	32.29ab	29.58a-d	37.33ab	32.3	4.76cd	4.00a	4.50bc	6.19bc	4.65
560	29.55b-d	31.54ab	34.50ab	36.33ab	31.9	4.77cd	3.98a	4.50bc	5.33bc	4.85
582	29.91a-d	34.38ab	33.44a-c	36.83ab	33.8	4.77cd	3.99a	4.50bc	5.71bc	4.73
585	26.71de	33.69ab	36.17a	36.00ab	33	4.75cd	4.03a	4.42bc	5.20bc	4.58
586	29.01b-d	36.78a	34.58ab	37.5ab	34	4.76cd	3.98a	4.50bc	4.99bc	4.56
588	29.82a-d	33.81ab	34.67ab	38.83a	34.5	4.74cd	4.01a	4.50bc	6.15bc	4.85
590	31.00a-d	32.92ab	34.17ab	34.83ab	33.4	4.88b-d	4.02a	4.58bc	5.98bc	4.86
605	34.58a	34.20ab	36.25a	39.67a	35	2.99e	3.97a	4.33c	4.11c	3.88
Gadam	18.97g-i	19.20ef	19.17d-f	18.33cd	18.8	5.00b-d	4.33a	5.33b	5.33bc	5
MUK 60	19.08g-i	19.43c-f	18.50ef	19.5cd	19.1	5.50b	3.99a	5.00bc	6.32bc	5.21
Obamo	16.65i	16.57f	16.00f	15.33d	16.4	5.25bc	4.01a	4.08c	6.53b	4.96
T53B	17.51hi	19.41d-f	20.17d-f	20.33cd	19.7	6.87a	4.50a	7.42a	9.68a	7.12
CV %	3.76	7.22	8.18	7.00		3.17	8.40	5.02	8.50	
SE	1.01	2.13	2.45	2.15		0.15	0.34	0.23	0.26	
Grand mean	26.93	29.53	29.95	32.30		4.81	4.08	4.65	5.62	

Note: Means in the same column followed by the same letter are not significantly different at $p \leq 0.05$ according to Tukeys range test.

4.2 Genotype x Environment Interaction for selected sorghum genotypes

Combined analysis of variance

The combined analysis of variance (ANOVA) across environments for grain yield and other agronomic characters of 25 sorghum genotypes is presented in Table 7. The genotypes and the environments differed significantly (p<0.01) for all the traits measured. Additionally, there was significant GXE for all the traits measured.

Table 7: Combined ANOVA Table for Sorghum Grain Yield Across four locations in western Kenya

Source of Variation	DF	Days to flowering	Early vigour	Plant Height	Panicle Length	Panicle Breadth	GY t/h
ENV	3	2258.09**	46.82**	76685**	363.46**	30.325**	3.301**
REP(ENV)	8	15.17	2.62**	3646**	10.51	0.099	0.039
BLOCK(REP*ENV)	48	13	0.695**	1085**	7.64	0.1335	0.099
GEN	24	163.52**	1.246**	31687**	377.3**	3.545**	1.995**
GEN: ENV	72	24.94**	1.136**	2014**	14.67**	0.611**	0.243**
Residuals	144	9.73**	0.44**	275**	5.83**	0.103**	0.111**
CV (%)		4.18	18.12	6.35	8.13	6.7	17.93
MSR+/MSR-		11.31	3.27	2.67	8.65	9.34	1.71
OVmean		74.68	3.66	261.29	29.69	4.79	1.85

DF: Degrees of freedom; **ENV**: Environment; **REP**: Replication; **GEN**: Genotype ; **MSR+/MSR- :** Mean square due to regression**; ****: significant at p < 0.05

4.2.1Partitioning of Genotype by Environment Interactions using AMMI Analysis

AMMI biplots were used to visualize GEI patterns and to measure genotypic adaptation and stability. The combined analysis of variance showed that genotype and environment main effects and their interaction were highly significant for all the traits measured (Table 8).

For grain yield, genotypes accounted for the highest in the total sum of squares due to variation 42.1%), environments accounted for 8.7% of the total sum of squares for variation while Genotype and Environment interactions accounted for the rest of the total sum of squares (15.4%). The cumulative percentage of the GEI that was justified by PC1, PC2 and PC3 was 100%. and the contributions of PC1, PC2 and PC3 were 55.1%, 23.5% and 21.4%, respectively (Table 8). For days to 50% flowering the variation was accounted for by environments, genotype and GEI as 41.2%, 23.9% and 10.9%, respectively. The contributions of PC1, PC2 and PC3 were 61.4%, 25.5% and 13.1%, respectively. High significant variation ($P \leq 0.001$) for Panicle length was accounted for by environments, genotype and GEI as 8.0%, 66.8% and 7.8%, respectively. The contributions of PC1, PC2 and PC3 were 55.1%, 27% and 18%, respectively. Low IPCA1 scores show low contribution to the GEI.

Table 8: Partitioning of the GEI for grain yield and other agronomic traits for Sorghum across four locations in western Kenya

SOV	DF	Days to 50% flowering			Panicle Length			Grain Yield		
		Mean Squares	Proportion	Accumulated	Mean Squares	Proportion	Accumulated	Mean Squares	Proportion	Accumulated
ENV	3	2258.09**	NA	NA	363.46**	NA	NA	3.30**	NA	NA
REP(ENV)	8	15.17	NA	NA	10.51	NA	NA	0.04	NA	NA
BLOCK(REP*ENV)	48	13.00	NA	NA	7.64	NA	NA	0.10	NA	NA
GEN	24	163.52**	NA	NA	377.30**	NA	NA	1.99**	NA	NA
GEN: ENV	72	24.94**	NA	NA	14.67**	NA	NA	0.24**	NA	NA
PC1	26	42.40	61.4	61.4	22.37	55.1	55.1	0.37	55.1	55.1
PC2	24	19.08	25.5	86.9	11.87	27	82	0.17	23.5	78.6
PC3	22	10.70	13.1	100	8.64	18	100	0.17	21.4	100
Residuals	144	9.73	NA	NA	5.83	NA	NA	0.11	NA	NA
Total	371	44.31	NA	NA	36.52	NA	NA	0.31	NA	NA

DF: Degrees of freedom;**; ENV**: Environment; **REP**: Replication; **GEN**: Genotype ; **GEN*ENV**: Environment genotype interaction; **REP(ENV): ; BLOCK(REP*ENV): ; PC**: Principal component; **Proportion**: % GEI ; **Accumulated**: Accumulation % GEI ******: significant at $p < 0.05$

Because of the maximum variability that was accounted for by the first two principal components (IPCA-1 and IPCA-2), they were used to plot a 2-dimensional AMMI biplots (Figure 3 to 8).

4.2.3 AMMI Stability analysis

Biplot graphs of the AMMI1 (PC1 *vs.* additive effects from varieties and environment) and AMMI2 models (PC2 *vs.* PC1) for grain yield are in shown in Figures 3 and 4, respectively. In the AMMI1 bi-plot the abscissa represents the mean of the environments and genotypes and the ordinate represents the PC1. Both the genotypes and environments in the right side of the abscissa are high yielding genotypes and environments (above the mean yield) while those in the left side are low yielding genotypes and the environments are unfavourable

environments(Yan and Tinker, 2006). The Biplot of grain yield vs. PC1 (Figure 3) illustrates that the high yielding and stable genotype had a higher grain yield (horizontal axis) and in terms of the first interaction item (PC1), which is shown on the vertical axis, had a minimum value and was near zero. The vertical line (ordinate) that divides the horizontal axis into two parts is the mean of grain yield and the genotypes that are located on the right side had a higher grain yield than the average. On the other hand, the horizontal line (abscissa) that divided the vertical axis into parts is the zero line for PC1.The stable genotypes are near the abscissa and have a minimum GEI. The genotypes that can be recommended in poor and weak locations have low grain yield performance (below average) but they should have a positive value of PC1.

Accordingly, the genotypes with highest grain yields were T53B, 588, 466, 586, 585 and 529 while the genotypes with the lowest grain yield were Obamo, 605, 536 and 512. The most stable genotypes with the least GEI were 565, 529, 466, T53B, 550 and 509. Gadam and 512 had low yields but positive PC1 hence can be recommended for weak environments.

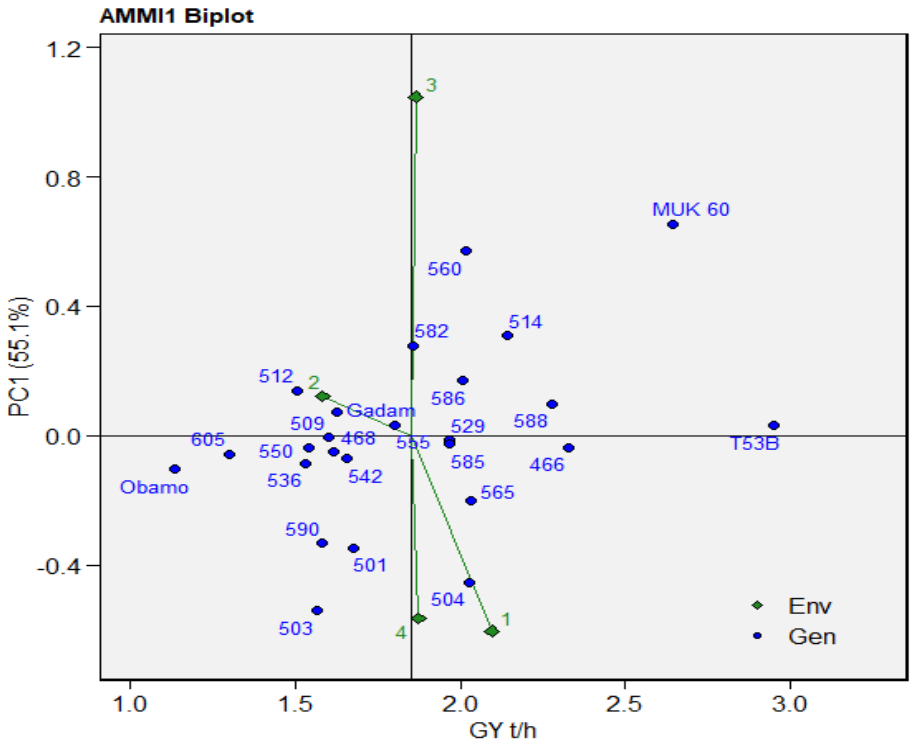

Figure 3: AMMI1 Biplot for additive effects vs. PC1 for Grain yield (t/ha) in 25 sorghum genotypes from four environments in Western Kenya. Numbers in Green colour represent sites/environment (1- Kibos, 2- Nyabisawa, 3- Godkwer, 4- Sega).

Environment 1 (Kibos) was the highest yielding while Environment 2 (Nyabisawa) was the least yielding. According to the correlation between PC1 and PC2 (AMMI 2 Biplot), the genotypes that were positioned near the origin had the least contribution for the GxE interaction and hence are stable, and the genotypes positioned near the x and y axis had more general adaptation. Therefore, genotypes T53B, 585, 555, 542 and 509 showed minimum interaction between genotypes and locations and are most stable. Genotypes 590, 565 and 605 had specific adaptation in Environment 1 while MUK 60 had specific adaptation in Environment 2. The genotypes with specific adaptation in Environment 3 were 582, 586 and 512. Genotype 503 had specific adaptation in environment 4. Genotypes

that had more general adaptation included 509, 585, 529, 542, 501, 555 and 466 (Figure 4).

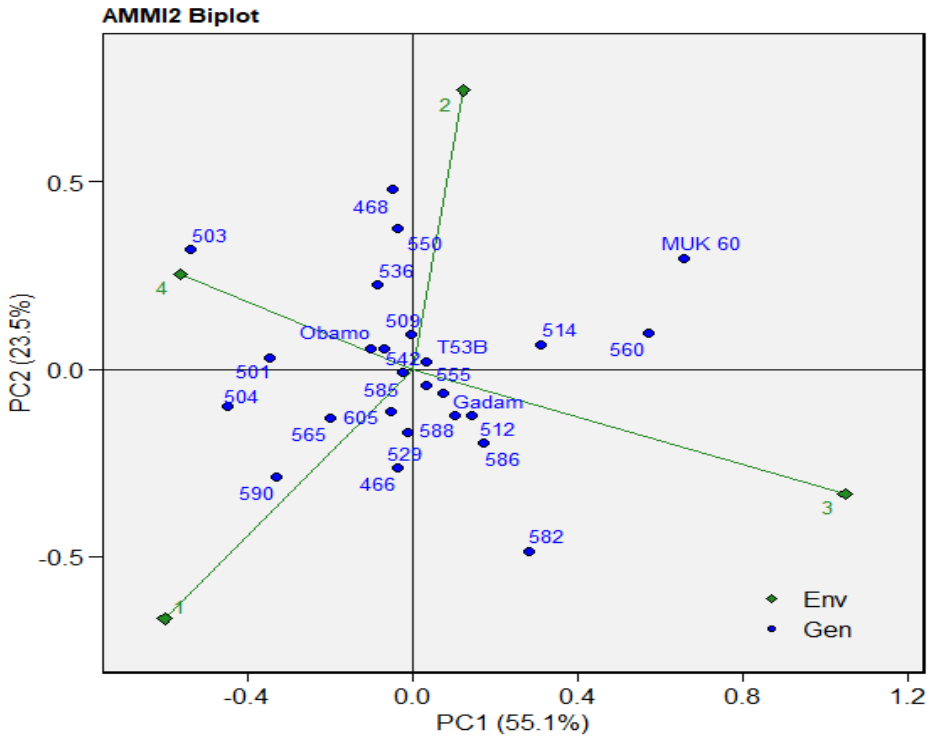

Figure 4: AMMI2 Biplot showing the two main axes of interaction (PC2 vs. PC1) for Grain yield (t/ha) in 25 sorghum genotypes from four environments in Western Kenya Numbers in Green colour represent sites/environment (1- Kibos, 2- Nyabisawa, 3- Godkwer, 4- Sega).

For Days to 50% Flowering, the genotypes and environments average was 74 days. The best genotypes with fewer days to reach 50% flowering were 514 and 512. Environments 2 (Nyabisawa) and 4 (Sega) had genotypes that had the least days to reach 50% flowering. The genotypes with the least days to 50% flowering were Gadam, 509 and 605. The most stable genotypes for this trait were 536, 529, T53B and 503. Genotypes 468, Obamo, 585

and 542 had more days to 50% flowering but positive PC1 hence can be recommended for weak environments with low fertility and low rainfall (Figure 5).

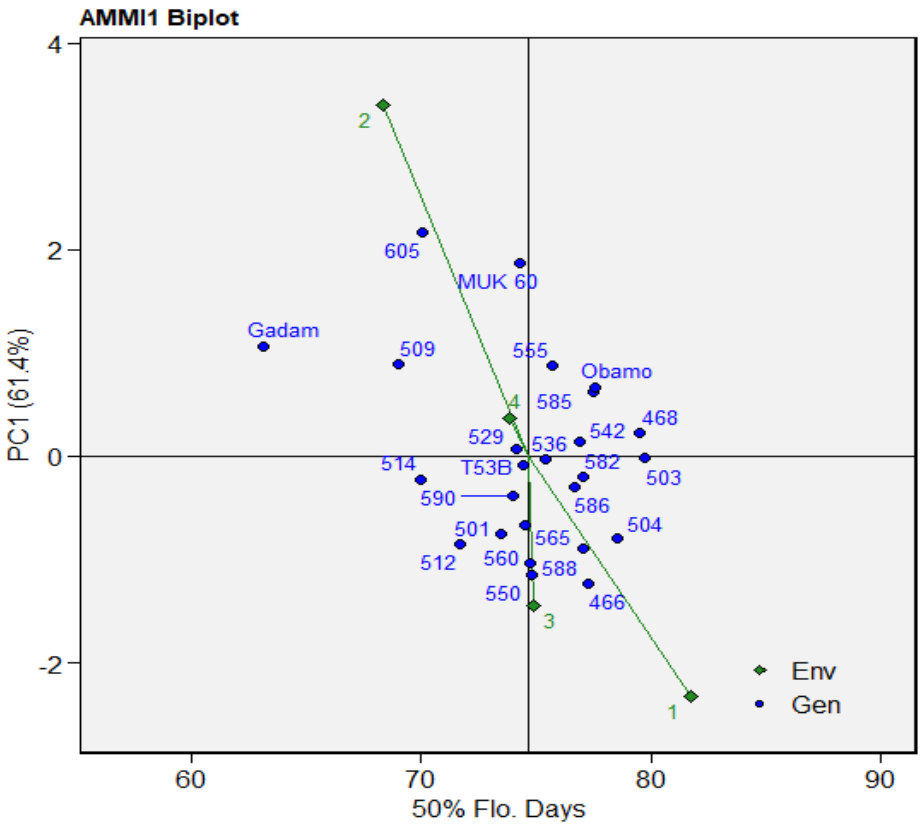

Figure 5: AMMI1 Biplot for additive effects vs. PC1 for days to 50% flowering in 25 sorghum genotypes from four environments in Western Kenya. Numbers in Green colour represent sites/environment (1- Kibos, 2- Nyabisawa, 3- Godkwer, 4- Sega).

According to the correlation between PC1 and PC2, Genotypes 536, 529, 586 and 590 showed the least interaction between genotypes and locations. Genotypes 588, 560, 565 and 514 had specific adaptation in Environment 1 while 555 and 501 had specific adaptation in Environment 2. The genotypes with specific adaptation in Environment 3 were 501, 550,504 and 512. Genotype 585 had specific adaptation in environment 4.

Genotypes that had more general adaptation included 503, MUK 60, Obamo and T53B. Gadam, 605 and MUK 60 could not be identified with a specific environment (Figure 6).

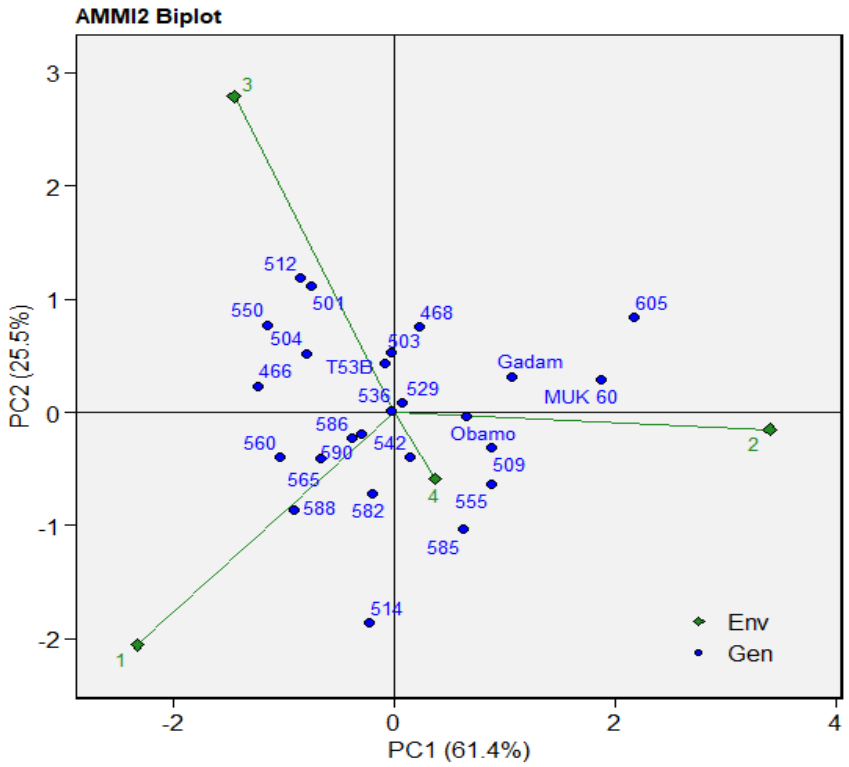

Figure 6: AMMI2 Biplot showing the two main axes of interaction (PC2 vs. PC1) for days to 50% flowering in 25 sorghum genotypes from four environments in Western Kenya. Numbers in Green colour represent sites/environment (1- Kibos, 2- Nyabisawa, 3- Godkwer, 4- Sega).

For Panicle Length, the genotypes and environments average was 29.7cm. The best performing genotypes were 605, 590, 555, 536 and 582. Environments 3 (Godkwer) and 4 (Sega) had genotypes with the highest average panicle lengths. The genotypes with the shortest panicle lengths were Obamo, Gadam, MUK 60, T53B and 468. These genotypes had also a positive PC1 hence can be recommended for weak environments (Figure 7). The most stable genotypes for this trait were 605, 514, 468 and 555.

Figure 7: AMMI1 Biplot for additive effects vs. PC1 Panicle Length in 25 sorghum genotypes from four environments in Western Kenya. Numbers in Green colour represent sites/environment (1- Kibos, 2- Nyabisawa, 3- Godkwer, 4- Sega).

According to the correlation between PC1 and PC2, Genotypes 536, 514, 560 and 590 showed the least interaction between genotypes and locations. Genotypes 550 and 542 had specific adaptation in Environment 1 while 466, 501, 586 and 585 had specific adaptation in Environment 2. The genotype with specific adaptation in Environment 3 was 509. Genotypes 512, 529 and 503 had specific adaptation in environment 4. Genotypes that had more general adaptation included 514, 468, 590, MUK 60, Gadam and 588. Obamo,504 and T53B could not be identified with a specific environment (Figure 8).

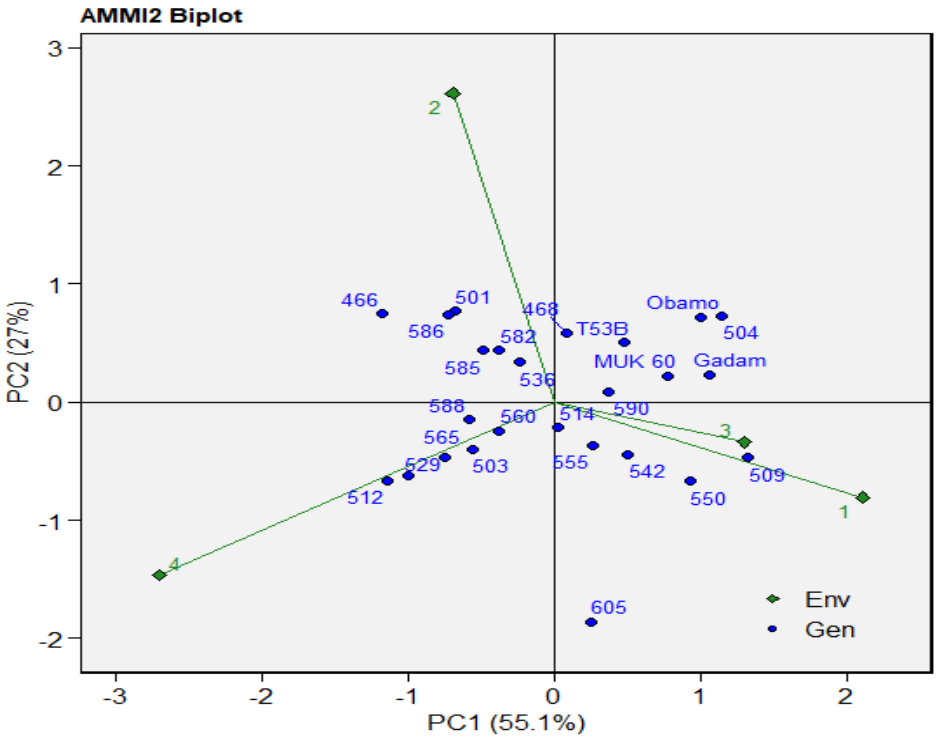

Figure 8: AMMI2 Biplot showing the two main axes of interaction (PC2 vs. PC1) for Panicle Length in 25 sorghum genotypes from four environments in Western Kenya. Numbers in Green colour represent sites/environment (1- Kibos, 2- Nyabisawa, 3- Godkwer, 4- Sega).

4.3 Determination of heterosis for selected traits

Nine crosses were generated using manual emasculation and pollination in the short rains of 2019. The small number of crosses produced was mainly due to self-pollination of the recurrent parents and to some extent partial self-incompatibilities between the SWR genotypes and the recurrent parents.

4.3.1 Estimates of Heterosis

Heterosis over respective mid parent (H1) and better parent (H2) for eight important attributes are presented in Tables 9 and 10. The F1s showed positive, negative and no heterosis for the traits studied.

Grain Yield per Plant (g)

The extent for heterosis for grain yield per plant ranged from -31.48% (RUMUK 154 X 514) to 194.27% (RUC26 X 586) and -49.39% (RUMUK 154 X 514) to 137.89% (RUC26 X 586) both over mid parent and better parent, respectively. The cross RUC26 X 586 expressed high positive heterosis over both mid-parent and better parent (194.27% and 137.89%, respectively) figure 9 (Table 9).

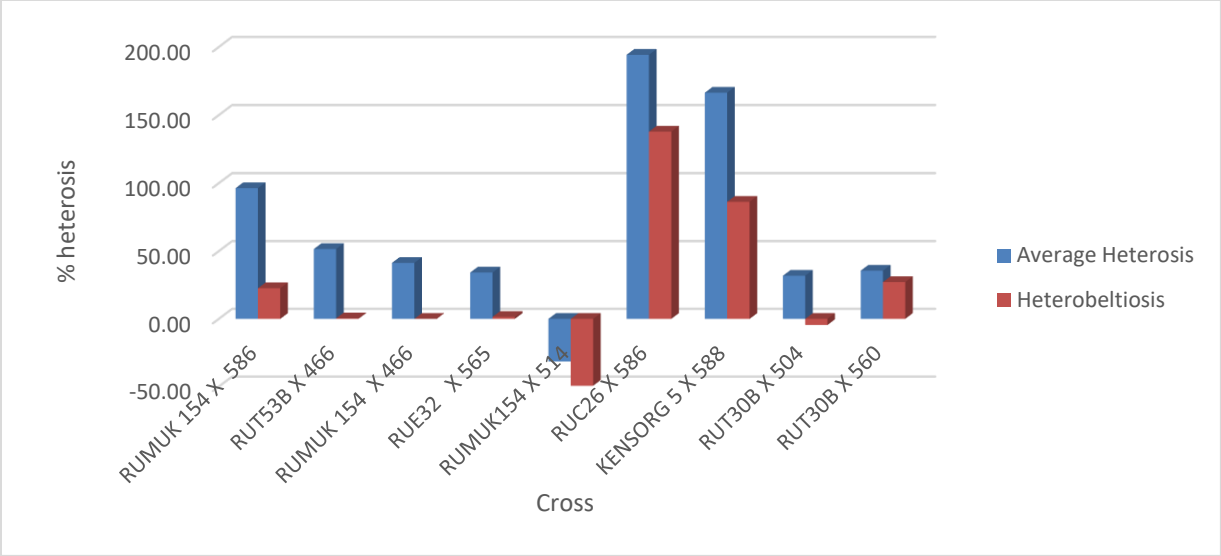

Fig 9. Graphical presentation of the nine cross combinations for heterosis for grain yield

100-Seed Weight (g)

For 100-seed weight, heterosis ranged from -25.28% (RUT30B X 560) to 55.26% (RUMUK 154 X 586) and from -37.54% (RUT30B X 560) to 18.95% (RUMUK 154 X 586) over mid parent and better parent, respectively. (RUMUK 154 X 586) exhibited high heterosis both over mid parent (55.26%) and better parent (18.95%) for this trait (Table 9).

Table 9. Estimates of Average heterosis (H1) and heterobeltiosis (H2) for Grain yield per plant, 100 seed weight, Days to 50% flowering, and Plant height

Cross	Grain Yield per plant		100 seed weight		Days to 50% flowering		Plant height	
	H1	H2	H1	H2	H1	H2	H1	H2
RUMUK 154 X 586	96.33**	22.62**	55.26**	18.95**	-8.86**	-6.49**	1.96**	-26.22**
RUT53B X 466	51.56*	0.38	7.48	1.32	-6.59**	-3.70**	23.26**	12.54**
RUMUK 154 X 466	41.33**	0.02	19.16**	-1	-4.29**	1.3	11.11**	-4.55
RUE32 X 565	34.23**	1.45	9.38*	-13.12**	-6.41**	-3.95**	11.71**	-16.22**
RUMUK154 X 514	-31.48**	-49.39**	21.08**	-13.18**	3.14**	6.49**	12.45**	-5.00*
RUC26 X 586	194.27**	137.89**	10.21*	4.44	4.04**	7.46**	31.68**	0.54
KENSORG 5 X 588	166.47**	86.35**	-1.22	-15.83**	1.82	5.00**	18.44**	3.58*
RUT30B X 504	31.85**	-4.51	17.18**	10.37*	0.61	3.75**	15.64**	11.59**
RUT30B X 560	35.59**	27.16**	-25.28**	-37.54**	-3.85**	-1.32	12.93**	3.25

* Significant at 5% level ** Significant at 1% level

Days to 50 percent flowering

Regarding days to 50% Flowering, Average Heterosis ranged between -8.86% and 4.04% and that over better parent ranged from -6.49% to 7.46%. Most of the Fl's exhibited negative heterosis (preferred) for this trait, both over better parent and mid-parent. The cross (RUMUK 154 X 586) had the best-preferred heterosis both over mid-parent (-8.86%) and better parent (-6.49%) for this trait (Table 9).

Plant Height

For plant height average heterosis varied from 1.96% (RUMUK 154 X 586) to 31.68% (RUC26 X 586) whereas heterobeltiosis for the same traits ranged between -26.22% (RUMUK 154 X 586) to 12.54% (RUT53B X 466). Crosses that exhibited negative

heterobeltiosis for this trait were (RUMUK 154 X 466), (RUMUK 154 X 586), (RUMUK 154 X 514) and (RUE32 X 565) (Table 9).

Panicle Length

Regarding panicle length, heterosis ranged from 0.11% (RUMUK 154 X 466) to 63.22% (RUT53B X 466) and -23.06% (KENSORG 5 X 588) to 39.22% (RUT53B X 466) over mid parent and better parent, respectively (Table 9). Crosses (RUT53B X 466) and (RUT30B X 504) recorded high positive heterosis over both mid parent and better parent for this trait (Table 10).

Number of Primary Branches per Panicle

Heterosis for number of primary branches per panicle ranged from -6.29% (RUMUK 154 X 586) to 21.74% (RUT30B X 504) and -26.79% (RUMUK 154 X 586) to 13.13% (RUT30B X 504) over mid parent and better parent, respectively. Of the crosses (RUT30B X 504) exhibited high heterosis over both the mid parent (21.74%) and better parent (13.13%) (Table 10).

Panicle Exertion

For panicle exertion heterosis ranged from -50% (RUT53B X 466) to 300% (RUT30B X 504) and -66.67% (RUT53B X 466) to 166.67% (RUT30B X 504) over mid parent and better parent, respectively. (RUT30B X 504) had the highest significant positive heterosis over both the mid parent and better parent for this trait (Table 10).

Table 10. Estimates of Average heterosis (H1) and heterobeltiosis (H2) for panicle length, primary branches, panicle exertion, and panicle breadth

Cross	Panicle length		Primary branches		Panicle exertion		Panicle breadth	
	H1	H2	H1	H2	H1	H2	H1	H2
RUMUK 154 X 586	7.77	-10.17*	-6.29	-26.79**	-45.8	-48.00**	20.66**	-5.88
RUT53B X 466	63.22**	39.22**	20.49**	-0.99	-50.00*	-66.67**	15.38*	7.14
RUMUK 154 X 466	0.11*	39.21	21.95**	-0.99	14.29	-33.33*	-3.45	-17.64**
RUE32 X 565	36.26**	8.77*	15.51**	10.20**	127.27**	38.89**	0	-14.29*
RUMUK154 X 514	17.23**	7.94*	3.45	-18.92**	42.86**	-23.08**	0	-23.53**
RUC26 X 586	20.39**	5.08	-2.08	-16.07**	-30.77**	-64.00**	30.11**	16.67*
KENSORG 5 X 588	17.53**	-23.08**	6.67	3.53	-16.28**	-28.00**	36.00**	6.25
RUT30B X 504	44.68**	25.92**	21.74**	13.13**	300.00**	166.67**	5.00**	-9.57
RUT30B X 560	49.03**	20.63**	13.99**	1.85	-6.67	-50.00**	23.08**	14.29*

Panicle Breadth

For panicle breadth, heterosis ranged from -3.45% (RUMUK 154 X 466) to 36% (KENSORG 5 X 588) and -23.53% (RUMUK154 X 514) to 16.67% (RUC26 X 586) over mid parent and better parent, respectively. (RUMUK 154 X 466) and (RUMUK154 X 514) exhibited no positive heterosis over both mid parent and better parent while (RUC26 X 586) showed high positive heterosis over both the mid parent (30.11%) and better parent (16.67%) (Table 10).

DISCUSSION

4.4.1 Performance of selected SWR Genotypes

The high mean grain yield in Kibos is attributable to the higher soil fertility levels in Kibos compared to the other sites. The higher soil fertility is due to the black cotton soil type which are deep and have good pH, with low acidity hence nutrient bioavailability. In Nyabisawa the soils were more sandy, shallow, also the pH there is low about 5.3 means are acidic and hence most nutrients are not available for plants. Additionally, Nyabisawa location experienced unexpected pre-flowering drought during the season that significantly affected performance. These results compare well with those of Muluneh and Kuru (2022), and Adugna (2007) who have reported genetic and phenotypic variabilities observed in different sorghum traits evaluated in different agro ecologies. The better performance of the improved variety checks is attributed to their good adaptation to the region. The high grain yields in some of the SWR entries is attributed to their good genetic potential and wide adaptation. Part of these introductions were well adapted to the Sahelian regions of Mali which have low altitude which to some extent might be similar to some areas around Lake Victoria basin which forms part of the Western Kenya block.

Some of the SRW genotypes such as 466 and 588 exhibited good performance like the checks and even outperforming some weak checks in some sites. This gives hope for further sorghum improvement in western Kenya as the SWR possessed some unique farmer preferred useful traits such as very large panicle size, big, bold and hard grain which is not easily eaten by birds. These traits can be transferred through introgression for sorghum improvement.

Early vigour results showed that there was differential performance of the genotypes for Early vigour was observed across the four Locations. Best performance for this trait by the SWR and checks was exhibited at Godkwer while worst was in Nyabisawa. The difference in performance for this trait across the sites may be attributed to differences in soil and rainfall intensity and amount during the seedling stage of growth. The variation in performance among the genotypes may be attributed to genetic differences among the genotypes tested. These results are in agreement with works of Aruna *et al.* (2016) who found variation in early vigour among 16 forage sorghum genotypes.

In this Study, most of the SWR genotypes showed good performance for days to 50% flowering and their performance compared well with those of checks and in some cases they were earlier than some checks. This implies that some of them could be adopted and grown in western Kenya by farmers as they have similar maturity with the checks.

Kibos location had the greatest number of days to 50% flowering while Nyabisawa had the least. The variation in flowering time might be caused by differences in temperature and rainfall. de Souza *et al.* (2021) found out that moisture stress pre-flowering accelerated flowering in sorghum genotypes. These results on different flowering time of sorghum genotypes are in agreement with Sheunda *et al.* (2019) who reported variation in flowering time among sorghum genotypes. Early flowering sorghum is preferred to counter the shortage of rainfall especially in drought-prone areas where sorghum is commonly cultivated (Belay and Meresa, 2017). Days to flowering predict maturity; early flowering varieties have a high possibility of maturing first escaping drought and other biotic and abiotic stresses.

Moisture differences between the locations might have caused variation in plant height. According to Assefa *et al.* (2010), moisture stress reduces rate of cell elongation and size which culminates into retarded stem growth and stem elongation. The SWR genotypes were much taller than most of the checks. Similar results on variation in height of sorghum genotypes were obtained by (May *et al.*, 2014). The large difference in height is due to the fact that the SWR Genotypes are bred from the guinea race sorghum which have genetically tall height. Studies have shown extremely high plant height and low sorghum height reduce the impact of the final yield. High plant height results in stem logging and difficulty in harvesting and spraying. However, (Ghosh *et al.*, 2015) reported the highest yield on the sorghum variety with the highest plant height among 20 varieties tested. Tall sorghum varieties are also recommended for animal feed purposes due to high above-ground biomass (Abduselam *et al.*, 2018). These findings emphasize the importance of plant height in determining the final yield of the crop.

The variation among the 4 locations may be attributed to differences in soil, temperature and rainfall. All the SWR entries performed well for this trait and they outperformed all the checks. Similar results on variation in panicle length among sorghum genotypes were reported in earlier works by Enyew *et al.* (2021) and Sheunda *et al.* (2019).

The small panicle breadth recorded in Nyabisawa as compared to other sites may be attributed to differences in temperature and rainfall. These results are in agreement with works of Enyew *et al.* (2021) who reported variations in panicle breadth among sorghum genotype.

4.5 Genotype x Environment Interaction, Stability and adaptation of Sorghum Genotypes

4.5.1 Genotype Environment Interaction

The AMMI analysis showed significant differences in genotypes, environments, GxE interactions indicating that both genotypes and the environment were different. These differences were expected as the sorghum genotypes tested were of diverse origin. Kenyan sorghum (checks) was from subspecies *bicolor* while the SWR were from subspecies *verticiflororum*. Similarly, the testing environments are known to differ agro-ecologically. These findings compare well with those of Sheunda (2019) in Sorghum; Rad *et al.* (2013) in wheat and Anowara *et al.* (2015) in rice who reported existence of GXE across locations. The AMMI analysis of variance of 25 sorghum genotypes tested over four environments revealed that 42.1% of the total sum of squares was attributable to the genotypes (G), 8.7 % to the environment (E) and 15.4% to GE interaction effects. The large variation accounted for by genotypes is further indication that they were genetically diverse mainly due to their origin/genetic background and also because some of them were pre-breeding materials related to the wild and could be in possession of novel genetic traits that are not yet available within the cultivated gene pools.

The small proportion of Sum of squares accounted for by the environmental variance indicated that the differences among the environments was not quite high as all the sites were within the Lake Victoria basin and this probably implies that there is no existence of mega environments. These findings agree with those of Rad et al. (2013) who reported significant effects of environmental variance on bread wheat grain yield. They are also in

agreement with those of many others (Yan et al., 2000 and Ahmed et al., 2011) who reported some variation due to environmental variance.

Bose *et al.* (2014) also reported larger Sum of squares variability attributed on rice genotypes due to genotype variability. Also Obsa (2019) reported larger Sum of squares variability attributed on bread wheat genotypes due to genotype variability.

In contrast, larger Sum of squares revealed due to environments on sorghum was reported by (Adugna, 2007; Amare *et al.*, 2019; Seyoum *et al.*, 2020).

The AMMI Component 1 (IPCA-1) and 2 (IPCA-2) indicates that the two AMMI components were adequately explained the variations existed on the yield of the tested sorghum genotypes due to GEI. The first two principal components of AMMI model are the most accurate in predicting total variation explained due to GEI (Bavandpori *et al.*, 2015; Gauch and Zobel, 1996).

The environments contributed the highest percentage to the total sum of squares are in agreement with those of Gethi *et al.* (2013) who reported that 64.5% of the total variation was attributed to environmental effects. Large proportions of variability explained by environmental effects indicate the larger contribution of the environmental effects on sorghum performance. Several studies have alluded to this finding (Amare *et al.*, 2019; Muluneh and Kuru, 2022; Seyoum *et al.*, 2020).

This results are in agreement with work of Enyew *et al.* (2021) who found that genotype was the major was the main contributor to variation in panicle length among sorghum landraces.

The effect of environment on the grain yield, Days to 50% flowering and panicle length could be attributed to growing temperatures, soil conditions, rainfall distribution and other environmental factors among the Four study sites during growth. Genotype effect on the yields of sorghum genotypes may have been attributed to the diversity of the Sorghum genotypes.

Genotype by environment interaction analysis is important in the identification of genotypes with high and stable performance across environments, and in cultivar recommendation for specific growing conditions (Lule *et al.*, 2014). Other studies also recommended specific genotypes for specific environments (Aruna *et al.*, 2016; Enyew *et al.*, 2021).

4.5.2 Stability and adaptation of Sorghum Genotypes

The major aim of plant breeding is to is to develop varieties that have high and stable production across a wide range of environments. This is done by developing genotypes with high productivity and thereafter evaluating them for adaptability in multi-locational trials in the different target environments (Tena *et al.*, 2019). The present study determined the stability and adaptability of sorghum genotypes using AMMI stability analysis. Genotypes considered most stable for grain yields could be recommended as potential candidates for hybrid development under a wide range of environmental conditions. Genotypes that had good grain yield but not very stable because they were found far from the biplot origin. Furthermore, Genotypes that were considered to have more general adaptation and could also be recommended for improving grain yield. These findings agree with findings of Enyew *et al.* (2021); (Muluneh and Kuru, 2022) who also identified superior genotypes across the test environments for grain yield.

Studies by Yan *et al.* (2007) suggested that genotypes with narrow adaptation showing high grain yield performance in specific environments should be recommended for specific target production areas.

Similarly, Muluneh and Kuru (2022) evaluated sixteen sorghum landraces and identified stable landraces with wide adaptability that were recommended to be incorporated in sorghum breeding program.

Genotypes with the shortest panicle that had a positive PC1 hence can be recommended for poor environments that have less than optimal soil fertility and rainfall. These results are in agreement with studies of Enyew *et al.* (2021) who identified sorghum genotypes in Ethiopia that had longer panicles and were stable.

The difference in performance of genotypes across different environments enables them to be classified for cultivation in either high or low yielding environments (Abuali *et al.*, 2014; Kandus *et al.*, 2010).

In this study, environments contributed differentially to the genotype stability for different traits. The IPCA1 scores indicated that environment 1 (Kibos) was the main contributor to the stability of genotypes in terms of Grain yield and days to flowering. In this study, AMMI2 biplots indicated that all environments were positioned far from the biplot origin for grain yield and panicle length while environment 4 (Sega) was placed close to the origin for days to 50% flowering. These results are similar to the observations reported by (Baraki and Gebremariam, 2018) who identified specifically adaptable sesame genotypes and genotypes widely adaptable in most of the environments for their oil content.

4.6 Heterosis for Selected traits

Most of the hybrids derived from locally adapted genotypes and sorghum wild relatives had higher grain yield and other traits that were evaluated except for days to 50% flowering which were reflected in the expression of heterosis. This demonstrated that there is potential in improving sorghum yields and its components by using hybrids derived from wild sorghum relatives. The average heterosis and heterobeltiosis in crosses varied significantly and this was due to the genetic diversity of parents used to generate the crosses as the parental materials were of diverse origins and to some extent from different races and gene pools. Similar findings have been reported by Ringo et al. (2015), Zhang et al. (2024) and Demisse (2023). The high positive heterobeltiosis (67%) and average heterosis (89%) for grain yield exhibited by the majority of the F1s is attributed to positive transgressive inheritance where the offspring's exhibited improved performance over the parents. This was expected due to high genetic diversity of the parental lines.

The cross (RUC26 X 586) expressed the highest positive heterosis over mid and better parent for grain yield per plant. The positive significant heterobeltiosis for grain yield per plant could have been contributed by the high scores for 100 seed weight and long panicle length. This finding also compares well with several other studies such as Rachman et al. (2022), Sheunda (2019), Schaffasz et al. (2019), (Sheunda, 2019) Ouma et al. (2012), and Zhang et al. (2024) who have reported Significant positive heterosis for grain yield per plant and on other agronomic traits.

For days to 50% flowering, 40% of the F1s had negative heterobeltiosis in comparison with parental genotypes while 60% of the F1s had negative average heterosis as compared to

parental genotypes. This was expected as the F1s had reduced flowering time compared to the parents which implies faster maturity and reduction of the crop reproductive cycle. Earliness is one of the key traits contributed by the wild sorghum which is an important contribution to sorghum adaptation and resilience to water stress which is predominant in the western and Eastern Kenya regions. These findings compare well with those of Sheunda et al. (2019), Crozier et al. (2020) and Veldandi et al. (2021b) who reported significant and negative heterotic values for this trait in sorghum. Further, these results are in agreement with the work of (Tiruneh et al., 2013) who reported negative heterosis in others crops such as common bean genotypes. The Lowest values for average heterosis and heterobeltiosis were expressed in RUMUK 154 X 586 which showed that this was among the top early maturing crosses. The early maturity in sorghum crosses has been attributed to additive gene effects (Makanda et al. (2009).

Most of the crosses showed positive heterosis and heterobeltiosis for plant height. The cross RUT53B X 466 and RUC26 X 586 particularly stood out for this trait probably because of the four possible patterns of dominance, over dominance, pseudo-over dominance, and epistasis (Li et al., 2015). Similar results on high positive heterosis for plant height have been reported by El-Mottaleb and Asran (2004) and El-Dardeer et al. (2011).

However, in Western Kenya, previous studies such as Gudu et al. (2013) have shown that majority of farmers prefer medium to short sorghum plants varieties compared to the tall ones. This is due to the fact that short sorghums require a relatively shorter period to maturity compared to taller ones and withstand lodging as well as easiness during harvesting (Hashimoto et al., 2021); Madhusudhana and Patil (2013). In this case therefore,

higher heterobeltiosis for plant height did not necessarily translate to positive outcome for the small holder farmers of western Kenya. Therefore, crosses with the most promising for plant height as they had negative transgressive inheritance and were shorter than their parents. These findings on heterosis for plant height compare well with those of Gaddameedi et al. (2020) who also reported negative transgressive inheritance for plant height in selected sorghum lines. Results for panicle Length showed that 78% of the F1s exhibited positive heterobeltiosis and the rest showed average heterosis. A longer panicle is generally associated with a greater number of grains and this is one of the attributes for higher grain yields in sorghum hybrids. These results compare well with those of Mengistu et al. (2020), Sheunda (2019), (Sharma and Sharma, 2006) and (Kanbar et al., 2011) who reported positive heterosis and heterobeltiosis for panicle length. However, they are contrary to those reported by Dinakar, 1985; Premalatha et al., 2006; Rachman et al., 2022 who reported negative heterosis for this trait although the reason for such results could not be established immediately. Heterosis of 100 seed weight show that 44% of the F1s showed positive heterobeltiosis and 78% of the F1s showed positive average heterosis. The cross (RUMUK 154 X 586) expressed high heterosis over mid and better parent for 100 seed weight. Significant better parent heterosis for 100-seed weight was reported by (Gaddameedi et al., 2020; Yimer and Jin, 2020).

Heterosis for panicle Breadth revealed 44% of the F1s showed positive heterobeltiosis and 67% of the F1s showed average heterosis for this trait. A Broader panicle is generally associated with a greater number of grains and this is one of the attributes for higher grain yields in sorghum hybrids. Similar positive heterosis for panicle breadth was reported by Ingle et al. (2018).

44% of the F1s showed positive heterobeltiosis and 78% of the F1s showed positive average heterosis for number of primary branches per panicle. The cross (RUT30B X 504) expressed high heterosis over mid and better parent for number of primary branches per panicle. Significant positive heterosis for Number of primaries per panicle was also reported by Prasuna (2012) and Ingle et al. (2018). Heterosis of Panicle exertion show that 22% of the F1s showed positive heterobeltiosis and 44% of the F1s showed positive average heterosis. Panicle exertion is an important attribute that often determines the quality of the grains. Poorly exerted panicle has the leaf sheath covering the panicle thus provides favourable conditions for fungi and insects to develop at the base of the panicle. The preferred well-exerted panicles were in two crosses (RUT30B X 504) and (RUE32 X 565). Similar results on positive heterobeltiosis and average heterosis on panicle exertion was also reported by Ringo et al. (2015)

CHAPTER FIVE

CONCLUSIONS AND RECOMMENDATIONS

5.1 Conclusions

There was significant variation among the sorghum lines tested for various phenotypic traits in all the four locations. This variation was mainly contributed by the wide range of diversity existing among the SWR and the checks. Some of the SWR genotypes 588, 586, and 585 provided promising traits such as early vigour, long panicles, few days to 50% flowering and larger grain size that could be used to improve yield and adaptation to drought.

Grain yield and other agronomic traits were highly influenced by GE interaction; the magnitude of Genotype effect was about five times that of environment effect for grain yield. Most of the genotypes such as 565, 466, 529, 550, and 509 further exhibited general adaptation while others such as 590, 512, and 605 showed more specific adaptation to different places in Western Kenya. This implies the need to select genotypes well adapted to a specific environment and exceptionally for broadly adapted genotypes.

The crosses exhibited both positive and negative heterosis for various traits which showed transgressive inheritance and hence possibility for further breeding using the SWR. The cross (RUC26 X 586) expressed high heterosis over both the better and mid-parent for yield and majority of phenotypic traits. This cross was the most promising and exhibited the best performance in most of the tested traits.

5.2 Recommendations

Further research is needed to screen the sorghum wild relatives against specific diseases and pests both in the field and the green house to determine their resistance. The grain quality and nutritional information of the crosses developed should also be determined.

The stable genotypes across the four environments may be used in future breeding programme further development of stable varieties. While the genotypes which performed well under unfavourable and favourable environment may play a role in the development of variety for the respective environments.

The crosses with high heterosis for grain yield and yield components should be included in sorghum breeding programs for western region of Kenya.

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APPENDICES

Appendix I: Analysis of variance for yield and yield components for parents and crosses

Source of Variation	df	Days to 50% flow	Plant height	Panicle length	Panicle breadth	Primary branches	Panicle exertion	100 sdwt	GY per panicle
Rep	2	0.788	3.82	1.511	0.2339	6.011	0.4091	0.01636	4.42
Treatment	21	46.708**	10616.38**	112.696**	4.791**	154.325**	199.6169**	0.66798**	3591.27**
Error	42	1.169	41.87	2.126	0.2458	4.369	0.8853	0.01474	14.92

* Significant at 5% level ** Significant at 1% level

Appendix II. Mean performance of parents and crosses for yield and yield contributing characters in sorghum

Entry	Days to 50% flow	Plant height (cm)	Panicle length (cm)	Panicle breadth (cm)	Primary branches	Panicle exertion (cm)	100 sdwt (g)	GY per plant (g)
466	86	230.5	25.5	6	50.5	6	2.01	31.48
504	85	276	27	5	49.5	6	2.41	37.08
514	82	240	31.5	4.5	55.5	13	3.11	33.48
560	76	310	32.33	6	54	10	3.17	72.39
565	80	370	28.5	5	44.5	18	2.82	19.08
586	81	370	29.5	4.75	56	25	2.48	17.49
588	85	307	26	4.5	42.5	25	2.4	26.03
RUC26	76	195	22	6	40	1	2.22	28.19
RUE32	76	185	17	7	49	4	1.66	37.3
KENSORG 5	80	230	22.5	8	40	18	1.69	65.29
RUMUK 154	77	165.5	19.67	8.5	31.5	1	1.32	70.21
RUT30B	80	256.7	20	7	42.5	2	2.12	82.68
RUT53B	81	279	18	7	32.5	2	2.27	96.98
RUC26 X 586	81.67	372	31	7	47	9	2.59	133.88
RUE32 X 565	73	310	31	6	54	25	2.45	37.84
KENSORG 5 X 588	84	318	20	8.5	44	18	2.02	121.67
RUMUK 154 X 466	78	220	25	7	50	4	1.99	71.86
RUMUK 154 X 586	72	273	26.5	8	41	13	2.95	86.09
RUMUK 154 X 514	82	228	34	6.5	45	10	2.7	35.53
RUT30B X 504	83	308	34	6.333	56	16	2.66	78.95
RUT30B X 560	75	320	39	8	55	5	1.98	105.14
RUT53B X 466	78	314	35.5	7.5	50	2	2.3	97.35
Grand Mean	79.62	276.26	27.07	6.55	46.82	10.59	2.33	63
CV %	1.4	2.3	5.4	7.6	4.5	8.9	5.2	6.1
Sed	0.88	5.28	1.19	0.4	1.71	0.77	0.1	3.15

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