

**Breeding Sweetpotato (*Ipomoea batatas* [L.] Lam.) for Drought
Tolerance in Kenya**

By

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Thesis Abstract

Sweetpotato (*Ipomoea batatas* (L.) Lam.) is an important food crop in East Africa including Kenya. The crop incurs high yield losses in production due to biotic (insect pests and diseases) and abiotic (drought, and heat) constraints. Among abiotic constraints, drought is the most important. Prolonged periods of drought in arid and semi-arid areas of Kenya have led to reduced quantity and quality of sweetpotato storage roots and in severe cases caused total crop failure. The objectives of this study were to: 1) determine sweetpotato production system constraints and farmers' coping strategies; 2) evaluate sweetpotato clones for yield performance and drought tolerance; 3) analyse genotype x environment interaction and stability for storage root yield of selected clones, 4) determine mechanisms of drought tolerance in sweetpotato, and 5) determine combining ability and heterosis for yield and drought tolerance traits under managed drought stress conditions.

To determine the production constraints and farmers' coping strategies, a survey was conducted in central, eastern and western Kenya. Out of 345 farmers interviewed, 60% were women, and 40% men. Farm sizes ranged from 0.4-0.8 ha, with 90% of sweetpotato cultivated on 0.2 ha or less. The main sweetpotato varieties were Vitaa, Kabonde and Bungoma and the majority of farmer's used their own conserved planting material which was conserved by leaving them in the field after harvest. About 35% of the farmers identified weevils as the major pest, and sweetpotato virus disease (SPVD) as the major disease, while 28% of the farmers identified drought as a major constraint. The farmers used clean seed, high yielding varieties, high planting density, and manure application as the main strategies to cope with sweetpotato production constraints.

Eighty four sweetpotato clones were evaluated under managed drought stress environments at KARI-Kiboko and KARI-Thika. Drought reduced the fresh weight of storage roots (FSR) (72.5%), fresh biomass weight (FB) (74.0%), marketable fresh storage root (MFSR) (80.7%), number of storage roots (NSR) (24.5%), days to permanent wilting point (DPWP) (0.3%), but seemed to increase percent root dry matter (% RDM) (-4.7%), harvest index (HI) (-2.6%), and chlorophyll content (CC) (-2.7%). Across the environments, genotypes 194555.7 (1.06), 421066 (1.05), Chingovu (0.94), 420014 (0.91), Excel (0.9), 199062.1 (0.87) and Unawazambane06-01 (0.81) gave higher FSR yields (kg plant⁻¹) than the local checks. Genotypes Nyarmalo and Polista were among the lowest yielding in the irrigated and non-irrigated conditions. Clones W119, 441725, and Xiadla-xa-kau were the highest yielding under the drought stress conditions.

The performance of 24 improved clones was evaluated in replicated trials at KARI-Thika and KARI-Kiboko using 24 sweetpotato clones grown under managed drought stress conditions for two seasons. AMMI, GGE biplots and regression analyses were conducted to determine stability of the clones. Mean FSR was significantly different ($P < 0.001$) in the two research sites with the environment contributing to 92.7% of the total variation, genotype 1.8%, and interactions 0.4%. AMMI and GGE biplots, and regression indicated the most stable clones to be 441725, Unawazambane06-01 and 189150.1, while Xiadla-xa-kau was the least stable.

To gather more information on drought tolerance mechanisms expressed in the sweetpotato genotypes, an experiment was conducted in the greenhouse using clones expressing different levels of drought tolerance in the field. The results showed more under-developed roots (pencil roots) in the drought stressed regimes than in the irrigated regimes and in the drought susceptible genotypes. Drought tolerant genotypes produced more FSR and NSR. The number of vine branches (NVB), vine tip pubescence (VTP) and mature leaf pubescence (MLP) increased with reduction of drought stress however, drought tolerant clones had reduced NVB. Drought stressed clones had shorter basal vine length (BVL), reduced CC, and reduced leaf growth (LG). Drought stress reduced growth of vines in terms of internodes length, internodes diameter, vine length, petioles length, and leaf CC. Overall, for the first time, the study demonstrated that drought stress in the first three months after planting, leads to the proliferation of non-edible pencil roots, which do not become edible storage roots even when drought stress is removed. Therefore, water is critical during this period for improved sweetpotato storage root yield, probably as a drought tolerant mechanism.

Combining ability for yield and drought tolerance of 15 F1 sweetpotato families generated through a half diallel mating of six parents was evaluated at KARI-Kiboko in 2012. Significant ($P \leq 0.05$) general combining ability (GCA) and specific combining ability (SCA) effects were recorded for root yield in both drought stress and no stress conditions, indicating that both additive and dominance gene effects were important in the inheritance of resistance to drought stress. Progenies from families G2, G5, G7, G8, G10, G12 and G15 had good SCA for fresh storage root yield, total biomass, number of days to permanent wilting point (DPWP), harvest index, and drought stress index (DSI). Progeny 8 from family G4, 5 and 8 from G15, had the highest mid and best parent heterotic effect (117-270%) for fresh storage root yield in both drought stress and no stress conditions. Progeny 6, and 7 from family G10, had the highest mid and best parent heterotic effect (165-234%) for fresh total biomass yield under no drought stress conditions. In conclusion, the progenies from families G2, G5, G7, G8, G10, G12 and

G15 that had high yield and biomass specific combining ability under drought and no drought stress indicated that they could be having drought tolerant genes, and therefore could be incorporated into advanced drought screening trials with the aim of releasing the best performing drought tolerant varieties. Secondly, the findings in this study lay a foundation for sweetpotato breeding programmes on drought tolerance. Thirdly, for the first time, this study uniquely combines yield performance, combining ability estimates, days to permanent wilting point and heterosis under contrasting moisture regimes to unmask the gene action of drought tolerance in sweetpotato, a milestone in science.

Declaration

I, Benjamin Musembi Kivuva, declare that

1. This thesis is a record of my own work; moreover, this work has never been presented before in any academic institution for an academic award.
2. The work reported in this thesis is my original research
3. This thesis does not contain other persons' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from those persons
4. This thesis does not contain other author's writing, unless specifically acknowledged as being sourced from other authors;,
 - a. Where other written sources have been quoted, then their words have been re-written but the general information attributed to them has been referenced
 - b. Where their exact words have been used, their writing has been placed inside quotation marks and referenced
5. Additionally, I acknowledge the sources of all information referenced in the work.

Signed.....Date.....

Benjamin Musembi Kivuva

As candidate's supervisors we agree to submission of this thesis for examination

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Dr. Julia Sibiya (Co-Supervisor)

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Dedication

To God Almighty

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Abbreviations

ABA	Absciscic Acid
ABS	Accelerated Breeding Scheme
ACCI	African Centre for Crop Improvement
AEA	Average Environment Axis
AEC	Average Environment Coordinates
AGRA	Alliance for a Green Revolution for Africa
AMMI	Additive Main effects and Multiplicative Interactions
ANOVA	Analysis of Variance
AOE	Average Ordinate Environment
ASALs	Arid and Semi-Arid Lands
AVDRC	Asian Vegetable Research and Development Center
BIO	Total fresh biomass weight
BVL	Basal Vine Length
CC	Chlorophyll Content
CIP	International Potato Centre
DAMSI	Days After Moisture Stress Initiated
DAP	Days After Planting
DDU	Degree Day Units
DM	Dry Matter
DPWP	Days to Permanent Wilting Point
DSI	Drought Sensitivity Index
F1	First filial generation
F2	Second filial generation
FAOSTAT	Food and Agriculture Organisation of the United Nations - Statistics
FPR	fresh weight of pencil roots
FS	Favourable Sweetness
FSR	Fresh Storage Root Weight
FV	Fresh Vine weight
FY	Favourable storage root Yields
GCA	General Combining Ability
GDU	Growing Degree Units
GEI	Genotype by Environment Interaction

GGE	Genotype by Genotype Environment Interaction
GMP	Geometric Mean Progression
H	Broad sense heritability
h^2	Narrow sense heritability
HI	Harvest Index
HS	High Starch Content
HY	High Yielding
IBPGR	International Board for Plant Genetic Resources
ICARDA	International Centre for Agricultural Research in the Dry Areas
IPGRI	International Board for Plant Genetic Resources (Bioversity)
IV	Improved Varieties
KARI	Kenya Agricultural Research Institute
KOPIA	Kenya Korea Government Cooperation Project
L	Landrace
LD	Leaf Diameter
LF	Low Fibre
LG	Leaf Growth
LL	Leaf Length
LRV	Length of Roots plus Vine braches
LSD	Least Significant Difference
LWP	Leaf Water Potential
m asl	Meters Above Sea Level
MFSR	Marketable Fresh Storage Root Weight
MLP	Mature Leaf Pubescence
MNR	Marketable Number of Storage roots
MoA	Ministry of Agriculture
MP	Mean Productivity
mRNA	Messenger Ribonucleic Acid
NB	Number of Vine branches
NGBK	National Gene Bank of Kenya
NPR	Number of Pencil Roots
NSR	Number of Storage Roots
NVB	Number of Vine Branches
OFSP	Orange Fleshed Sweetpotato

PCA	Principal Component Analysis
PL	Pencil roots Length
PRA	Participatory Rural Appraisal
PRI	Pencil Root Index
PWP	Permanent Wilting Point
QTL	Quantitative Trait Loci
r	Pearson's correlation coefficient
R ²	Coefficient of determination
RCBD	Randomised Complete Block Design
RDM	Root Dry Matter
RGR	Relative Growth Rate
RLI	Root Length Index
RVL	Root plus Vine Length
RWC	Relative Water Content
SCA	Specific Combining Ability
SPCSV	Sweetpotato Chlorotic Stunt Virus
SPFMV	Sweetpotato Feathery Mosaic Virus
SPSS	Statistical Package for Social Sciences
SPVD	Sweetpotato Virus Disease
SSA	Sub Saharan Africa
SSI	Stress Susceptibility Index
STI	Stress Tolerance Index
SWP	Soil Water Potential
UNESCO	United Nations Educational, Scientific and Cultural Organization
USDA	United States Department of Agriculture
VBL	Vine Branches Length
VD	Vine Diameter
VDM	Vine dry matter
VL	Vine Length
VTP	Vine Tip Pubescence
WARDA	West Africa Rice Development Authority
WFSP	White Fleshed Sweetpotato
WUE	Water Use Efficiency
YR	Yield Reduction

Thesis Introduction

1. Importance of sweetpotato

Sweetpotato (*Ipomoea batatas* (L.) Lam.) is an important food, feed and vegetable crop in most tropical developing countries. The crop is ranked fifth economically after rice, wheat, maize, and cassava, sixth in dry matter production, seventh in digestible energy production, and ninth in protein production in the developing countries (Stathers et al., 2005; Thottappilly and Loebenstein, 2009). World production is about 131 million tonnes yr⁻¹, on approximately 9 million ha with mean estimated yields of 13.7 tonnes ha⁻¹ (FAOSTAT, 2009). About 97% of the world production is found in the developing countries. The crop is widely grown in Africa, Asia, and Latin America, with China accounting for 52% of the crop grown on approximately 4.7 million ha (FAOSTAT, 2009). In sub-Saharan Africa (SSA), sweetpotato is the most widely grown root crop and about 9.9 million tonnes of storage roots are produced on an estimated 2.1 million ha (FAOSTAT, 2009).

In Kenya, sweetpotato is an important staple crop (Hagenimana et al., 2001). Its production and utilization varies depending on where it is grown in the country, the time of year, and income group. In most parts of the country, the storage roots are boiled and eaten, or chipped, dried and milled into flour which is then used to prepare snacks and baby weaning foods (Hagenimana et al., 2001). Sweetpotato provides essential nutrients including carbohydrates, proteins, minerals, and vitamins (Stathers et al., 2005). Its storage roots provide 25-30% as carbohydrates and 2.5-7.5% as protein of its dry weight, respectively. It also provides 200-300 mg 100 g⁻¹ of potassium (K), 0.8 mg 100 g⁻¹ of iron (Fe), 11 mg 100 g⁻¹ of calcium (Ca) and 20-30 mg 100g⁻¹ of vitamin C of its dry matter (Stathers et al., 2005; Çalifikan et al., 2007) as well as copper, zinc and manganese, vitamin B2, B6 and E, while the yellow and orange fleshed storage roots provide pro-vitamin A. Sweetpotato is also used in industries to produce starch, natural colorants, and fermented products. The fermented products include wine, ethanol, lactic acid, acetone, and butanol (Winarno, 1982; Clark, 1988; Duvernaya, et al., 2013). All the plant parts of sweetpotato and its culls are used as livestock feed (Claessens et al., 2008). Fresh storage roots are also sold in the market for income generation (Githunguri et al., 2007)

The acreage under sweetpotato has been rapidly increasing in Kenya, in recent years. This increase has been associated with factors such as: 1) decreasing soil fertility in most of the agro-ecological zones of the country, 2) the removal of subsidies for fertiliser and seeds for major crops such as wheat and maize as part of trade liberalisation policies, 3) devastating

pests and diseases of major crops such as wheat and maize, 4) growing understanding by consumers that sweetpotato is a healthy crop to consume rather than a poor man's food, and 5) the growing shift of sweetpotato from a subsistence crop to a commercial crop (Stathers et al., 2005). However, the increase in sweetpotato acreage has not been commensurate with increased productivity due to production constraints.

2. Constraints to sweetpotato production

Sweetpotato production in Kenya faces several constraints (Goldsworthy and Fisher, 1984; Collins, 1995; Ames et al., 1996; Njeru et al., 2004; Gichuki et al., 2006; Pua and Davey, 2007). These constraints include: abiotic constraints (drought, and soil nutrient deficiencies), socio-economic constraints (poor agronomic varieties, poor post-harvest handling and storage facilities, lack of processing skills, lack of clean seed materials, poor seed distribution system, and insufficient capacity), and biotic constraints (weeds, insect pests and diseases). Consequently, the average storage root yield in Kenya is below 9 t ha⁻¹ (Table 1). However, its production potential may be well above 20 t ha⁻¹, depending on the variety.

Table 1. The average area of production and the yields of sweetpotato in central, eastern and coastal Kenya

Year	Central			Eastern			Coast		
	Area ^a	Yield ^b	Yield (t ha ⁻¹)	Area ^a	Yield ^b	Yield (t ha ⁻¹)	Area ^a	Yield ^b	Yield (t ha ⁻¹)
2003	3.6	27.3	7.6	6.7	34.6	5.2	0.5	4.1	8.2
2004	45.4	387.5*	8.5	7.4	12.4	1.7	0.8	5.3	6.6
2005	37.3	284.7*	7.6	5	16.5	3.3	1	8	8.0
2006	7.2	15.9	2.2	5.6	62.6	11.2	1	9.3	9.3
2007	-	-	-	5.7	62.6	11.0	0.9	7.5	8.3
Mean	23.4	178.9	6.5	6.1	37.7	6.5	0.8	6.8	8.1

Where: ^aunits in '000ha, ^bunits in '000 t yr⁻¹, * figures abnormally high.

Source: (MoA, 2009).

3. Drought

Drought is a major abiotic constraint to crop production especially in the warm and hot tropics (Bennett, 2003; Amede et al., 2004). Drought begins when the readily available soil water in the root zone is exhausted (Kramer, 1983). Drought resistant varieties produce relatively high yield within the range of their production potential under conditions of limited water availability. These drought resistant varieties may express various resistance

mechanisms including escape, tolerance, avoidance, or recovery from drought stress (Ekanayake, 1990; Ahmad et al., 2009). Therefore, the presence of one or more of these drought resistance mechanisms in various combinations can render a variety drought tolerant at a given stage of its growth cycle (Amede et al., 2004).

In sweetpotato, drought stress is detrimental during the crop establishment and storage root filling stages (Ekanayake, 1990). It alters the sink-source relationship by affecting photosynthates production, translocation and partitioning. Prolonged periods of drought reduces yield, root quality, and in severe cases causes total crop failure (Anioke, 1996). In general, drought at the storage root initiation stage results in lower numbers of smaller sized storage roots which reduces sweetpotato yield.

4. Breeding for drought tolerance

In eastern, southern, and western Africa, breeding high yielding sweetpotato varieties, for drought, dual purpose human and animal feed use, and orange fleshed sweetpotato (OFSP) with high superior nutritional qualities are being undertaken (Grüneberg et al., 2009). To undertake this regional task, breeders in the region need to embrace strategies for breeding narrowly and broadly adapted varieties. This requires breeding strategies that enable evaluation of genotype by environment effects, to identify genotypes with good performance across ecological zones or specific to a given country or location (Bantayehu, 2009). However, the breeders should ensure that the variety released (end products) satisfies the preferences of the farmers (end users), for the farmers to be receptive to adoption of the developed varieties and technologies. This justifies why this study was preceded by a survey using a structured questionnaire to gather the information on sweetpotato production constraints and preferences prioritised by farmers in Kenya.

Studies have been conducted in various locations worldwide, using different methods, in order to determine drought tolerant genotypes. Newell et al. (1994) estimated drought tolerance in sweetpotato using the detached leaf moisture loss method, and reported that drought tolerant genotypes had lower moisture loss than susceptible genotypes. Similar findings have been reported in cowpea and wheat (Walker and Miller, 1986; Amede et al., 2004). Walker and Miller (1986) reported that drought tolerant cowpea genotypes had higher leaf water content than the susceptible ones 48 hours after detachment.

Mkandawire et al. (2008a, b) studied the effect of drought stress on sweetpotato yields during the dry season. In their study, delay in planting after the onset of rainfall, implied that the crop would suffer drought stress at later growth stages. The authors recorded significant

genotypic differences in yield and dry matter (DM) among five clones. The most drought tolerant clone had the highest plant stand count (37,032 plants ha⁻¹), the highest root number (108,782 ha⁻¹), and the highest yield (18.25 t ha⁻¹). The variety with the lowest plant stand count (that is, least tolerant to drought) also had the lowest yields of 9.65 t ha⁻¹ (Mkandawire et al., 2008b). A two week delay in planting relative to onset of rains at the experimental sites, (with harvesting done after same number of days) reduced yield from 23.57 t ha⁻¹ to 21.76 t ha⁻¹, while a four week delay further reduced the yield to 18.01 t ha⁻¹. In addition, significant interaction of drought and genotype was also reported (Mkandawire et al., 2008b). Therefore, their study demonstrated that the delay in planting relative to onset of rains is critical in environments with frequent terminal drought stress conditions.

Githunguri et al. (2007) subjected nine elite sweetpotato clones to both field and organoleptic evaluations in semi-arid parts of eastern Kenya. The authors reported that clones 566632, 440248, 420009, 420094 and K135 were fairly drought tolerant, while organoleptic tests on fibre content showed that all clones were acceptable to the farmers. Moreover, improved varieties such as Ejumula, Carrot C, Carrot Dareslaam, Zambezi, and NASPOT5 were being promoted for use by farmers in different ecological zones from where they were bred (Mwanga et al., 2003). Yet, these improved varieties have not been screened for drought tolerance under the farmers' field condition where they are being cultivated. This suggests that breeders should incorporate effective genotype by environmental interaction evaluation in order to identify clones with broad and/or narrow adaptation.

Indira (1989) screened 100 sweetpotato clones for drought tolerance during the dry season under field conditions at the Central Tuber Crop Research, Trivandrum, India between 1983 and 1987. The clones were evaluated on the basis of physiological and biochemical characteristics and only maintenance irrigation was applied to the experimental genotypes. The results indicated that drought tolerant clones had lower inorganic phosphate, higher specific leaf weight, higher percentage of epicuticular wax, higher relative water content, lower desiccation rate, higher leaf hairiness, and lower stomatal conductance relative to susceptible genotypes (Indira, 1989). The author opined that, hairs on the leaf increased reflectance of the light, with the light being deflected to lower leaves, thus increasing the photosynthesis of lower leaves, leading to yields similar to non-hairy genotypes that performed well under no drought stress conditions.

At La Trinidad, in the Philippines, Anselmo et al. (1998) evaluated seedlings from a polycross of eight local sweetpotato landraces during the dry season. In their work, the

seedlings were irrigated to field capacity for one month after planting (until established), then irrigation withheld until harvest (150 DAP). Scores on drought were made at 79 and 100 days after planting (DAP) and yielding ability of genotypes at harvesting used also as an indicator of drought tolerance. Their results enabled the identification of F1 recombinants with high storage root yield and thus drought tolerant.

Drought tolerance is a polygenic trait and is not well understood in sweetpotato. Breeders working on drought tolerance programmes in sweetpotato, therefore, need to understand combining ability and inheritance of the genes responsible for drought tolerance. Unfortunately, no drought tolerant sweetpotato varieties have been bred and released in Kenya, despite drought episodes being frequently experienced, hence this study was proposed.

5. Problem statement

In Kenya, about 59,200 ha of land are grown with sweetpotato annually with an annual production of about 567,600 tonnes. The productivity level (9.53 t ha^{-1}) is far below the potentially achievable ($20\text{-}50 \text{ t ha}^{-1}$) depending on the environment and varieties grown. The low productivity has been attributed to a number of biotic, abiotic and socio-economic constraints. Moreover, over 80% of Kenya's land does not receive adequate rainfall, necessitating the need to develop drought tolerant varieties for cultivation in these areas. Also, little or no breeding work has been done in Kenya towards breeding sweetpotato for tolerance to drought stress. Therefore, there is an urgent need to establish a breeding programme for developing drought tolerant sweetpotato clones to mitigate drought stress effects. This intervention will assist in meeting the increasing demand for sweetpotato, as a healthy food (for vitamin A deficiency correction), for income generation, and feed use.

Although, the International Potato Center (CIP) has identified sweetpotato germplasm that can be used as sources of drought tolerant genes, it is impossible to introgress these genes into high yielding, locally adapted, drought susceptible genotypes using a conventional backcross breeding approach. This is due to several factors including frequent cross incompatibilities, the complex inheritance of most traits in sweetpotato due to polyploidy ($2n=6x=90$), and the need to maintain heterozygosity to avoid inbreeding depression in F1 breeding populations. To overcome these breeding constraints, drought tolerant lines need to be crossed with a higher number of deserving genotypes using a combination of paired and poly-cross breeding and successful progenies screened for drought tolerance. Moreover, there is also a need to understand the mechanisms of drought tolerance and genes responsible for drought tolerance and their inheritance for effective selection and

breeding procedures. In addition, drought is highly correlated to ecological zones and thus any drought study also requires analysis of genotype x environment interaction (GEI). The GEI for sweetpotato genotypes has not been well explored in Kenya. It would therefore, be important to determine the magnitude of GEI and yield stability of sweetpotato clones and the advanced genotypes. This will help to identify the most suitable testing environments for evaluating drought tolerance of sweetpotato in Kenya.

6. Research objectives

The overall goal of this study was to contribute towards improved production of sweetpotato by resource poor farmers, through the breeding of drought tolerant genotypes with farmer desired traits.

6.1 Specific objectives

The specific objectives of the study were:

- (i) To determine sweetpotato production constraints and farmers' coping strategies through a participatory rural appraisal (PRA) and survey.
- (ii) To screen sweetpotato germplasm and populations for drought tolerance.
- (iii) To analyse genotype x environment interaction effects for storage root yield of parental genotypes and F1 genotypes of sweetpotato in Kenya.
- (iv) To examine phenotypic drought tolerance mechanisms of sweetpotato
- (v) To conduct a genetic study of drought tolerance in sweetpotato and estimate combining ability and heterosis in the test crosses.

6.2 Assumptions

During the studies the following assumptions were made:

- (i) Sweetpotato landraces in Kenya and CIP clones were cross compatible and had high heritability values for storage root yield and drought tolerance.
- (ii) Drought tolerance in sweetpotato could be increased without compromising storage root yield.

7. Research hypotheses

The following research hypotheses were tested:

- (i) Drought is a major constraint in sweetpotato production and farmers in Kenya prefer specific traits that meet their production criteria.
- (ii) High levels of tolerance to drought are available in local sweetpotato landraces and plant introductions.

- (iii) Sweetpotato storage root yield performance is affected by genotype x environment interaction.
- (iv) Sweetpotato responds to moisture stress through various mechanisms.
- (v) The inheritance of genes for resistance to drought and other agronomic traits is controlled by both additive and non-additive gene action.

8. Structure of the thesis

The thesis is structured according to the objectives, where, each objective is presented in chapters aimed at publishing in a refereed journal and, therefore, some contents may be found overlapping across the chapters.

The thesis outline is as follows:

- Abstract
- Introduction to thesis
- Chapter 1: A review of the literature relevant to the research study
- Chapter 2: Identifying the farmers production practices and constraints
- Chapter 3: Evaluation of sweetpotato germplasm for drought tolerance
- Chapter 4: Genotype x environment evaluation of parental sweetpotato genotypes
- Chapter 5: A study on mechanism for drought tolerance in selected genotypes of sweetpotato
- Chapter 6: Inheritance of drought tolerance in sweetpotato
- Chapter 7: Overview

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Chapter 1

Literature Review

1.1 Introduction

Sweet potato is an important crop in several countries of the world (FAOSTAT, 2009). Sweet potato root production is hindered by several biotic and abiotic constraints (Gichuki et al., 2006). Recent research efforts have been directed towards developing varieties with improved yield and nutritional value, adaptation to low fertility, drought tolerance, and pest and disease resistance (Kapinga, et al., 2007). In addition, multiplication and distribution of clean cuttings, promotion of improved processing, and marketing skills of released varieties has also been emphasized (Stathers, et al., 2005; Kapinga et al 2007). All these efforts have contributed to increases in sweetpotato root yield, but this is still far below the potential yield production levels (Fuglie, 2007; Shields and Fletcher, 2013). Therefore, sustainable improvement of sweet potato production in East Africa require breeding varieties that combine high yield with resistance or tolerance to drought, pest and diseases, high beta carotene and minerals such as iron, zinc, and boron (Stathers, et al., 2005). Moreover, the improved yield impact will only be felt once skills on production, processing, and marketing of sweet potato are transferred to the farmers. (Gichuki et al., 2006; Ames et al., 1996). Therefore, this review commences with general introductory information on sweetpotato, followed by breeding objectives of sweetpotato, which narrows down to breeding for drought tolerance. The review concludes by discussing the breeding mating designs, selection methods, and genotype by environment interaction effect on sweetpotato breeding trials.

1.1.1 Origin of sweetpotato

Sweetpotato was domesticated in either South America or Central America more than 5000 years ago (Rosse et al., 2001). Ancient sweetpotato is grouped into three distinct clusters: Kumara, Camote and Batata (Denham, 2013). These three groups form the two gene pools in the modern sweetpotato. The gene pools are; Carribean and Central America (Northern) gene pool comprising batata and camote and northwestern South American (Southern) gene pool comprising Kumara (Denham, 2013). Batata and Camote also dominate in the New Guinea and Eastern Pacific gene pool. Thus since its domestication, sweetpotato has been cultivated in two widely separate areas; tropical America and Southwest Pacific (Polynesia). Therefore, sweetpotato is believed to have moved from its centre of diversity (America), to

caves of Peru then to Pacific Polynesia and South East Asia possibly by seafarers before Columbus at around 1200-1300 AD (Denham, 2013).

The crop was rapidly introduced to Europe from tropical areas of the Americas by European explorers around 1500 AD. The Portuguese primarily introduced it to Europe, Africa, South Asia, East and Southeast Asia (Yen, 1976). Moreover, the Spanish introduced sweetpotato into the Philippines in the 16th century, from where it spread to other islands and the East Asian mainland. It is also believed that sweetpotato was spread from island to island across the Pacific, through boats by indigenous people (Rossel et al., 2001). Secondary centres of genetic diversity of sweetpotato that are genetically distinct from those found in their original centre of diversity evolved separately from those of its American ancestors, such as in Papua New Guinea and in other parts of Asia. Today sweetpotato is cultivated in 117 countries in tropical and subtropics. Asia is the highest producer followed by Africa and the Americas. In addition, the inhabitants of the Pacific islands are among the largest per capita consumers of sweetpotato in the world today (Rossel et al., 2001).

1.1.2 Botany of sweetpotato

Sweetpotato is also referred to as batata, camote, boniato, batata doce, apichu, or kumara in Latin America (Stathers et al., 2005). It was botanically described in 1753 by Linnaeus as *Convolvulus batatas*, but Lamarck, in 1791, re-classified the crop into the genus *Ipomoea* on the basis of the stigma shape and the surface of the pollen grains (Thottappilly and Loebenstein, 2009). Hence, the crop belongs to the family of Convolvulaceae, tribe of Ipomoeae, genus *Ipomoea*, sub-genus *Eriospermum*, section *Eriospermum*, and species *batatas*. Therefore, the botanical name of sweetpotato was changed to *Ipomoea batatas* (L.) Lam.. The storage organ of sweetpotato is a root. However, many authors have erroneously referred sweetpotato storage root as tuber (a tuber is a fleshy underground stem or a shoot).

The centre of diversity of the wild relatives of *I. batatas* is within the Americas, except *I. littoralis*, found in Australia and Asia. Cultivated *Ipomoea batatas* (L.) Lam.. has 13 wild relatives. They comprise: two tetraploids ($2n = 4x = 60$), namely *I. tabascana* and *I. tiliacea* (Austin, 1979; Austin and Huaman, 1996); nine diploids ($2n = 2x = 30$) namely *I. cynanchifolia*, *I. grandifolia*, *I. lacunose*, *I. xleucantha*, *I. littoralis*, *I. ramosissima*, *I. tenuissima*, *I. triloba*, and *I. umbraticola*; and two polyploids namely *I. cordatotriloba* (*I. trichocarpa*), which is either $2x$ (diploid) or $4x$ (tetraploid) and *I. trifida* which may be $2x$ (diploid), $3x$ (triploid), $4x$ (tetraploid), and $6x$ (hexaploid) (Huamán and Zhang, 1997). Moreover, *I. peruviana* from Peru and Ecuador was initially considered a wild relative of *Ipomoea batatas* (L.) Lam., but now is classified as *I. setosa*, and is used as a root stock for

sweetpotato grafting. Also, *I. gracilis* was initially considered as wild relative of *I. batatas* from Australia, but is now classified in section *Erpipomoea* (McDonald and Austin, 1990). Crossing *I. cordatotriloba* x *I. lacunosa* and *I. cordatotriloba* (diploid) x *I. batatas* (hexaploid) produced hybrids *I. xleucantha* (diploid), and *I. grandifolia* respectively (Austin, 1978).

The cultivated *I. batatas* is a hexaploid of $2n = 6x = 90$ with basic chromosome number $x = 15$ and is grown throughout the tropics with wide diversity. The closest relative of cultivated *I. batatas* is *I. trifida* which exists in $2x$ (diploid), $3x$ (triploid), $4x$ (tetraploid), or $6x$ (hexaploid) forms. This wild relative is believed to be one of the ancestors of the cultivated sweetpotato. Plants from the diploid *I. trifida* seeds produce small storage roots (Grüneberg et al., 2009).

Polyploid plants have more than two homologous pairs of chromosomes (Tate et al., 2005; Sleper and Poehlman, 2006). There are two types of polyploids; allopolyploids and autopolyploids (Sleper and Poehlman, 2006). The breeding behaviour of allopolyploids is very similar to diploid. However, polysomic inheritance in polyploids is prone to meiosis disorders, which reduces fertility in flowers of autopolyploids (Acquaah, 2007). Meiosis disorders may result due to complete infertility, and less seed formation hence necessitating asexual propagation (Hawkes, 1979). Hybridisation of diploid and tetraploid plants results in the formation of triploid plants ($3x$), and further doubling of chromosomes forms hexaploids. It is hypothesized that this is how sweetpotato evolved from diploid ($2x$) to tetraploid ($4x$) and then hexaploid ($6x$). Consequently, sweet potato has two closely related chromosomal sets: Set 1 = $B_1B_1B_2B_2$ and set 2 = $B_1B_1B_2B_2B_2B_2$ (Austin and Huaman, 1996).

1.1.3 Flowering in sweetpotato

Sweetpotato flowers are formed in auxiliary inflorescences of 1-22 buds that open mainly after daybreak (Huamán and Zhang, 1997). The colour of the flowers varies from white to lavender. Its anthers may be superior or inferior to stigma. The flower pistil carries two ovaries, each containing two ovules and thus the seed capsules contain one to four seeds that may be glabrous or pubescent. Sweetpotato seeds are viable for over 20 years and require either acid or mechanical scarification to germinate (Huaman, 1987). Sweetpotato flowering is generally sensitive to day length and profuse flowering tends to occur when the day becomes shorter. However, there are no undesirable traits reported that are associated with flowering. Sweetpotato has complex compatibility and sterility systems. The crop has sporophytic self-incompatibility controlled by multiple alleles, in one or two loci, which may make development of F_1 hybrids challenging. Additionally, cross pollination in sweetpotato is largely restricted to intra-specific rather than inter-specific hybridization (Huamán and Zhang, 1997).

1.1.4 Growth requirements for Sweetpotato

Sweetpotato is a perennial crop but cultivated as an annual in the tropics and subtropics (Purseglove, 1968). It grows well in fertile, high organic matter, well-drained, light, and medium textured soils with a pH range of 4.5-7.0 (Wolfe, 1991; Ahn, 1993). Heavy and poor textured, poorly drained soils that have frequent water-logging and poor soil aeration impedes the growth of storage roots, reducing their size and yield. Water logging in early growth stages hinders the establishment of roots, and in later growth stages causes decay of the storage roots (Ahn, 1993). Sandy loam soils that are light and well-drained are the best for growing sweetpotato. The crop is very sensitive to aluminium toxicity, which occurs at pH below 4.5, and may lead to death of the crop within six weeks (Ames et al., 1996).

Sweetpotato grows at latitudes ranging from 40°N to 32°S. The crop grows in temperature ranges of 15°C to 35°C; with an optimum of 24°C (Goldsworthy and Fisher, 1984). It is grown at altitudes from sea level to 3000 meters above sea level (m asl) along the equator (Huaman, 1987). It requires about five months of frost-free growing conditions with abundant sunshine with photoperiod of 13–15 hours. However, both flowering and storage root formation are promoted by short day lengths, and warm nights. Due to its short growth period, it can be grown during the warm summer months in temperate zones.

Sweetpotato requires annual rainfall of 750–1000 mm, with a minimum of 500 mm in the growing season (Ahn, 1993). The crop grows best where light intensity is relatively high. The nutritional disorders of sweetpotato include nitrogen deficiency, phosphorus deficiency, potassium deficiency, magnesium deficiency, boron deficiency, iron deficiency, acid soils, aluminium toxicity, and salinity (Ames et al., 1996). Initial growth of foliage requires application of N fertiliser, but an excess of N can lead to more foliar growth than storage root growth. Potassium is required especially during storage root growth and the crop is an efficient user of phosphorous. Sweetpotato vines smother weeds after establishment and may only require weeding once.

1.2 Constraints to sweetpotato production

The main biotic constraints of sweetpotato in the tropics are sweetpotato weevil (Woolfe, 1992; Stathers et al., 2005; Shonga et al., 2013; Ehisianya et al., 2013), alternaria blight, sweetpotato virus disease (SPVD) (Ames et al., 1996; Mwanga et al., 2002; Miano, 2008; McGregor et al., 2009), and root-knot nematodes (*Meloidogyne* spp) mostly found in the temperate zones (Mwanga et al., 2002; Grüneberg et al., 2009). Moreover, SPVD is a combination of sweetpotato chlorotic stunt virus (SPCSV) and sweetpotato feathery mosaic virus (SPFMV), (Clark, 1988; Miano, 2008; McGregor et al., 2009). In summary, there are

about 20 viruses or virus like diseases, about 35 bacterial and fungal diseases, about 20 nematodes, and about 20 insect pests that affect sweetpotato (Martin and Jones, 1986; Ames et al., 1996; Ndunguru and Kapinga, 2007).

Moisture stress due to drought is becoming a major abiotic constraint to crop production worsened by climate change (Amede et al., 2004; Claessens et al., 2012; Nakashima and Yamaguchi-Shinozaki, 2013). Soil moisture availability determines the external water status at the boundaries of the plant (soil and air) and in the internal plant water status within the tissue of the plants. Moisture stress begins when the readily available soil water in the root zone is exhausted (Kramer and Boyer, 1995). Drought stress reduces photosynthesis, and translocation of assimilates thus effectively reducing the yield (Anselmo et al., 1998; Anjum et al., 2011). However breeding drought tolerant varieties may ensure high yield production under conditions of limited water availability (Sorrells et al., 2000). Mechanisms such as drought escape, drought tolerance, drought avoidance, and drought recovery enable the crop to tolerate drought and produce some yield (Ekanayake, 1990; Sorrells et al., 2000). Drought tolerant sweetpotato varieties produce higher quantity and quality of yields in absence of sufficient rains and irrigation compared to other varieties.

1.2.1 Moisture stress

Drought may occur in the early, middle, or end of the cropping season, which triggers multiple and mixed responses during the stress and recovery time (Mundree et al., 2002). This phenomenon complicates studies of the genes responsible for drought tolerance. Moreover, interactions of the genotypes with environmental factors such as soil chemistry, soil texture and weather complicate drought tolerance studies (Sorrells et al., 2000; Jaleel et al., 2009). Thus, drought evaluation experiments may require use of greenhouse or drip irrigated rain-out shielded fields where water can be precisely controlled (Laurie et al., 2013). Additionally, field trials should be large enough and replicated to eliminate micro environmental errors (Amede et al., 2004). Also, screening for drought in sweetpotato is further complicated if drought tolerance is measured using yield components (e.g. number of storage roots M^{-2} , number of storage roots $plant^{-1}$, root weight $plant^{-1}$, dry matter instead of the yield ha^{-1} , because each component is sensitive to drought at different times and in different modes (Makihara et al., 1999).

Root growth characteristics play important roles in drought stress tolerance in plants (Ahmad et al., 2009). Deep rooted varieties that continue to grow by tapping water from deeper layers are bred for upland areas with deep soils and unreliable rainfall. Likewise, in lowland areas with unreliable rainfall, genotypes with roots with the capacity to penetrate the

hardpan layer of compacted soil at about 20-25 cm below the soil surface are bred (Champoux et al., 1995; Ray et al., 1996).

The desired traits for drought tolerance in crops include its ability to; 1) reduce water loss to the soil and to air, 2) maintain cell turgor pressure for a long time, 3) survive loss of cell turgor pressure, 4) protect cells against oxidative damage caused by continued absorption of radiation when the stomata is closed thus preventing photosynthesis and, 4) to recover after water is available (Ahmad et al., 2009; Anjum et al., 2011)

1.2.2 Plant response to drought stress

Crops under water stress undergo three stages of dehydration; alarm, resistance and exhaustion (Amede et al., 2004). The stage of alarm occurs under mild drought stress where assimilation and transpiration are similar to normal well watered plants and plant soil water uptake meets evapo-transpiration requirements (Mundree et al., 2002). The resistance stage occurs when the photosynthetic capacity of the plant is reduced below the maximum potential level due to drought stress. At this stage, the plants develop adjustment mechanisms and regulatory metabolic processes to cope with the water stress (Anjum et al., 2011). Finally, the exhaustion stage occurs when the plants strive to survive and delay death due to prolonged drought stress. Once the crop reaches this stage, its recovery after rain or irrigation depends on genotype and duration of the water stress (Sinclair and Ludlow, 1986).

Plants manifest different types of responses to moisture due to water stress (Jaleel et al., 2009; Anjum et al., 2011; Nakashima and Yamaguchi-Shinozaki, 2013). During rapid water stress, plants tend to orientate leaves parallel to incident light. Cell growth and expansion is diverted to restitution of physiological integrity, and stomatal adjustment (Arve et al., 2011). Moreover, under long term water stress, crops tend to reduce leaf area while increasing root density modifying root leaf ratio (Ahmad et al., 2009). Usually, root depth and density are used to determine the level of drought tolerance of genotypes. Also, crops under water stress alter plant cell solute concentration to reduce the osmotic cell potential while maintaining cell turgor pressure (Mundree et al., 2002; Arve et al., 2011). This allows turgor related physiological processes such as stomata movement and cell growth to go on despite low water potential. Some plants modify soil plant water gradient through cell solute concentration, hence increasing the amount of water transpired and leading to yield increase (Mundree et al., 2002). Solute concentration in plant cells occurs through cellular water loss, breakdown of primary metabolites (protein, carbohydrates and fats), and translocation of assimilates (solute) to the cell sinks that increases cell solute concentration (Kramer and Boyer, 1995; Mundree et al., 2002). Under moderate levels of drought stress, roots may

absorb and accumulate inorganic macro and micro ions such as potassium, calcium, sodium, chloride, magnesium in cells, coupled with reduced cell growth, hence reducing osmotic potential (Munns, 1988). For example, tepary beans are more drought tolerant than common beans because they possess higher osmotic adjustment potential. Thus, transferring the osmotic adjustment gene from tepary beans to common beans can improve their drought tolerance (Parsons and Howe, 1984).

The rate of transpiration in crops depends on size of the transpiring area, the number and size of stomata, and the conductivity of the cuticle (Amede et al., 2004). Stomatal transpiration accounts for 90% of crop water loss (Anjum et al., 2011; Ahmad et al., 2009). This is followed by water loss through the cuticles, which is influenced by its thickness, and presence or absence and type of wax (Monneveux and Belhassen, 1996). Additionally, leaf rolling, leaf colour or leaf reflectance influence transpiration (Arve et al., 2011). Early seedling establishment, early high vigour, rapid canopy development, and leaf area maintenance minimize evaporation while maximizing transpiration and are termed as drought tolerance mechanisms (Subbaro et al., 1995). Stomata closure is one of the first steps of defence against drought stress in many crops because it is a more rapid and flexible process relative to other mechanisms like root growth or reduction of leaf area. The effect of drought stress on stomata closure may be measured by the CO₂ fixation rate. Thus, drought tolerant genotypes maintain higher CO₂ fixation even at prolonged drought stress. Crops under mild water stress tend to have increased root growth and root density but reduced shoot growth and evapo-transpiration (Ahmad et al., 2009). Stomatal closure is an effective survival strategy for intermittent stress, although it may not work for terminal stress (Amede et al., 2004).

1.2.3 Water use efficiency

Plants open stomata to admit CO₂ for photosynthesis, and to transpire water (Mundree et al., 2002). Stomatal conductance is more strongly correlated to photosynthetic parameters than soil water status itself (Anjum et al., 2011). Leaves and stems may transpire through non-stomatal surfaces. Plants transpire to cool during high air temperatures and transport soil nutrients and chemicals synthesized in the roots to the leaves through the transpiration stream (Peuke et al., 2002). Crop production per unit transpiration is referred as water use efficiency (WUE). The ratio of photosynthesis (A) / transpiration (T) is referred as transpiration efficiency (Peng et al., 1998). Water productivity per unit of evapo-transpiration is the mass of crop production divided by the total mass of water transpired by the crop and lost from the soil by evaporation. Plants transpire several hundred times more water than is present in their tissues at any one time. Drought water stress reduces photosynthesis, total

dry matter accumulation, and yield, depending on time, duration and severity of the drought stress (Boonjung and Fukai, 1996; Anjum et al., 2011).

Translocation is less affected by water stress than the photosynthesis and transpiration (Boyer, 1976). Thus, late sowing for example in a month after the onset of rains exposes the ability of a genotype to translocate reserves to the sink during the onset of the terminal drought (Ludlow and Muchow, 1990). In most crops, the assimilate reserves originate from pre-anthesis to post-anthesis events, depending on the amount of reserves in the stem, therefore the availability of these reserves is dependent on the timing of water stress (Amede et al., 2004).

1.2.4 Drought tolerance mechanisms

Plants respond to drought through various mechanisms (Mundree et al., 2002; Nakashima and Yamaguchi-Shinozaki, 2013). Some of the drought resistant mechanisms are; synchrony of fast growth stages to water supply, early growth vigour, stomatal regulation, developmental plasticity, increased root depth and density, leaf area maintenance, synchrony of storage root filling to water supply, mobilization of assimilates from source to sink, and osmotic adjustment of roots and shoots (Mundree et al., 2002; Amede et al., 2004; Nakashima and Yamaguchi-Shinozaki, 2013). Traits that indicate drought tolerance are; biomass, growth vigour, root depth and density, storage roots per vine, storage root weight, storage root yield, early maturity, degree of translocation, production efficiency, and drought sensitivity index, plant water potential, osmotic potential, relative water content (RWC), and relative growth rate (RGR) (Amede et al., 2004; Painawadee et al., 2009; Anjum et al., 2011; Arve et al., 2011; Ciarmiello et al., 2011).

Plants cope with drought through: 1) drought avoidance, by development of deep roots that penetrate and explore deeper and greater soil volume, 2) drought escape where short duration crops complete their lifespan before soil moisture from fairly reliable rainfall vanishes, and 3) drought tolerance where plants adapt to slow onset of drought by modifying their chemical constitution to retain as much water as possible through osmotic adjustment to protect themselves from irreversible damage during stress (Ludlow and Muchow, 1990; Mitra, 2001; Mundree et al., 2002; Bennett, 2003).

Drought avoidance mechanism occurs where primary and secondary leaves continue expanding at decreasing soil water potential (SWP). This mechanism is detected by determining both the leaf area at moderate drought stress and leaf water potential (LWP) at 50% transpiration reduction (Amede et al., 2004). Drought escape is where the crop will

cope with low soil water through earliness of development, plasticity of growth, and efficient water uptake by increased rooting depth and density and increased hydraulic conductivity (Mundree et al., 2002). Drought tolerance arises through osmotic regulation that maintains cell turgor measured by determining SWP and LWP at decreasing relative water content (RWC) (Amede et al., 2004; Yang and Miao, 2010; Anjum et al., 2011). Also, drought tolerance arises through the plant having low critical soil water potential (SWP) for non-recovery upon re-watering measured by determining RWC and LWP below which plants will not recover (Amede et al., 2004).

Other mechanisms include efficient conservation of tissue water by leaf rolling and shrinkage, reduction of cuticle water loss through wax deposits, regulation of stomata aperture and osmotic adjustment (Anjum et al., 2011). Plants may also cope with incident light intensity by producing new growth at a time of the year with moderate light intensity, under shading by plants within a canopy, or leaves on individual plants. Plants also control light absorption through reduction of leaf reflectance using leaf hairs, waxes and leaf orientation adaptation. At the cellular level, water stress is reduced by absorption of excitation energy by chlorophyll, as well as dissipation of excitation energy as heat through the xanthophyll cycle. Also, plants reduce water stress through active oxygen formation and free radical scavenging defence mechanism through enzymatic and non-enzymatic antioxidants (Amede et al., 2004). The excess free radicals cause drought induced photo-oxidative damage referred to as leaf chlorosis or necrosis when the crop is exposed to high light intensity coupled with drought stress and or mineral deficiency (Mundree et al., 2002; Anjum et al., 2011).

1.3 Breeding for drought tolerance

1.3.1 Sources of drought tolerance

Development of drought tolerant varieties through conventional breeding requires making crosses (Sleper and Poehlman, 2006; Acquaaah, 2007). The choice of the right parent increases the number of promising recombinant genotypes among the best families. Good parents should have good combining ability and good performance for all traits (Pfeiffer and McClafferty, 2007). Parents with drought tolerant characteristics are selected from genotypes that have evolved under drought conditions (Sleper and Poehlman, 2006). Crosses are made to ensure good recombination of genes responsible for drought tolerance. Genotypes with large root volume, deeper root growth, early maturity, small foliage, thick leaves and trichomes, low canopy temperature, are crossed with drought susceptible

parents and the gene frequency increased through recurrent selection, backcross, three way crosses or modified double crosses (Sorrells et al., 2000; Pfeiffer and McClafferty, 2007).

Sometimes wild relatives are used as the source of drought tolerance genes in various crops. For instance, West Africa Rice Development Authority (WARDA) has introduced genes for drought tolerance into *Oryza sativa* from the African cultivated rice *Oryza glaberrima* (Sorrells et al., 2000; Bennett, 2003). The International Centre for Agricultural Research in the Dry Areas (ICARDA) has introduced drought tolerance into *Hordeum vulgare* from *Hordeum spontaneum* (Sorrells et al., 2000; Bennett, 2003). The International Potato Center (CIP) is enhancing the drought tolerance of potato using indigenous potato germplasm from the Andes. Further, CIP and its collaborators have also identified drought tolerant sweetpotato lines. However, cross pollination barriers and absence of suitable donors for drought traits has hindered progress in screening for tolerance in sweetpotato (Bennett, 2003).

1.3.2 Drought evaluation and screening methods

Different experimental methods have been developed for evaluating drought stress. These include; field experimentation (Zhang et al., 2009; de Paiva Rolla et al., 2013), pot experiments (de Paiva Rolla et al., 2013), chamber house experiments (Thwe et al., 2013), nutrient solution experiments (Mia et al., 2010), rain out shelters (Dodig et al., 2012), rhizotron experiments (Chapman et al., 2011; Poverigiani et al., 2012), and petri dish experiments (Afzal et al., 2012). These types of experimentation methods enable some level of drought simulation depending on how they are designed and they all have limitations. It is difficult to quantify roots, and ensure homogeneity in soil properties, and soil moisture as well as day and night soil temperature in field experiments.

Pot experiments are labour intensive, have limited number of treatments, root growth is restricted by pot size, and pots generally do not sustain plant growth resource demands to maturity. Chamber house experiments, on the other hand, have limited space and are very expensive, while nutrient solution experiments are less precise, and labour intensive. Rainout shelters induce heat stress and have higher relative humidity leading to slow induction of water stress, and also leakage effects. Rhizotron experiments allow only a few treatments to be tested, and they are bulky and labour intensive. Petri dish experiments require supplementing with field or pot experiments and may not reflect the reality in the field. Therefore, the choice of any type of these experimentation methods requires consideration of their strength and their shortcomings. In this study, field experiments and experiments in the greenhouse were conducted.

Selection for drought tolerant varieties involves selecting for reduced non transpiration uses of water, reduced transpiration without reducing yield, increased yield without increasing transpiration and salinity tolerance lead to increased water use efficiency (WUE) (Sorrells et al., 2000; Bennett, 2003; Anjum et al., 2011). Transpiration may be reduced without reducing yield by developing waxy-cuticle, rapid stomata closure, cooling mechanisms for leaves, rapid canopy closure, and a thicker more intact casparian strip (Mundree et al., 2002; Jaleel et al., 2009). Production may be increased without increasing transpiration through short maturity duration, high seedling vigour, higher harvest index (HI), C₄ photosynthesis, more photosynthesis per unit transpired water, more dry matter allocated to grain after stress, and leaf stay green (ability for the leaf to remain green under moisture stress) (Sorrells et al., 2000; Anjum et al., 2011).

Several indices have been developed to measure stress tolerance (Rosielle and Hamblin, 1981). These include the stress susceptibility index (SSI) (Fischer and Maurer, 1978), stress tolerance index (STI) (Fernandez, 1992), the tolerance and mean productivity index, (Rosellie and Hamblin, 1981) and the geometric mean progression (GMP) (Fernandez, 1992).

Stress susceptibility index expresses yields under water stress as a function of yield under no water stress. It measures how much genotypes reduce their performance under drought conditions as compared to their performance in well-watered conditions. The drought sensitivity index (SSI) ranks the genotypes as, SSI 1=neutral, >1 sensitive, <1 tolerant. Thus, SSI is calculated as follows; $SSI = [1 - (D/C)] / [1 - (Dm/Cm)]$ (Fisher and Mauer, 1978), where, D is yield of genotype under drought, C is yield of genotype under normal moisture, Dm is mean yield of all genotypes under drought and Cm is mean yield of all genotypes under normal moisture. Genotypes with low SSI values are considered to be stress tolerant (Bruckner and Froberg, 1987).

The STI proposed by Fernadez (1992) is estimated based on geometric mean productivity as follows: $STI = (Y_p * Y_s)/Y_p^2$: where, Y_s is the mean yield estimated under stress, and Y_p is the mean yield estimated under non-stress environments. Higher values of STI indicate higher stress tolerance and yield potential for a genotype. The TOL and MP indices are calculated as $TOL = Y_s - Y_p$ and $MP = (Y_s + Y_p)/2$. where; Y_s is yield under water stress, Y_p is yield under non-stress environments and mean productivity (MP) as the average yield of Y_s and Y_p, i.e. Thus large values of TOL that indicate more tolerance to stress, coupled with large values of MP is favoured (Rosielle and Hamblin, 1981). GMP is used to assess drought resistance under stress and non-stress environments and is expressed as $GMP =$

$\sqrt{Y_S * Y_P}$ (Fernandez, 1992). High GMP indicates drought resistance (Ramirez and Kelly, 1998).

Martin and Carmer (1985) reported variation of sweetpotato clones for tolerance in field and greenhouse using high root yield as an indicator of tolerance for nine stress conditions namely: heavy soil, space competition, competition with maize, shading, flooding, drought, acidity, salinity, and weevil infestation. In this work, up to 30.9% of the plants showed high stress tolerance. Correlations between yield and multiple stresses were low but significant indicating tolerance to various stresses occurred together (Martin and Carmer, 1985). Saraswati et al. (2004) screened 15 genotypes of sweet potato for drought in the greenhouse at James Cook University, Townsville, North Queensland and reported that plant biomass, main stem length, internode diameter, internode length, leaf number and area and root weight decreased in response to water stress. They also concluded that drought tolerance is associated with the lowest percentage of growth reduction, less water consumption, higher leaf water potential, and delayed wilting under imposed drought stress conditions.

1.3.3 Identification of drought related genes

Genes responsible for drought tolerance have been identified through various ways. These include studying the anabolic and catabolic pathways for metabolites that accumulate in drought stressed plants; these metabolites include proline, glycine, betaine, trehalose, and ABA (Mundree et al., 2002; Anjum et al., 2011). They also involve studying drought response regulatory gene expression and the changes in protein synthesis under drought stress in plants (Sorrells et al., 2000; Mundree et al., 2002; Arve et al., 2011; Nakashima and Yamaguchi-Shinozaki, 2013). Mapping QTL for drought tolerance, using segregating populations as well as studying and isolating natural or artificial drought tolerance directed mutants and transgenic plants, may also lead to identification of drought tolerance genes (Sorrells et al., 2000; Mundree et al., 2002; Arve et al., 2011).

Increased drought tolerance is dependent on finding the most appropriate alleles of drought tolerance genes and pyramiding them (Sorrells et al., 2000). This is done by screening the population with standardized phenotyping protocols followed by detailed genetic analysis for the best performing materials in segregating progenies (Bennett, 2003). These segregates perform well because of either positive alleles at a number of QTL of small effect, or positive alleles at one or two major genes (QTL of large effect) (Bennett, 2003). In general, a few QTL of large effect are of greater interest and useful for a crop breeding program than many QTL with smaller effects. This is because they can accurately be used as screening markers for the trait (Bennett, 2003).

1.3.4 Sweetpotato breeding

Mating designs are important in the breeding of any crop as they are used to evaluate parents, and develop F1 recombinant crosses that form the base population for selection (Hallauer et al., 2010). They also help to generate synthetic populations, and provide information for estimating gene action and genetic gains (Hallauer et al., 2010). In sweetpotato, mating designs such as polycross, diallel, or North Carolina design I may be used (Jones et al., 1987; Mwangi et al., 2002; Chiona, 2010).

The diallel mating design is used to study the polygenic action (Hayman, 1954; Hallauer et al., 2010). Its analysis is based on general combining ability (GCA) and specific combining ability (SCA) (Griffing, 1956b). GCA and SCA enable distinguishing between the average performance of parents and their crosses, respectively (Johnson and King, 1998; Acquah, 2007). The GCA indicates the relative value of the population in terms of frequency of favourable genes, and identifies superior parents for use in intra-population breeding programmes (Acquah, 2007). On the other hand, the SCA indicates the predominant direction of the deviations due to dominance in a population (Viana and Matta, 2003; Acquah, 2007).

An evaluation of at least five parents in a partial diallel has been reported to give reliable estimates of GCA (Stuber, 1980). Genetic component analysis done using partial diallel on SPVD resistance in Uganda indicated that GCA:SCA range of 0.51-0.87, meaning GCA effects were more important than SCA ratios (Mwangi et al., 2002). Resistant parents exhibited high GCA meaning additive gene effects were predominant in the inheritance of resistance to SPVD. The narrow sense heritability of 31-41% and broad sense heritability of 73-98% (moderate–high) was reported meaning genetic gain for SPVD resistance could be accomplished easily by mass selection (Mwangi et al., 2002).

After making crosses in sweetpotato breeding, visual selection that eliminates genotypes that do not meet the lowest acceptable values for each trait is done (Grüneberg et al., 2009). This is followed by index selection for yield and nutritional quality based on the desired genetic gain. Further, the remaining clones are selected against pests and diseases done by visual selection. The last 100-200 clones enter into late breeding stages, but are also used as parental materials for the next cycle of recombination and selection (Grüneberg et al., 2009).

Each sweetpotato seedling is potentially a new variety (Chiona, 2010). The seedlings are clonally propagated, whereby; about 40-60 cuttings per plant are produced under rapid multiplication (Stathers et al., 2005). The breeder may reduce the selection cycles from five

years to about a year or two and get the best genotype for tolerance to abiotic and biotic factors using accelerated breeding scheme (ABS) (Grüneberg et al., 2009). Use of higher selection intensity (5-20%) and many environments results in optimum genetic gain (Wricke and Weber, 1986). Crosses and multiplication are done during early selection and late selection stages, reducing the phases into 3 stages in 3 years and, the clone that fails test in each stage are discarded (independent culling) (Wricke and Weber, 1986). About 90 cuttings of sweetpotato per plant can be obtained in 3-4 months (Stathers et al., 2005). Visual evaluation and selection is conducted in poor resource environment and selected clones are further evaluated in more environments (Pesek and Baker, 1969). Potential clones selected from previous selection cycle are subjected to high selection pressure, upon which 2-5 clones are finally selected for variety release (Grüneberg et al., 2009). The five phases of selections in sweet potato are summarized in Fig. 1.1.

Parent A	X	Parent B	Parental crosses: many crosses are done as much as possible
F _{A1}		F _{B1}	F1 seedling developed
F _{A1} clones	→	F _{B1} clones	A clones: Evaluation plots, visual screening, few traits measured, visual selection done, small single row plots of 3-5 plants used, not replicated. The evaluation get close to optimum response to selection, usually done in two sites (Grüneberg et al., 2004)
F _{A1} clones		F _{B1} clones	B clones: Promising clones selected and planted in plots of 2-3 locations
F _{A1} clones	→	F _{B1} clones	C clones: Good clones are selected for further trials
F _{A1} clones		F _{B1} clones	D-clones: Selection for advanced trials and potential release

Figure 1.1: Breeding process of sweetpotato

Source: Grüneberg et al., 2009

For example, a mass selection programme of 350 sweetpotato genotypes from Taiwan, Japan, New Guinea, Hawaii, Nigeria, Thailand, Peru, Cuba, Philippines, Puerto Rico, New Zealand, Guatemala, Uruguay, Cook Islands, Marquesas Islands, Spain, and Canada from the previous wide gene populations was used by Jones in mass selection (Jones et al., 1987). The plants were allowed to undergo open-pollination. About 3000 seeds were collected, germinated and grown in the greenhouse. Among them, 700 genotypes representing all possible crosses were trellised. After open pollination, seed from 200 of the 700 plants were selected to start the next cycle. In the third cycle the number selected as seed parents was reduced to about 100 among 700 trellised plants. After a two-year evaluation, the best 25-30 selections are identified and their seed used to start the next

selection cycle. Selections from the mass selection populations can be tested directly for genotype potential or may provide a source of parental material for a polycross nursery.

1.3.5 Participatory rural appraisal (PRA)

The research priorities of sweetpotato vary with specific regions and countries (Fuglie, 2007). This variation may be explained by the agro ecological variations within the countries. Also, global warming has led to sporadic weather changes causing further agro-ecological variations (Jaetzold et al., 2006; Shields and Fletcher, 2013). Therefore, there is need to establish the farmers' priority research needs before initiating a breeding research programme. This requires gathering of information from the farmers on their preferences, practices and priority research needs. The information is collected through conducting participatory rural appraisal (PRA).

Participatory rural appraisal methods include: 1) focused group discussions which may involve use of pictures and cards with drawings representing various traits to assist the farmers during the discussions, 2) farmers interviews and discussions with structured questionnaires where farmers may use matrix scoring (farmers compare varieties of choice (rows) with the listed traits (columns) giving a score for each trait), and pairwise ranking (traits of interest are compared pair by pair and farmers choose the trait they prefer and give reasons), 3) review of relevant articles, 4) and questionnaire surveys (Fuglie, 2007; Sibiya et al., 2013b; Mmasa et al., 2012; Odonde et al., 2013). In sweetpotato, PRA study areas are selected randomly by considering; sweetpotato growing areas, coverage of the attitude ranges, and representation of different agro-ecological zones (Mmasa et al., 2012; Odonde et al., 2013). In some cases, the selection of study area is based on production data at the extension offices. Liaising with local leaders and agricultural extension officers is also required. However, in some cases, the accessibility of the target areas may be considered during selection of study area. Once the study area is selected, enumerators are trained on study tools and questionnaires prior to data collection. The respondents in most cases are the farmers' households' heads. Additionally, gender balance is considered whereby; males, females, elderly and youthful farmers are involved in the study (Shields and Fletcher, 2013)

Participatory rural appraisal studies collect both quantitative and qualitative data. Data analysis is done to generate means and frequencies for presentation of the results. Usually, descriptive and inferential statistics are used to describe the results (Degu et al., 2013). Therefore, PRA involves both farmers and researchers, which improves the probability of breeding varieties that address the needs of the end users (Gibson et al., 2008).

1.3.6 Gene action and heritability

Sweetpotato is a hexaploid ($2n=6x=90; x=15$) and each of its genes may be represented by six alleles. Thus, the segregation ratios after crossing are varied and complicated, but may be simple when a single dominant allele is present (Falconer and Mackay, 1996; Sleper and Poehlman, 2006). However, the majority of important traits in sweetpotato appear to be inherited quantitatively.

Sweetpotato is highly heterozygous, and requires crossing with improved genotypes to evaluate the genetic value of the mother plant and estimate heritability, genetic advance and heterosis (Sleper and Poehlman, 2006). Heritability is the measure of the degree of correspondence between phenotypic values and breeding values (Sleper and Poehlman, 2006). A high estimate indicates that good parents tend to give the best progeny on average and *vice versa*. Narrow sense heritability (h^2) estimates of over 0.60 in sweetpotato indicate adequate genetic advance will be achieved. However, minimum values of about 0.30 by regression and 0.40 by variance-covariance with precise selection methodology are acceptable. Mwangi et al. (2002) reported narrow sense heritability of 31-41% and broad sense heritability of 73-98% on SPVD resistance in Uganda indicating genetic gain for SPVD resistance could be accomplished easily by mass selection. Genetic advance is the gain in performance of mean phenotype of the offspring of the selected parents, relative to mean phenotype of the whole parental generation (Acquaah, 2007). Heterosis is also referred as panmitic mid-parent heterosis and indicates the average excess in vigour exhibited by F1 hybrids over the mid parent and reduces by 50% in F2 (Acquaah, 2007; Sleper and Poehlman, 2006). In highly heterogeneous clonal plants, transgressive segregation is normally evaluated rather than heterosis (Rieseberg et al., 1999).

Jones (1969) reported high heritability estimates of ten vine traits, which reflected phenotypic changes of the ten vine traits, while additive component of variance was predominant (Jones, 1969). Diallel analysis of 8 sweetpotato clones for the quantitatively inherited trait of fusarium wilt resistance, reported significant GCA/SCA of $87\%=V_a$, and heritability estimates on basis of parent offspring regression of $V_d=13\%$, $H=70\%$, $h^2=50\%$ (Collins, 1977). In addition, Jones (1969) reported about 13.9% genetic advance of fusarium resistance on 40 randomly selected sweetpotato clones associated with additive genetic variance (V_a) with selection intensity of 10% and predicted genetic gain of 10.5%. Jones et al. (1976a) selected sweetpotato genotypes for desirable production and market qualities, with multiple resistance to pathogens, nematodes and insects in six generation single year cycles and reported high frequencies of flowering and seed set, attractive root shape orange flesh, thin cortex, acceptable yield resistance to fusarium wilt, southern root

nematode and a number of insects pest excluding weevil. Moreover, increased flowering, reduced leaf whorl purpling, decreased leaf diameter, decreased root weight, fewer smooth skinned types, and increased vine length in six random crossing generations, is reported (Jones, 1972; Jones et al., 1976b). Maluf et al. (1983) reported high positive correlation of vine length and number of internodes per vine (NIV) ($r=0.717$), which had vine length $H=0.46$, $(NIV)=H=0.403$, number of marketable roots (NMR), $H=0.598$ and thus root yielding can be improved through selection for increased NMR.

1.4 Genotype x environment (GE) interaction and stability

The performance of a genotype is influenced by its genotype and the environment in which it is grown (Yan and Tinker, 2006; Yan et al., 2007; Choukan, 2011;). Environmental effects vary from season to season (Sorrells et al., 2000; Yan et al., 2007; Mohammadi and Amri, 2013). Thus, genotypes need to be evaluated in various environments and seasons to select the best genotype for a particular environment. Genotype x environment interaction is used to determine whether to select for a wide or specific adaptation, the choice of sites for selection, whether selections in early generations can be conducted under stress or stress free environments, and whether to perform multi environment testing of large numbers of genotypes or subject fewer lines to intensive trait based selections (Yan et al., 2007; Bantayehu, 2009). Significant GE interactions indicate that the parental crosses interact with environment, and if not, then the additive gene effect is constant under different environment conditions (Sorrells et al., 2000; Yan and Tinker, 2006; Yan et al., 2007; Bantayehu, 2009; Mohammadi and Amri, 2013).

Several methods are used to analyse GE interaction and phenotypic stability (Piepho, 1998; Truberg and Huhn, 2000; Bantayehu, 2009). These methods include: analysis of variance, regression analysis, risk assessment, ranking methods, pattern analysis (cluster analysis), principal component analysis (PCA), factor analysis, additive main effects and multiplicative interaction (AMMI) model, and GGE biplot (Lin et al., 1986). This review focuses on AMMI, GGE biplots and regression analysis.

1.4.1 Additive main effects and multiplicative interaction model (AMMI)

Additive main effects and multiplicative interaction model (AMMI) is an advanced form of principal component analysis for interpreting GE interaction (Gauch and Zobel, 1989; Crossa et al., 1991). There are a number of models generated from AMMI. AMMI0 uses the additive genotypic and environmental means to describe the data matrix and thus ranks genotypes identically at each environment ignoring GxE. AMMI1 considers the main effects as well as one principal component analysis (IPCA 1) to interpret the residual matrix. AMMI2 considers the main effects in addition to IPCA1 and IPCA2 for non-additive variation (Misra et al.,

2009). Subsequent models consider an additional IPCA; however, the higher order of multiplicative principal components that are not significant can be ignored giving a reduced model.

AMMI analysis of data of 9 clones of sweetpotato evaluated across 14 locations in Peru, showed that the choice of location was of significance in sweetpotato selection (Grüneberg et al., 2005). Three environmental groups were observed whereby at least one environment from each group could be used as a test site for sweetpotato adaptability tests (Grüneberg et al., 2005). AMMI biplot analysis of data of 17 genotypes of sweetpotato evaluated across three sites in Kenya showed wide variability among environments and less among genotypes (Mwololo et al., 2009). Genotypes (Ex-shimba, Kemb10, Japanese, Jonathan, Zapallo and SPK004) with large principal component scores and high yields were adapted across environments. Genotypes with PCA values close to zero and low yield in all the environments (i.e., Ejumula, Jubilee, Muibai and Sponge) were stable and did not benefit from favourable environments. Genotypes (Marooko, Muibai, 440015, K135, Salyboro and Jewel) at or near the middle of the biplot did not show a distinct pattern of stability or adaptability and could be considered adapted to either favourable or adverse environments. Overlapping genotypes in the biplot (Muibai and Marooko, 440015 and K135, Ejumula, Jubilee and Sponge, Sponge and Bungoma, and Jewel and Salyboro) indicated cross-over interaction in the different environments (Mwololo et al., 2009).

1.4.2 Genotype, and genotype x environment (GGE) biplots

Analysis of variance is an additive model that describes the effects due to genotype and environment and their interaction but does not determine genotype by genotype environment interaction (Kaya et al., 2006; Yan and Tinker, 2006). Genotype and genotype x environment interaction biplots enable the assessment of multi-environment yield trials (Kaya et al., 2006; Yan and Tinker, 2006; Choukan, 2011). The phenotype of a crop is a combination of genotype (G), environment (E) and genotype x environment interaction (GEI) (Sleper and Poehlman, 2006; Acquah, 2007). Moreover, E explains most of phenotypic variation and G and GEI contribute a small proportion of the variation (Yan, 2001, 2002). The measured yield is a combined effect of G, E and GEI, but, the interaction of G and GEI probably defines the genotype performance under multi environment trials (Kaya et al., 2006; Yan and Tinker, 2006). This is why GGE interaction is put together and analysed and a plot displayed that describe genotype performances on various environments in multi environment trials (Yan, 2001, 2002; Kaya et al., 2006). GGE biplot displays data graphically in a two way table, involving genotypes on one hand and their performance on various environments (Yan et al., 2000; Yan, 2002; Yan and Tinker, 2006; Mohammadi and Amri, 2013). GGE biplots reveal which genotypes won where (i.e. the yield performance of genotypes and their

stability on various environments), and the power of environment to discriminate the yield performance of the genotypes experimented (Yan and Tinker, 2006)

The GGE biplots are constructed by plotting the first two principal components (PC_1 and PC_2) derived from subjecting environment-centered yield data to singular value decomposition (Yan and Tinker, 2006; Yan et al., 2007;). In the biplot, a vector is drawn from the biplot origin to each marker of the traits to facilitate visualization of the relationships among the traits. The correlation coefficient between any two environments is approximated by the cosine of the angle between their vectors. Acute angles indicate a positive correlation; obtuse angles indicate a negative correlation and right angles no correlation (Yan and Tinker, 2006; Yan et al., 2007). The length of the vector describes the discriminating ability of the environment (Yan and Tinker, 2006). A short vector indicates that the environment is not related to other environments, that there is a lack of variation, or it is not suitable for genotype discrimination (Yan and Tinker, 2006; Yan et al., 2007; Choukan, 2011; Sibiya et al., 2013a).

1.4.3 Regression

Large genotype (G) x environment (E) interactions make it difficult to identify the superior genotypes (Sullivan et al., 2002). A significant GEI is either crossover or non-crossover (Kaya et al., 2006; Sleper and Poehlman, 2006). Genotypes that have significant change of rank from one environment to another have crossover GEI and thus are unstable and could be tested for specific environments (Yan and Tinker, 2006; Bantayehu, 2009;). Genotypes that do not have significant change of rank across environments are stable and thus can be used over a wide range of environments (Mohammadi and Amri, 2013). The stability behaviour of the genotypes may be determined using regression analysis (Eberhart and Russell, 1966; Becker and Léon, 1988; Ngeve, 1993). The slope of a regression curve determines the response of the genotype on a particular environment. In a regression plot, genotypes found far from the regression line are not stable, while the ones close to the line are stable across environments (Eberhart and Russell, 1966; Becker and Léon, 1988; Ngeve, 1993). Moreover, the position of the genotypes on the regression plot indicates whether it is high or low yielding (Eberhart and Russell, 1966).

1.5 Summary

The literature review has shown that drought tolerance trait is; polygenic, inversely related to the harvestable yield, and is highly variable across environments (Anjum et al., 2011). Selection pressure for drought stress traits under field conditions in most cases are not uniform (Ahmad et al., 2009). Therefore, these calls for management of the environment to ensure genotypes under drought tolerance evaluation are subjected to uniform, and

sufficient drought stress selection pressure. Drought trait is affected by several loci associated with morphological traits, leaf rolling genes, root morphology root/shoot ratio, osmotic adjustment, root thickness, root volume, and leaf stay (Ahmad, 2009).

Furthermore, this review has shown that sweetpotato is mostly self-incompatible, auto-hexaploid, and some genotypes don't flower at all. Also, the genotypes that flower have some level of sporophytic cross incompatibility (Hawkes, 1979; Huamán and Zhang, 1997). Therefore, sweetpotato breeding requires selection of flowering; compatible parents and the breeder may or may not control self-pollination. However, the non-flowering genotypes may be grafted on to *I. setosa* or grown under short daylight hours to trigger them to flower. Additionally, proper pre-planning is required to ensure flowering is synchronized for effective cross pollination

This review has also indicated that drought stress lead to crops only attaining 25% of their yield productivity potential (Ahmad et al., 2009). The review has indicated that drought stress causes osmotic stress which leads to cell dehydration, that hinders cell metabolic functions, reduces crop growth, and lowers yield and biomass (Anjum et al., 2011; Nakashima and Yamaguchi-Shinozaki, 2013). Moreover, dehydration reduces photosynthesis and photosynthetic pigments, translocation and transpiration (Jaleel et al., 2009). Further, drought stress leads to production of reactive oxygen species which damage cell DNA, protein and lipids (Anjum et al., 2011; Nakashima and Yamaguchi-Shinozaki, 2013). The DNA damages interfere with protein synthesis affecting essential function of the cell. Protein denaturation affects the function of the whole plant. Lipid peroxidation leads to cell membrane solute leakages, which interfere with cell membrane function, causing cell metabolic imbalances (Mundree et al., 2002; Anjum et al., 2011). Additionally, drought stress reduces stomatal conductance and CO₂ uptake, as well as water use efficiency (Anjum et al., 2011; Nakashima and Yamaguchi-Shinozaki, 2013). The overall impact of drought stress is quantity and quality reduction of the harvestable part of the crop. However, excessive severe stress results in irreversible cell damage and death of entire crop.

Moreover, the review has shown that the crops respond to drought stress in different ways (Ahmad et al., 2009; Anjum et al., 2011). From the review, drought stress dehydration; 1) triggers ABA production which signals closure of guard cells to reduce water loss through transpiration, 2) causes mesophyll cell wall folding reduce leave surface area exposed to light, formation of multiple vacuoles in bundle sheath cells, 3) and replacement of water in vacuoles with compatible solutes and less molecular weight molecules, and protein proline (Nakashima and Yamaguchi-Shinozaki, 2013), 4). Production of anti-oxidant protein gene XVPer1 that protect DNA from reactive oxygen species, XVSAP1 that protects membrane

linkage, XPgols, and ALDRXV4 that trigger osmo-protection by formation of proteins that confer drought tolerance (Mundree et al., 2002; Anjum et al., 2011; Nakashima and Yamaguchi-Shinozaki, 2013). Therefore, drought tolerance mechanisms involve photosynthetic pigments, stomata protective changes, scavenging of reactive oxygen species, enzymatic and non-enzymatic systems, cell membrane integrity, stress protein production, harvesting of light by carotenoids and protecting oxidative damage (Mundree et al., 2002; Anjum et al., 2011; Nakashima and Yamaguchi-Shinozaki, 2013). Thus, genotypes that; 1) tolerate cellular dehydration, 2) have minimal water loss due to evapo-transpiration, 3) maintain favourable water status for leaf development under moisture stress conditions, 4) have drought escape ability, 5) have ability to recover from drought stress and form new leaves from bud after a dry spell, 6) have waxy thicker leaf layer and deep rooting, are most likely, drought tolerant (Ahmad, 2009). In conclusion, it is the ability of a crop to sense and respond to the stress before irreversible damage occurs, that breeders exploit to develop drought tolerance varieties.

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Chapter 2

Assessment of Production Constraints and Farmers' Preferences for Sweetpotato Genotypes

Abstract

Sweetpotato is one of the most important staple food crops in Kenya and it has a significant role not only for food security but also as a potential commercial crop. Its production is hindered by numerous biotic, abiotic and social factors. This study was aimed at determining the farmers' preferences of sweetpotato varieties, production constraints and farmers' coping strategies. A baseline survey was conducted in central, eastern and western Kenya between September and December 2012. A structured questionnaire was randomly administered to a total of 345 farmers in the three sub-regions, with each region covering four administrative units. Data on households demographics, sweetpotato varieties grown, sources of seed, cultural practices, and production constraints were collected and analysed using statistical package for social scientists (SPSS, 2007). Results indicated that 60% of the farmers interviewed were women and family sizes varied between 3-5 persons in 55% of the households. Farm sizes varied between 0.41-0.8 ha with 90% of sweetpotatoes being grown on 0.24 ha or less. The main food crops grown on the surveyed farms included maize, beans, sweetpotato, cassava, sorghum, and pigeon peas, while the main cash crops were; kale, banana, sugarcane, bean, maize, sweetpotato and groundnut. The average sweetpotato yield on the farms surveyed ranged from 5.5-7.4 t ha⁻¹. The preferred sweetpotato varieties were Vita, Kambu 10, and Kabonde because they were orange fleshed with high beta carotene. Moreover, 50% of the farmers used planting material from their previous crop, which was conserved by leaving in the field. Production constraints in the three regions were basically similar, with 35% of the farmers identifying weevils as the major pest, and sweetpotato virus disease (SPVD) as the major disease. Drought was identified by 28% of the farmers as a major production constraint. Farmers indicated the use of clean seed, high yielding varieties, high planting density, and manure application as some of the strategies they used to cope with the production constraints. To improve sweetpotato production in Kenya, these production constraints need to be addressed.

Key words: Food security, farmers' preferences, production constraints, households, sweetpotato genotypes

2.1 Introduction

Sweetpotato is a major crop in most eastern and southern African countries such as Uganda, Rwanda, Kenya, Tanzania, Ethiopia, Zambia, Mozambique and South Africa (FAOSTAT, 2009; Shonga et al., 2013). In Kenya, about 59.2 thousand ha of land are grown to sweetpotato annually with an estimated productivity of 9.53 t ha^{-1} , which is less than the world average of 14.1 t ha^{-1} (FAOSTAT, 2009). The crop is grown from sea level to 2200 m asl in various agro-ecological zones with major production concentrated in the arid or semi-arid areas of Kenya. The crop is mostly harvested in piece meal and stored on a flexible time schedule, which qualifies it as food security crop (Ekanayake, 1990). In rural areas, sweetpotato storage roots are boiled and eaten or chipped, dried and milled into flour which is then used to prepare snacks and baby weaning foods (Kidmose et al., 2007). Some farmers also sell fresh storage roots in the market for income generation. Likewise, some companies contract farmers and buy the storage roots, cook them, place them in a tin for local and probably export markets. In some developed countries, light industries also, use sweetpotato as an industrial raw material to produce starch, natural colorants and fermented products such as wine, ethanol, lactic acid, acetone, and butanol (Winarno, 1982; Clark, 1988; Duvernaya et al., 2013). Importantly, farmers use almost all parts of the sweetpotato plant as livestock feed (Claessens et al., 2008).

Recently, many organisations have been promoting the breeding and use of orange-fleshed sweetpotato with the aim of ensuring food security, income generation and reducing vitamin A deficiency. The consumption of orange fleshed sweetpotato, rich in pro-vitamin A helps in ensuring normal vision especially in the night, healthy skin and mucous membranes, proper cell growth, reproduction and immunity to diseases such as measles, malaria, respiratory diseases and diarrhoea in the body (Stathers et al., 2005; Ishiguro et al., 2007; Ndolo et al., 2007). Also, deep orange fleshed sweetpotato roots are reported to be rich in Fe (50 ppm DM) and Zn (40 ppm DM) with about 3.5%-9.5% DM protein, in storage roots, stems and leaves (Çalifikan et al., 2007; Grüneberg et al., 2009). This illustrates the inherent potential of sweetpotato which is unexploited in many African countries including Kenya. In addition, the poor exploitation may be attributed to production constraints and lack of capacity for value addition.

The production of sweetpotato is below the potential level in many parts of Kenya. Sweetpotato has a yield potential of $20\text{-}50 \text{ t ha}^{-1}$ of storage roots in the tropics (Çalifikan et al., 2007). This yield potential is yet to be realized as farmers in sub-Saharan Africa (SSA) produce on average, less than 10 t ha^{-1} (Rees et al., 2003).

These low yields are as a result of several socio-economic, biotic, and abiotic constraints which have not been adequately addressed. Socio-economic constraints in the production of sweetpotato include, poor post-harvest handling and storage facilities, lack of processing skills, lack of clean seed, and poor seed distribution system and poor agronomic varieties (Goldsworthy and Fisher, 1984; Collins, 1995; Ames et al., 1996; Njeru et al., 2004; Gichuki et al., 2006; Pua and Davey, 2007). The major biotic factors affecting sweetpotato include pests (sweetpotato weevil, weeds, and nematodes) and diseases (viruses, alternaria blight, and root rots among others). Yield losses of 20-78% due to viruses (Zhang et al., 2006) and 45% due to sweetpotato weevil (*Cylas formicarius*) have been reported (Lagnaoui et al., 2000). Virus and weevil infected plants also become susceptible to other pests and diseases resulting to yield loss of up to 100%. Other diseases affecting sweetpotato include alternaria blight, bacterial wilt and fusarium wilt (Ames et al., 1996). Yield increases of 160% (40.8 t ha⁻¹) due to use of virus-indexed planting materials has been reported (Zhang et al., 2006). Also, an annual benefits worth \$145 million (11.6 billion shillings) due to using virus-indexed sweet potato seeds has been reported in China (Fuglie et al., 1999).

Abiotic constraints affecting production of sweetpotato include drought stress and soil nutrient deficiencies. Drought stress reduces the quantity and quality of the storage roots and vines, in sweetpotato. A sustainable remedy for addressing this constraint would be introducing multiple drought stress tolerance genes into sweetpotato varieties (Amede et al., 2004). Thus research in Kenya and other countries with poor yields need to address adequately these constraints to boost sweetpotato production.

Participation of farmers in identifying the research problem and being engaged in the search for a research solution (participatory breeding) improves the adoption of the developed varieties and technology (Stathers et al., 2005). This ensures varieties that meet the needs of the farmers are developed and the scenario where a breeder addresses a problem which is not the priority of the farmers is avoided. A PRA and survey conducted prior to a research project enable farmers and breeders to collaboratively identify production constraints and the preferred characteristics of varieties to be developed. Regionally, the characteristics of varieties of sweetpotato preferred by farmers vary. For example, white fleshed sweetpotato with 28-32% dry matter (DM) is preferred in Brazil and most countries in SSA. In east Africa, white fleshed varieties with DM of 26-29% are preferred, a trend that is changing with the awareness of vitamin A rich orange fleshed sweetpotato varieties. In west Africa, genotypes that are less sweet with high DM, dark orange flesh, cylindrical but tapering at both ends of the storage roots are preferred (Grüneberg et al., 2009). Additionally, the information gathered from PRA and surveys helps the breeder to outline: 1) the stages and implementation of the project within the available resources, 2) materials and methods

required for carrying out the research work, 3) the constraints and challenges anticipated and their possible solutions (Ndolo et al., 2001; Stathers et al., 2005). In this study, a survey using a structured questionnaire was conducted in western, eastern and central Kenya in order to identify farmers' sweetpotato production constraints and variety preferences.

2.2 Materials and methods

2.2.1 Study area

The study was conducted in eastern, western, and central Kenya (Fig. 2.1) in September 2012 just before farmers harvested the crop. In eastern Kenya, two counties namely Machakos (longitude: 36.9°E-37.6°E and 0.7°S-1.7°S) and Makueni (longitude: 37.0°E-38.7°E and latitude: 1.4°S-3°S) were selected (Fig. 2.1). Their elevation ranged from 400-2100 m asl and about half of the total land is under agricultural use (Claessens et al., 2012). The soils are deep, friable, and of low fertility especially deficient in nitrogen, phosphorus and soil organic carbon. The soil texture varies from sandy clay loam to sandy clay. This region has semi-arid climatic conditions with bimodal rainfall characterized with low, variable and unreliable rainfall. The annual rainfall ranges from 500-1300 mm of which short rains occur from November - January and long rains from March - June (Jaetzold et al., 2006). The average annual temperature ranges from 15°C-25°C. Long term observation indicates drought episodes occur after every four to five years in this region (Tiffen et al., 1994).

In western Kenya, Homa Bay county was selected. Homa Bay lies at latitude: 0°-1.5°S and longitudes: 34°E-35°E (Fig. 2.1). The soils in Homa Bay are moderately drained, deep, dark brown clay loam, which is moderately fertile. The area receives bimodal rainfall where the long rains come March - April and short rains in September - December. Temperatures range from 22-32°C and the altitude is about 1225 m asl and the rainfall ranges from 1000-1250 mm annually (Jaetzold et al., 2006).

In Central Kenya, Murang'a and Kirinyaga counties were selected. Murang'a lies at latitude: 0.5°S-1°S and longitude 36.7°E-37.5°E and Kirinyaga lies at latitude: 0.15°S-0.7°S and longitude 37.3°E-37.9°E (Fig. 2.1). In both Murang'a and Kirinyaga counties, the soils are well drained, fertile, deep, volcanic red loam usually referred as nitisols. The area receives bimodal rainfall with long rains in March - April and short rains in September - December. Temperatures range from 14-26°C and the altitude range was 1500-2000 m asl while the rainfall ranges from 1500-1800 mm annually (Jaetzold et al., 2006).

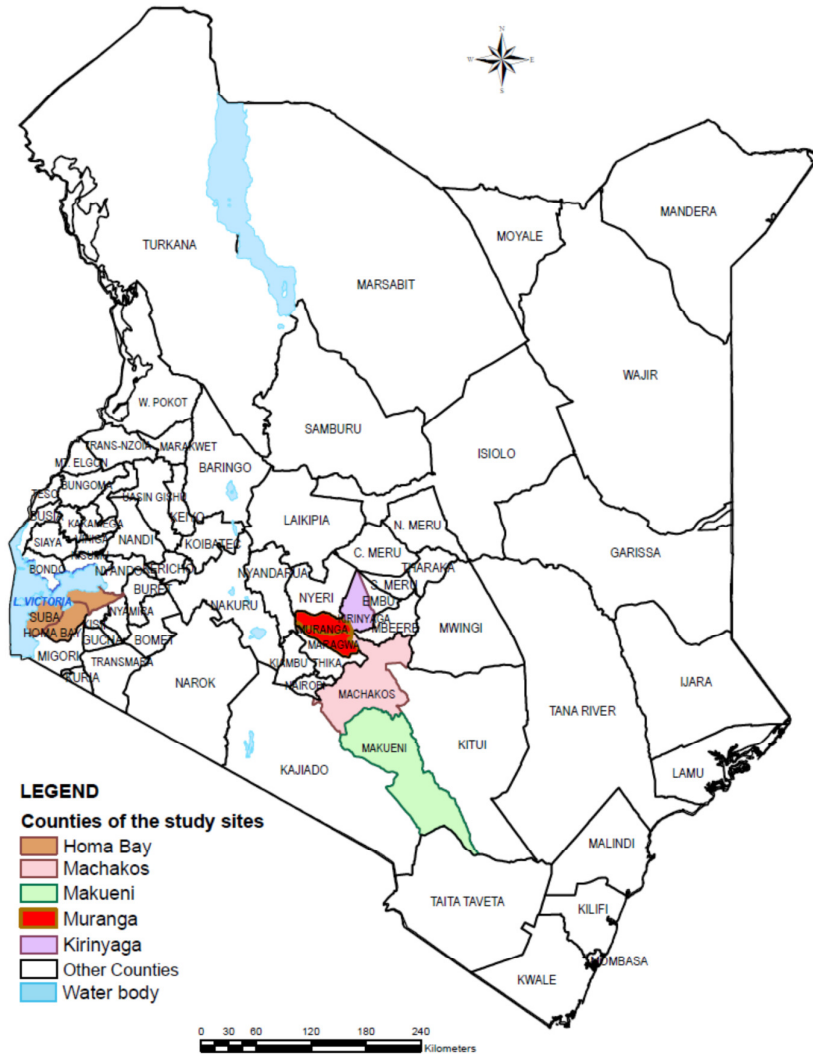


Figure 2.1: A map of Kenya showing the regions where the survey was conducted

2.2.2 Sampling procedures and data collection

Four districts were selected in each region (eastern, central and western Kenya) with the assistance of the extension officers. Sweetpotato farmers were selected from two divisions in each of the selected districts but spread across the villages of the divisions, with the help of extension officers in the localities. Structured questionnaires were administered to the farmers by a multidisciplinary research team comprising of a breeder, agronomist, and socio-economist. A community leader accompanied the survey team as a guide. For individual interviews, the household head present was interviewed. In cases of language barrier, a member from the community or household was asked to translate. Data on household demographics, farmers’ agronomic and crop husbandry practices (farming systems, planting time, cropping pattern, and use of fertilizers and manures), current

varieties grown, planting material sources, and production constraints were collected. About 30 copies of the questionnaire were administered in each district. A total of 345 farmers were interviewed in all the regions (Appendix 2.1).

2.2.3 Data analysis

The collected data were entered into excel spread sheets. The data were analysed using Statistical Package for Social Sciences (SPSS, 2007). Cross tabulations were used in the analysis and the percentage respondents were calculated and presented in the results.

2.3 Results

2.3.1 Farmers interviewed in four selected districts/divisions

The proportions of farmers interviewed in each district/division are shown in Fig. 2.2.

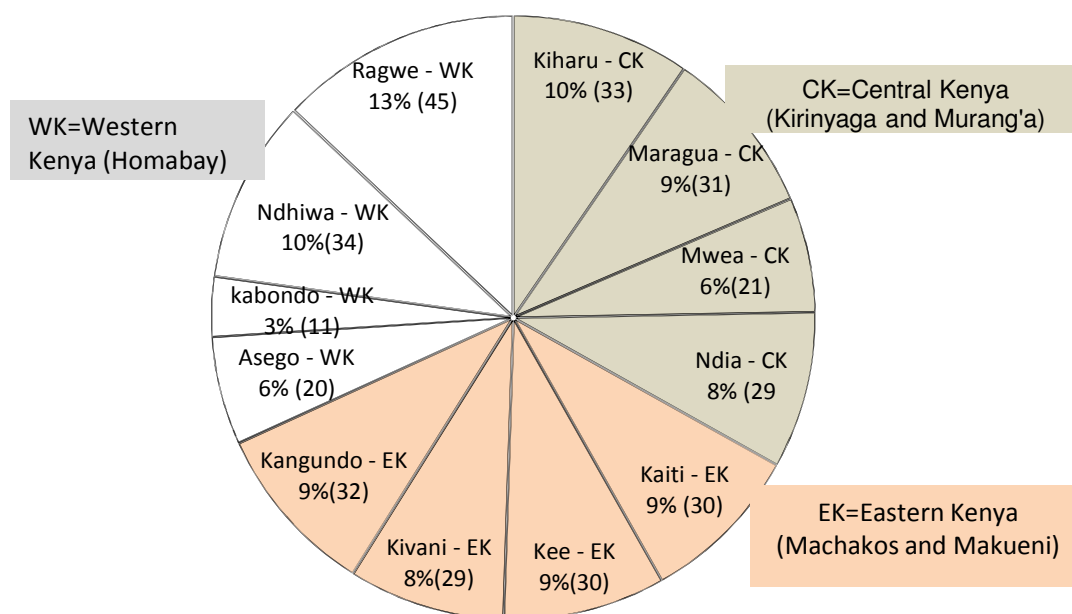


Figure 2.2: The proportions (%) of interviewed farmers in the four districts/divisions selected in eastern, central and western Kenya

2.3.2 Demographic information

About 60% of the farmers interviewed were women, and the majority of the farmers were between 41-50 years. Most farms ranged between 0.41–0.8 ha (32%) in size, with sweetpotato being grown on an average of 0.24 ha. Family sizes averaged 3-5 persons (55%), and the majority of the household members were between 21-40 years (Fig. 2.3).

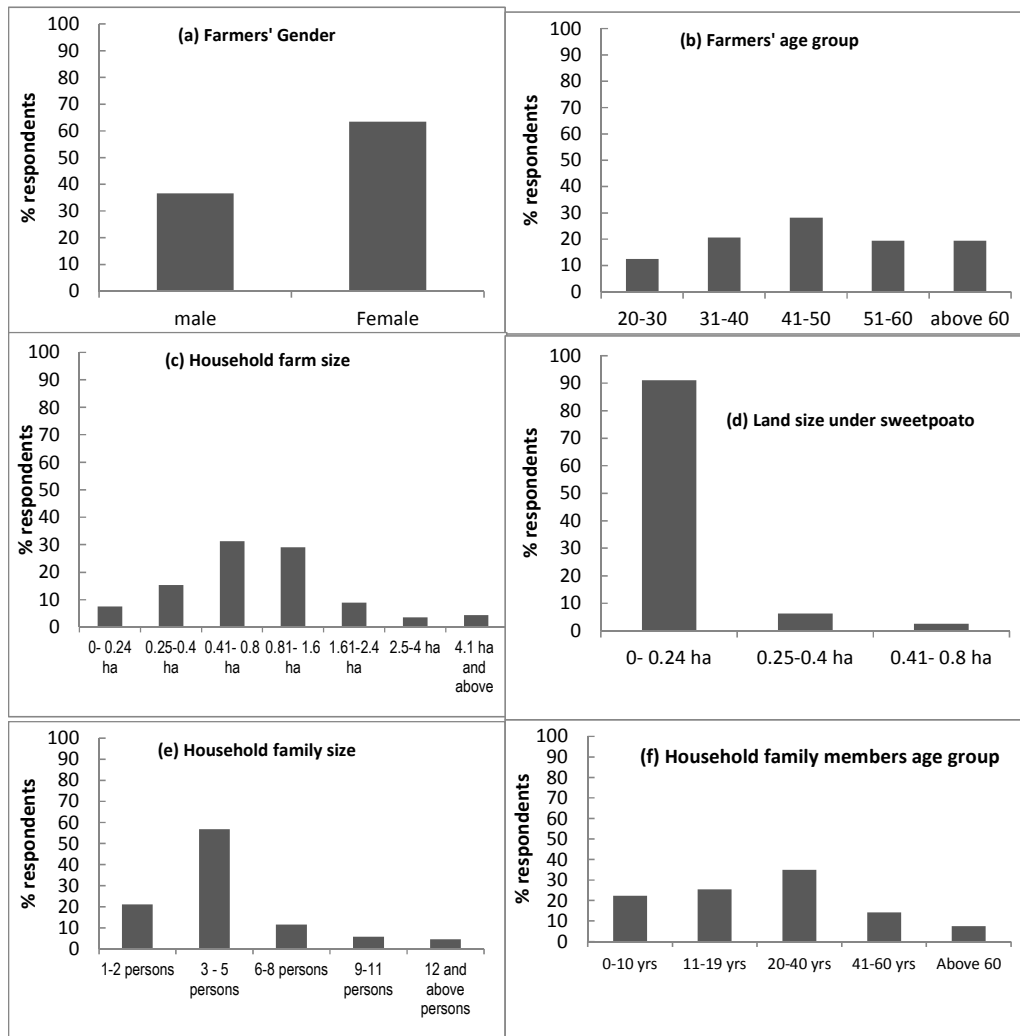


Figure 2.3: The (a) gender, (b) farmer's age group, (c) household farm size, (d) sweetpotato farm size, (e) family size, and (f) age group of household members of the farmers interviewed.

2.3.3 Food and cash crops grown by the farmers in the regions

The food crops identified by about 10% and above of the respondents were; sweetpotato, beans, maize, cassava, sorghum, and pigeon peas. The cash crops identified by about 5% and more of the respondents were kale, banana, sugarcane, beans, maize, sweetpotato and groundnut (Fig. 2.4).

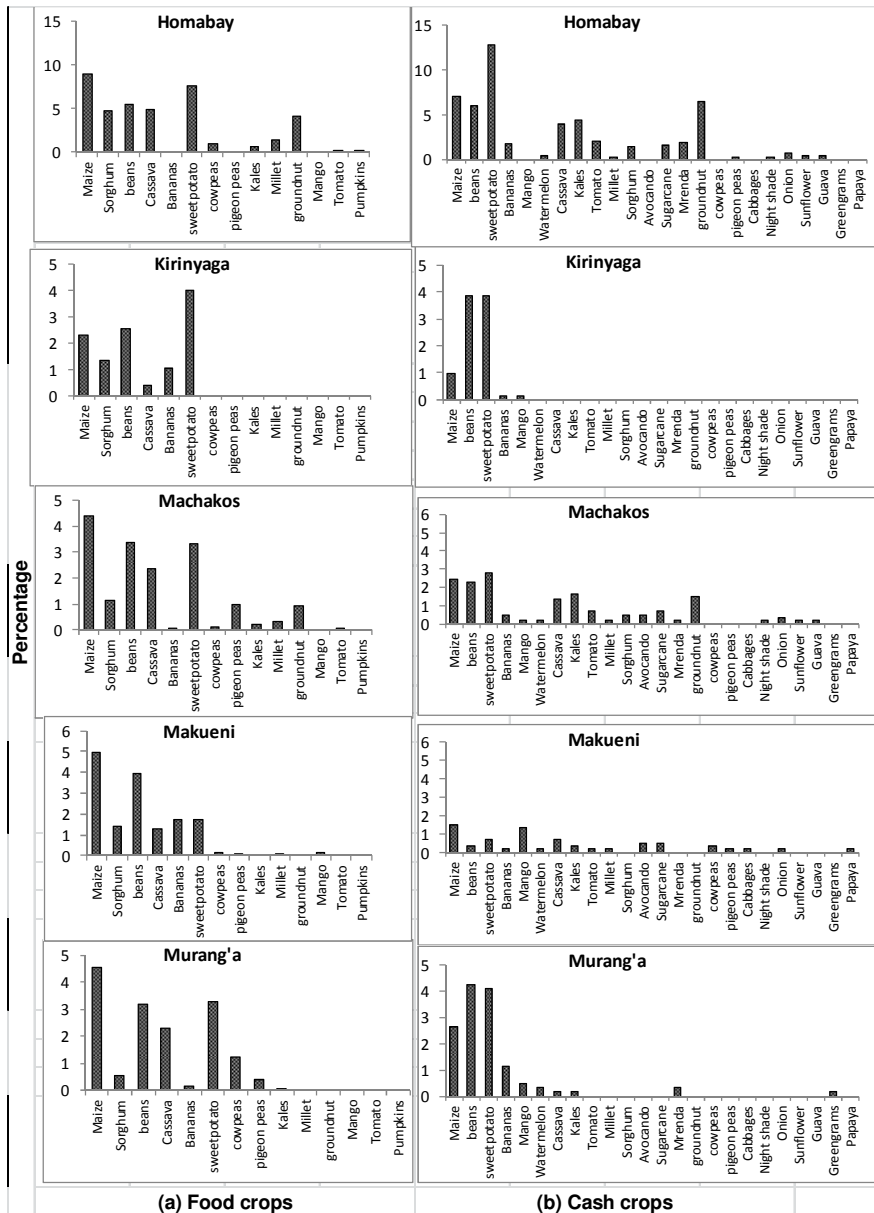


Figure 2.4: The food crops and cash crops grown by the farmers interviewed (%) in different counties

2.3.4 Sweetpotato varieties grown by farmers

The varieties Vitaa (13%), Kembu 10, and Kabonde (12%) were grown by most of the farmers. Qualities of the most preferred genotypes were; orange fleshed (OFSP), favourable sugar content (FSC), favourable starch content (FSC), low fibre content after cooking (LF), do not overcook in normal cooking time (NO), high yielding (HY), and improved varieties (IV). The less preferred were white fleshed (WFSP), high starch content (HS), local landraces (LL), and favourable storage root yield (FY) (Table 2.1).

Table 2.1: Varieties and the percent of respondent farmers growing them per region and across the surveyed regions

Genotype	Western Kenya (%)	Central Kenya (%)	Eastern Kenya (%)	Total (%)	Why preferred
Vitaa	3	4	6	13	OFSP,FS,HS,LF,NO,HY,IV
Kembu10	3	4	5	12	OFSP,FS,HS,LF,NO,HY,IV
Kabonde	3	5	5	12	OFSP,FS,HS,LF,NO,HY,IV
Bungoma	0	5	4	9	FS,HS,LF,NO,HY,IV
SPK 04	0	5	4	9	FS,HS,LF,NO,HY,IV
Kiganda	0	5	4	8	FS,HS,LF,NO,HY
Maruko	0	5	3	8	FS,HS,LF,NO,HY
Mwavuli	2	1	4	7	WFSP,HS,L,FY
Amina	2	0	3	5	WFSP,HS,L,FY
Mwei umme	2	0	3	4	WFSP,HS,L,FY
Mvita	0	0	1	1	WFSP,HS,L,FY
Kiluu	0	0	1	1	WFSP,HS,L,FY
Blanketi	2	0	0	2	HS,L,FY
Kalambyanyerere	2	0	0	2	HS,L,FY
Kunyikibonjwi	1	0	0	1	HS,L,FY
Nilikuja Kuzaa	1	0	0	1	HS,L,FY
Nyakeya	1	0	0	1	HS,L,FY
Nyasoda	1	0	0	1	HS,L,FY
Nyatonge	1	0	0	1	HS,L,FY
Odhieyo	1	0	0	1	HS,L,FY
Total	27	34	39	100	-

OFSP=orange fleshed sweetpotato, FS=favourable sweetness, HS=high starch content, LF=low fibre content after cooking, NO=do not overcook in normal cooking time, HY=high yielding, IV=improved varieties, while the less preferred were WFSP=white fleshed sweetpotato, HS=high starch content, L=landraces, and FY=favourable yield

2.3.5 Cultural practices

The majority of farmers (50%) used sweetpotato planting material from their previous crop or from their neighbours (34%). Only 8% of the farmers used certified planting materials (Fig. 2.5). Sixty percent of the farmers planted sweetpotato on ridges. Results on cropping type indicated that 38% of farmers practiced mixed cropping, 35% monocropping and 20% intercropping with other food crops (Fig. 2.5). Most farmers (45%) used manure and less than 10% of the farmers used inorganic fertilisers. However 55% of the farmers did not use any fertiliser in sweetpotato production (Fig. 2.5).

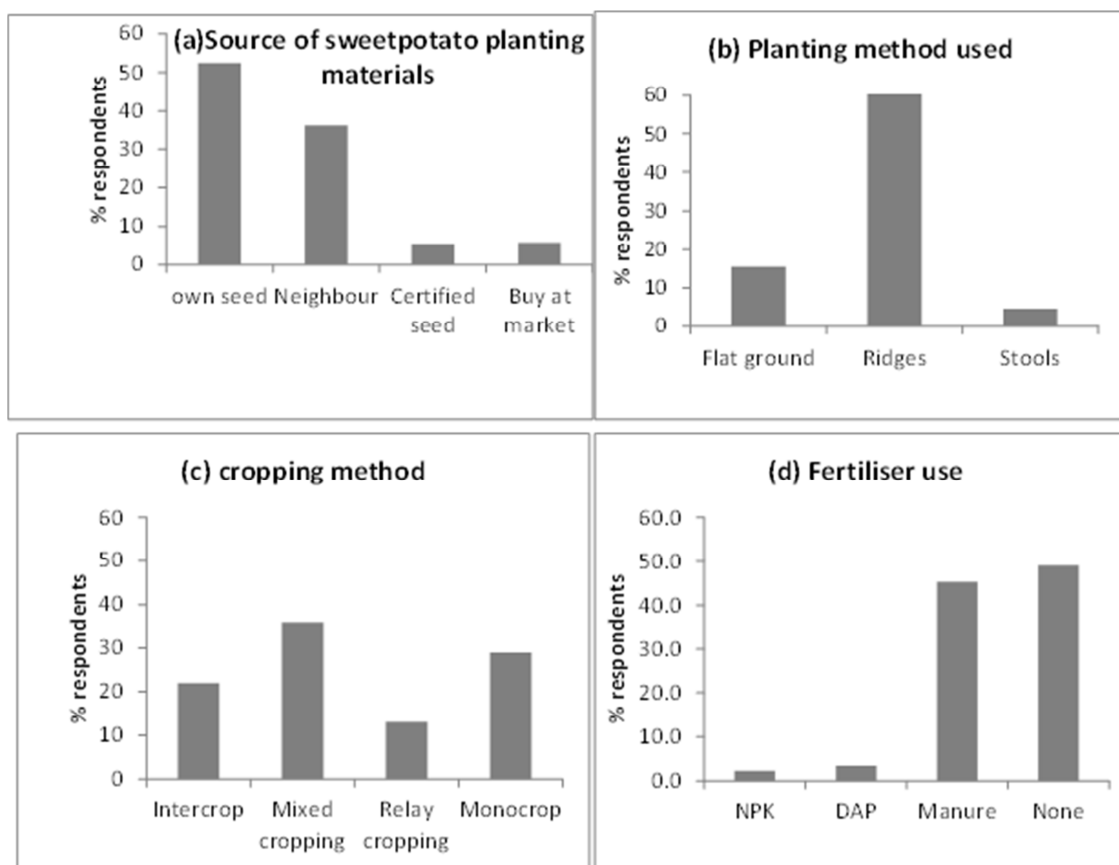


Figure 2.5: Cultural practices by sweetpotato farmers in Kenya (a) sources of planting materials, (b) planting method used, (c) cropping system and (d) fertiliser use.

2.3.6 Sweetpotato planting material conservation method

Most farmers (33%) conserved planting materials in the field, while the rest used other methods as indicated in Table 2.2

Table 2.2: Methods of sweetpotato seed conservation by farmers (%)

Conservation method	Western Kenya	Central Kenya	Eastern Kenya	%Total
Left on-farm	15	8	10	33
Plant after harvest	3	3	6	12
Wet land	2	5	4	11
Irrigated nursery	5	2	4	11
Under shade	1	4	5	10
Plant on soil embankment	3	3	3	9
Put in a hole	2	3	2	7
Do not conserve	2	2	3	6

2.3.7 Sweetpotato farmers' yields

The on-farm sweetpotato produced average yields of 5.5-7.4 t ha⁻¹, while a few produced about 3.5 t ha⁻¹ and below or 10 t ha⁻¹ and above (Fig. 2.6).

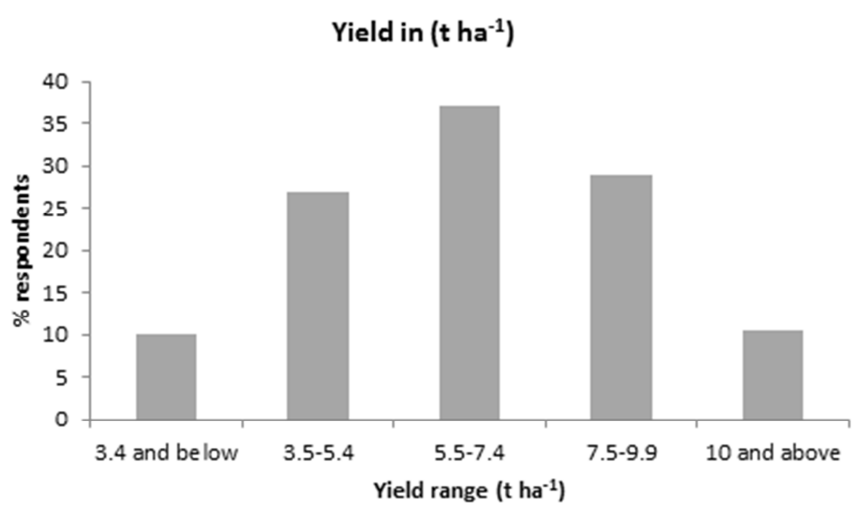


Figure 2.6: The sweetpotato yield of the households interviewed

2.3.8 Sweetpotato production constraints

Most farmers (28%) identified drought associated with hard soil pan as a major land preparation and planting constraint, as well as lack of clean and enough planting materials (18%) and high cost of inputs (11%). Drought (26%) was again the major constraint during harvesting, which led to increased damages inflicted to the storage roots during harvesting (19%) (Fig. 2.7; Table 2.3 a).

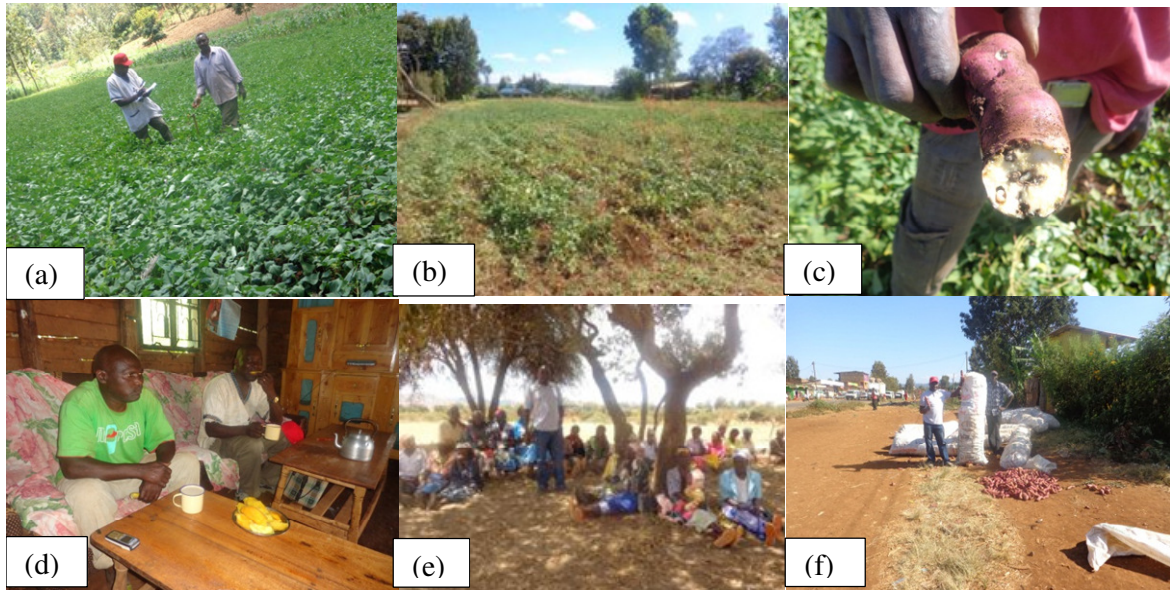


Figure 2.7: A photograph showing (a) sweetpotato crop under no drought stress, (b) under drought stress, (c) weevil infested storage root, (d) sweetpotato meal, (e) group of farmers who were interviewed, (f) sweetpotato packaging for sale, taken in the field during the participatory rural appraisal (PRA) survey interviews

Table 2.3a: Percent respondents on sweetpotato land preparation, planting and harvesting constraints during the PRA survey interviews

Constraint	Western Kenya	Central Kenya	Eastern Kenya	% Total
<i>Land preparation and planting constraints</i>				
Drought resulting to soil hard pan	10	6	13	28
Lack of clean, enough planting material	8	4	7	19
High cost of inputs	2	3	5	10
Lack of funds	4	2	3	9
Lack of ploughing oxen	2	2	2	6
Scarcity of manure	2	2	3	7
Lack of machinery	1	2	3	6
Water logging	2	1	2	5
Weeds	2	2	2	6
Labour scarcity	1	1	2	4
Total	34	25	42	100
<i>Harvesting constraints</i>				
Drought causing hardpan making digging out the roots difficult	7	9	10	26
Some storage roots damaged while harvesting	2	5	12	19
Roots damaged by moles	2	6	4	12
Weevil infestation	2	4	3	9
Labour shortage	1	4	2	6
Lack of funds to hire harvesting labour	1	2	2	5
Expensive labour	1	2	2	5
Pricked by thorny weeds while harvesting	1	2	2	4
Get poor yields after investing heavily	1	2	1	4
In piece meal harvesting, the small sized are harvested, leaving the large sized deep in soil	2	1	1	4
Some storage roots left underground	1	1	2	3
Roots damaged by hippopotamus	1	1	1	3
Total	22	39	42	100

The main pest and disease constraints were weevils (35%), and viruses (40%) (Fig. 2.7; Table 2.3b).

Table 2.3b: Percent respondents on sweetpotato pests and disease constraints of farmers interviewed

Constraint	Western Kenya	Central Kenya	Eastern Kenya	% Total
<i>Pests</i>				
Sweetpotato weevil (<i>Cylas spp.</i>)	10	14	11	35
Red spider mite (<i>Tetranychus cinnabrinus</i>)	5	6	9	21
Moles	11	3	4	18
Leaf worms (<i>Spodoptera littoralis</i>)	6	3	4	13
Whitefly (<i>Bemisia tabaci</i>)	1	3	3	7
Aphids (<i>Aphis gossypii</i>)	3	1	2	6
Total	36	30	33	100
<i>Diseases</i>				
Unaware	9	10	8	27
SPVD (SPFMV + SPMMV)	12	18	10	40
Alternaria blight (<i>Alternaria bataticola</i>)	7	12	5	24
Fungal Black Rot (<i>Ceratocystis fimbriata</i>)	2	4	3	9
Total	30	44	26	100

SPVD = Sweetpotato virus disease, SPFMV= Sweetpotato feathery mottle virus (transmitted by aphid potyvirus) and SPMMV= Sweetpotato mild mottle virus (SPMMV) transmitted by whitefly-transmitted potyvirus

2.3.9 Farmers' coping strategies for the constraints

Farmers coped with soil hardpan as a result of poor rains (drought) by irrigation (41%) while 36% suggested use of drought tolerant varieties. A majority of farmers (36%) stated that they would maintain planting materials and multiply it in wetlands to ensure they had clean and enough planting materials at the onset of rains. Also, farmers indicated that they used high yielding and drought tolerant varieties (59%) to address poor yields if available (Table 2.4a)

Table 2.4a: Percent respondents on strategies of coping with sweetpotato land preparation, planting and harvesting constraints during the PRA survey interviews

Constraints	Farmers' coping strategy	Western Kenya	Central Kenya	Eastern Kenya	Total
Soil hard pan due to drought	Irrigation	20	8	13	41
	Use oxen	7	4	3	14
	Wait for rains	5	2	4	11
	Drought tolerant varieties	15	9	12	36
	Total	45	23	32	100
Lack of clean, enough seed	Plant after harvest	12	3	2	17
	Buy from market or multiplier	7	10	4	21
	Maintain and multiply in wet land,	13	9	14	36
	Maintain and multiply in irrigated nursery beds	11	8	7	26
	Total	43	30	28	100
Weeds	Weeding regularly	10	7	6	23
	High planting density	11	11	15	37
	Manure application	6	11	5	22
	Fertilizer application	1	2	1	4
	Total	43	30	27	100
Poor yields	High yielding variety	19	17	22	59
	Fertilizer application	3	4	5	13
	Manure application	11	6	11	29
	Total	34	28	39	100

The coping strategies of the farmers on pest constraints were mainly use of clean planting materials (20%), use of crop rotation (15%) and early harvesting practice (15%). On diseases, majority farmers (24%) again used clean planting materials as control for virus disease, followed by crop rotation (22%) and use of resistant clones (19%) (Table 2.4b).

Table 2.4b: Percent respondents on strategies of coping with pests and disease constraints on sweetpotato production of farmers interviewed

Constraints	Farmers' coping strategy	Western Kenya	Central Kenya	Eastern Kenya	Total
Pests	Resistant varieties	4	6	3	13
	Early harvesting	6	5	4	15
	Crop rotation	6	3	6	15
	Irrigation	3	3	4	10
	Using clean seed	6	6	8	20
	Manure application	3	3	4	10
	Chemical spray	2	2	3	7
	Trapping	3	1	2	6
	Scaring away	2	0	1	4
	Total	35	29	36	100
Diseases	Using clean seed	8	8	8	24
	Early harvesting	7	5	4	16
	Resistance varieties	6	6	7	19
	Crop rotation	6	7	9	22
	Irrigation	4	4	4	11
	Chemical spray	2	2	4	7
		Total	34	31	35

2.4 Discussion

2.4.1 Demographic information

The majority of the 345 farmers interviewed were women. Most of the women had 1-5 children; the majority of the female farmers aged 21-40 and many household had children aged 0-10 years. This indicates the need to promote growing of OFSP as a source of vitamin A especially for the children aged 3-10 years and the lactating mothers in these households. In many households men are the head and decision makers even concerning farming activities. However, most of the men work and reside in the urban areas, which explains why the majority of the farmers interviewed were women. The absence of men on the farms causes delays in decision making which in turn causes delays in farm preparation and planting and consequently contributes to poor yields. Considering both gender, most farmers were aged between 41-50 years. This could be explained by the tendency of young

people moving to urban centres in search of work after finishing school/college. The majority of the household farm sizes were also small with sweetpotato grown on 0.5 acres and below. Results from this study were in agreement with those reported by Shonga et al. (2013) who reported that farmers grew sweetpotato on characteristically small sized plots in Ethiopia. This is because farmers try to produce enough for subsistence use, because there is no long term storage method for sweetpotato after harvesting. If the sweetpotato crop is ready for harvesting, leaving storage roots un-harvested will result to considerable losses as they lose their quality and are typically infested heavily by weevil. Similar findings were reported by Mmasa et al. (2012) in Tanzania who further recommended the increase of land area under sweetpotato production in order to boost productivity.

2.4.2 Food and cash crops, and sweetpotato varieties

Farmers classified almost all the food crops also as cash crops. Many of the farmers interviewed used part of their produce for food and sold the rest to generate cash income. However, increased commercialization of the crop and the fact that supermarkets and hotels are retailing sweetpotato storage roots and French fries is an indication that sweetpotato is a potential cash crop, which farmers could produce in large scale for income generation.

The varieties Vitaa, Kembu 10, and Kabonde were grown by most of the farmers. These varieties have high beta carotene and thus are used as health foods. Moreover, sensitization of orange fleshed sweetpotato as source of vitamin A has created a demand for these varieties, hence generating market. Moreover, this also shows that farmers were receptive to improved and released varieties compared to local landraces.

2.4.3 Cultural practices

Sweetpotato planting materials were mainly recycled from the previous crop, since only a very small portion of the farmers indicated they used certified planting material. This shows that either most farmers do not understand the importance of using clean and certified planting materials or do not have an alternative. This partially explains why sweetpotato yields continue to be low. Fuglie (2007) conducted survey work on sweetpotato constraints across many countries, and similarly found that lack of clean and enough planting material was a major constraint in most of African countries. In this study, farmers preferred to use manure rather than inorganic fertilisers such DAP and NPK, while a large number of farmers did not use any fertiliser. The farmers believe inorganic fertiliser makes the sweetpotato grow vegetatively and results in tasteless storage roots. Some believe that sweetpotato does not require a lot of soil nutrients and thus would do well with low soil fertility. These arguments may not be too far from the truth; however, research is required towards the development of a fertilisation model that improves the yields of sweetpotato but maintaining

the palatability qualities. Most farmers used ridges in planting sweetpotato, probably because this planting method leads to better yields than the other types of cultivation (Githunguri and Migwa, 2007). Mixed cropping with other food crops was the most preferred method, meaning farmers prefer planting crops in a mixture to spread the risk of failure to harvest in case of drought or any other unexpected constraint. However, some farmers planted sweetpotato as a monocrop, which suggests that the perception of the farmers on the value of the crop is changing.

2.4.4 Sweetpotato planting material conservation method

Most farmers leave the sweetpotato planting materials in the field. Consequently, the materials are heavily infested with virus and other pests and diseases. The aftermath is a reduction of the yield by 50% relative to the previous crop. These results are similar to those reported by Namandaa et al. (2013) who demonstrated that sweetpotato planting material sourced from swamp or irrigated on farm plots were infested with virus and getting it from volunteer plants after rains led to planting delays. In this study, roots conserved under sand and planted 10 cm deep and watered for 5-10 weeks before the onset of rains produced enough clean planting materials at the onset of the planting season. There is significant need to develop a working system of developing clean and enough planting materials for sweetpotato ready at the onset of the rains. Most farmers preferred higher planting densities, that is, 75 x 30, 60 x 60 and 75 x 60 cm, indicating a preference for intensive farming to maximise the productivity of their scarce land. This is supported by Belehu (2003) who reported that high density resulted in increased yield of sweetpotato. Also, higher density planting suppresses the weeds and at the same time minimises evaporation of soil moisture, resulting to improved yield (Kivuva et al., 2005)

2.4.5 Sweetpotato yields

Most sweetpotato yields on-farm ranged 5.5-7.4 t ha⁻¹, which is below the average production of 9 t ha⁻¹ in Kenya. Shonga et al. (2013) in their review on sweetpotato production constraints reported average sweetpotato yield in Ethiopia of 8 t ha⁻¹ relative to 18 t ha⁻¹ in the Asian countries. This indicates production constraints need to be addressed to improve the productivity of the sweetpotato.

2.4.6 Sweetpotato production constraints and coping strategies

Most farmers identified drought associated with hard soil pan, lack of clean and enough planting material and high cost of inputs as major constraints for land preparation and planting. Shields and Fletcher (2013) reported similar results in Uganda. This calls for researchers to devise methods of breaking the soil hardpan, and production of enough and clean sweetpotato planting materials. Breeding drought tolerant varieties, especially the

deep rooted, may also minimise storage root yield losses due to soil surface hard pan and weevil infestation. This also concurs with Mmasa et al. (2012) who reported shortage of planting material, lack of capital, drought and pests and diseases as sweetpotato production constraints in Tanzania

The major constraint experienced during harvesting was drought. Thus there is need for ways of simplifying harvesting when terminal drought occurs making the soil surface hard to break. Irrigating the field softens the soil surface and simplifies harvesting. Also, use of oxen and tractors would simplify the harvesting, hence, reduce root damages during harvesting. But these practices are not readily available to poor farmers. Research is also required for the best way to effectively control moles that cause damage to sweetpotato storage roots. Farmers engage the services of skilled mole trappers, which is expensive to sustain.

Most farmers in this study identified weevils as a major pest and sweetpotato virus disease (SPVD) as a major disease affecting their crop. This concurs with Ngailo et al. (2013), who reported that SPVD reduced yields 50-80% in Tanzania. They also indicated that the cheapest control method for the resource poor farmers was breeding for resistance. In this study, most farmers used unconventional weevil control methods such as manure application, which improves soil structure and irrigation which reduced the soil cracking and thus reduced the weevil infestations. This is similar to results by Ehisianya et al. (2013) in Nigeria who reported that a mixture of 50 ml of neem seed oil extract and 30 ml of diazinon in either 2 or 10 litres of water and cuttings dipped for 30 minutes (unconventional weevil control method) controlled *Cylas puncticollis* by 35.5%. However, data collected also showed a number of farmers were ignorant of pests and diseases that affected sweetpotato. This implies that there is need to sensitize farmers on diseases and other aspects of sweetpotato. Degu et al. (2013) also reported the need to improve the capacity for farmers to take up and continue with developed varieties and technologies. The lack of resistant varieties as well as disease and pest free sweetpotato planting materials were the major hindrance to pest and disease control. Thus breeders need to identify resistant varieties as well as promote production of clean seed to improve sweetpotato production. This is in agreement with results of work done on resistant gene expression on sweetpotato virus resistance (McGregor et al., 2009). Furthermore, Tefera et al. (2013) have also reported SPVD as a major constraint of sweetpotato production in Ethiopia. They also, reported that *Alternaria blight* was a constraint even though not serious, which concurs with the findings in this study.

As coping strategies some farmers indicated used clean planting materials, and improved varieties tolerant to drought, pests and diseases in order to have improved yields. This

implies that farmers are willing to embrace research technologies aimed at improving sweetpotato production.

2.5 Conclusion

Varieties Vitaa, Kemb 10, and Kabonde were grown by most of the farmers interviewed in this study which indicated that farmers were receptive to adoption of improved OFSP varieties. The farming households comprised groups of persons aged 0-10 years and 21-40 years (comprising young children and lactating mothers), thus, there is a need to promote breeding and production of OFSP varieties which are rich in beta carotene. Research on use of inorganic fertilisers, such as DAP and NPK, to boost production is required since most farmers never used any soil fertility enhancing method. Both infrastructural and personnel capacity building is required on alternative skills and better methods of conserving sweetpotato planting material to maintain them clean and also to control weevil and viruses infestation. Intensified research is required towards generating resistance varieties to drought, weevil, and virus which were the major constraints to sweetpotato production found in this study. Lastly, appropriate technology and seed multiplication and distribution method is required to ensure availability of clean and enough planting materials at onset of rains.

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Appendix

Appendix 2.1: Baseline questionnaire to determine current production practices and constraints in sweetpotato production

Section 1. Interviewee identification information

County _____ Division _____
Location _____ Sub-location _____
Village _____
Name of farmer: _____
Interviewed by _____
Date of interview _____
Farm size _____ (acres/hectares) GIS location _____ Altitude
above sea level _____ AEZ _____

Section 2. Socio-demographic characteristics of the household

2.1 Gender of farmer:

1=Male [] 2=Female []

2.2 Age of farmer (years) _____

2.3 Level of formal education of farmer:

1=None []

2=Primary []

3=Secondary []

4=Tertiary []

5=Other (specify) []

2.4 Marital status of household head:

1=Single []

2=Married []

3=Divorced []

4=Widowed []

5=Other (specify) []

2.5 Household size

Age group (years)	How many of the household members live at home and their age group	
	Males	Females
0 to 10		
11 to 15		
16 to 20		
21 to 40		
41 to 60		
Above 60		
Total		

2.6 Farmer's economic activities

2.6.1 Farming activities 2.6.1.1: Crops grown and acreages

(a) Food crops

- i. _____ acreage _____
- ii. _____ acreage _____
- iii. _____ acreage _____
- iv. _____ acreage _____

(b) Cash crops

- i. _____ acreage _____
- ii. _____ acreage _____
- iii. _____ acreage _____
- iv. _____ acreage _____

Section 3. Sweetpotato production

3.1 Which varieties of sweetpotatoes do you grow and how?

Variety name	acreage	Cropping method Mono=1 Intercrop=2 Mixed cropping=3	spacing	Irrigation=1 (specify type) Rain fed=2
Variety 1				
Variety 2				
Variety 3				

3.2 Planting material

Variety name	Source of planting material own vines=1 neighbour=2 Buy from local market=3 Other sources=4 (specify)	Price if bought (give source/price)	Conservation method of planting materials
Variety 1			
Variety 2			
Variety 3			

3.3 Soil and fertility Management:

3.3.1 How do you prepare land for planting?

Variety name	Dig by hand=1 Plough with oxen/donkey= 2 Plough with tractor = 3, Other= 4specify	Cost per acre (Kshs)
Variety 1		
Variety 2		
Variety 3		

3.3.2 Method of planting

Variety name	Flat ground=1 Ridges=2 Other=3 (specify)	Cost per acre for planting and holes preparation (Kshs)
Variety 1		
Variety 2		
Variety 3		

3.3.3 Which fertilizer do you apply for planting and at what rate?

Variety name	Fertilizer for planting NPK=1 DAP=2 Animal manure=3, Other= 4 (specify)	Rate	Cost per hectare of fertilizer plus labour for application (Kshs)
Variety 1			
Variety 2			
Variety 3			

3.3.4 Which fertilizer do you apply for top dress and at what rate?

Variety name	Fertilizer for planting CAN=1 Urea=2 Animal manure=3, which one? other= 4 (specify)	Rate	Cost per acre of fertilizer plus labour for application (Kshs)
Variety 1			
Variety 2			
Variety 3			

3.3.5 If intercrop or mixed cropping with which crops?

Variety name	acreage	Cropping method Intercrop=1 Mixed cropping=2	Crops intercropped/mixed with	spacing
Variety 1				
Variety 2				
Variety 3				

3.3.6 What constraints do you encounter during land preparation and planting of sweetpotato?

Section 4. Pests and diseases

4.1 List the most important pests you see in your sweetpotatoes

Pest name	Var1	Incid %	Sev 1-5	VaR 2	Incid %	Sev 1-5	Var3	Incid %	Sev 1-5
Pest 1									
Pest 2									
Pest 3									

Where: Var=Variety, Sev=severity, Incid=incidence

4.2 Pest control method

Pest name	Method 1	Cost ha ⁻¹ (Kshs)	Method 2	Cost ha ⁻¹ (Kshs)	Method 3	Cost ha ⁻¹ (Kshs)
Pest 1						
Pest 2						
Pest 3						

4.3 List the most important diseases you see in your sweetpotatoes

Disease name	Var1	Incid %	Sev 1-5	VaR 2	Incid %	Sev 1-5	Var3	Incid %	Sev 1-5
Disease 1									
Disease 2									
Disease 3									

Where: Var=Variety, Sev=severity, Incid=incidence

4.4 Disease control method

Variety name	Method 1	Cost ha ⁻¹ (Kshs)	Method 2	Cost ha ⁻¹ (Kshs)	Method 3	Cost ha ⁻¹ (Kshs)
Disease 1						
Disease 2						
Disease 3						

4.5 What is your major constraint in pests/disease control in sweetpotatoes?

4.5.1 In disease control?

- i. _____
- ii. _____
- iii. _____

4.5.2 In pests control?

- i. _____
- ii. _____
- iii. _____

Section 5. Sweetpotatoes harvesting

5.1 How long do your sweetpotatoes take in the farm to harvest?

Variety	Period in months
Variety 1	
Variety 2	
Variety 3	

5.2. How do you harvest your sweetpotatoes storage roots?

Variety	Dig by hand hoe=1 Plough with oxen/donkey= 2 Plough with tractor = 3, Other=4 (specify)	Harvest procedure Piecemeal=1 All at once=2 Other= 3 (specify)	Cost of harvesting ha ⁻¹ (Kshs)	Yields ha ⁻¹
Variety 1				
Variety 2				
Variety 3				

5.3 How do you store your sweetpotatoes after harvesting?

- i. _____
- ii. _____
- iii. _____
- iv. _____

5.4 What constraints do you encounter in sweetpotatoes harvesting?

- i. _____
- ii. _____
- iii. _____
- iv. _____

Section 6 Utilization processing and marketing

6.1 For what purpose do you utilize/grow your Sweetpotatoes?

Variety name	Utilization Food=1, Sell=2 Animal feed= 3, Other= 4 (specify)
Variety 1	
Variety 2	
Variety 3	

6. 2 If utilize sweetpotatoes as food list various ways you use it as food e.g. grinding into flour for thick porridge?

- i. _____
- ii. _____
- iii. _____
- iv. _____
- v. _____

6.3. What constraints do you encounter in utilization, processing and marketing?

6.3.1 Utilization

- i. _____
- ii. _____
- iii. _____
- iv. _____

6.3.2 Processing

- i. _____
- ii. _____
- iii. _____
- iv. _____

6.3.3 Marketing

- i. _____
- ii. _____
- iii. _____
- iv. _____

Chapter 3

Evaluation of Sweetpotato Genotypes for Tolerance to Drought Stress

Abstract

A total of 84 sweetpotato clones were evaluated at Kenya Agricultural Research Institute (KARI), Kiboko and Thika between May 2011 and September 2012 for tolerance to drought. The experiments were planted in a split plot design with drought stress and no drought stress conditions as whole plots, and clones as subplots arranged in a 14 x 6 alpha lattice design with two replicates. Approximately 30 cm long vine cuttings of each clone were planted 10 cm deep on 25 cm high beds, in single rows of 6 hills spaced at 30 x 90 cm. The field study was also validated in greenhouse box experiments at KARI-Muguga. Data on growth and yield characteristics were recorded and analysed using Genstat 14th edition. Across sites, data indicated that, genotype, environment, and their interaction significantly differed for fresh storage root weight (FSR) (kg plant⁻¹), total fresh biomass weight (FB) (kg plant⁻¹), marketable fresh storage root weight (MFSR) (kg plant⁻¹), harvest index (HI), and days to permanent wilting point (DPWP) at ($P \leq 0.05$). Comparing data on both environments, drought stress caused a reduction of FSR (72.5%), FB (74.0%), MFSR (80.7%), NSR (24.5%), DPWP (0.3%), but seemed to increase percent root dry matter (%RDM) (-4.7%), HI (-2.6%), and chlorophyll content (CC) (-2.7%). Based on FSR across the environments, genotypes 194555.7 (1.06), 421066 (1.05), Chingova (0.94), 420014 (0.91), Excel (0.9), 199062.1 (0.87) and Unawazambane06-01(0.81) gave higher storage root yields (kg plant⁻¹) than the local checks. Genotypes Nyarmalo and Polista were the lowest yielding clones in both drought stress and no drought stress environments. Genotypes W119, 441725, Xiadl-xa-kau had the highest DPWP (81), had high yields under drought stress, and had drought sensitivity index (DSI) ≤ 1 , an indication that they were drought tolerant. Moreover, genotype 194555.7, Unawazambane06-01, 189150.1, Tanzania, and Chingova had DSI < 1 and high storage root yield under drought stress and no drought stress conditions, and thus, may be used in drought tolerance breeding programme.

Key words: Sweetpotato genotypes, drought stress, biomass, harvest index, storage root yield, drought tolerance.

3.1 Introduction

The increasing population pressure in developing countries has led to increased human activities leading to reduction of agricultural land (Kiage, 2013; VÄgen-Tor et al., 2013). This has led to an expansion of agricultural activities to arid and semi-arid lands (ASALs). These ASALs have frequent droughts resulting in low crop production (Amede et al., 2004). Thus, a remedy for the low crop production in ASALs due to drought stress is urgently required. The most common interventions are water application through irrigation and breeding for drought tolerant crops. The latter approach is more appropriate for sweetpotato farmers in sub-Saharan Africa, as it is not capital intensive.

The natural source of water for plants is rainfall, which infiltrates in the soil (Tardieu, 1996). Plants extract the soil water together with nutrients and the water is assimilated into the plant cells with part of it lost to the atmosphere through evapo-transpiration. Failure of rainfall causes soil water to diminish and plant cells experience water stress leading to cell dehydration and ultimately senescence (Lisar et al., 2012). Once the plants exhausts the readily available soil water in the root zone, water stress begins (Kramer and Boyer, 1995). Water stress affects photosynthesis and translocation of assimilates (Mundree et al., 2002). However, some plants device mechanisms of tolerating the drought stress to some extent through escape, avoidance, tolerance, or recovery of drought, with extreme drought stress leading to crop death (Ekanayake, 1990; Cruz De Carvalho, 2008). A drought tolerant genotype produces economically good yield under soil moisture stress. Therefore, drought tolerant sweetpotato genotypes should produce higher quantity and quality of yields in absence of sufficient rains and irrigation compared to other genotypes. These drought tolerant genotypes may be identified through screening of germplasm under managed drought stress conditions.

The yield of most crops is used as an indicator for the capacity to tolerate moisture stress (Anjum et al., 2011). Drought in sweetpotato reduces both the quantity of storage root yield and above ground vine (forage) and their respective quality (Mundree et al., 2002). Research to determine the drought stress tolerance ability of sweetpotato genotypes is yet to be conducted in Kenya. Breeding for drought tolerance exploits the recombination of alleles from donor genotypes to develop more drought stress tolerance genotypes. It is against this background that the screening of sweetpotato genotypes under drought and non-drought conditions was conducted.

Several studies have been conducted by other researchers who used different parameters to evaluate drought tolerance in sweetpotato. Anselmo et al. (1998), evaluated local high

yielding sweetpotato germplasm in Sweden and was able to distinguish genotypes with drought tolerance based on the marketable storage roots yield. Heerden et al. (2008), on the other hand, reported that drought stress reduced photosynthesis, above ground biomass, and yield of genotypes A15 and Resisto evaluated, but photosynthesis per unit area was reduced more in the less tolerant genotype Resisto. Laurie et al. (2004) used a rapid drought screening box method by planting about 15 cm long vine cuttings of the sweetpotato clones in boxes filled with sterile media and media moisture maintained at field capacity up to 15 days after planting after which irrigation water was withheld. They identified W119 as tolerant, Excel as neutral to tolerant, A15 as neutral, Resisto as neutral to susceptible and Bosbok as susceptible. Maquia et al. (2013) also reported that the genotypes Chingova, Naspot 5, SPK 004, and Resisto were drought tolerant.

Despite these studies, information on the drought tolerance of landraces and released clones in Kenya is unknown. Because only roughly 20% of the land in Kenya receives adequate rainfall, there is great need for the development of drought tolerant crops (Jaetzold et al., 2006). Thus, identification of sources of drought tolerance from the locally adapted clones and other sources from the region would be useful for establishing a sweetpotato breeding programme. The aim of this study was to identify drought tolerant clones from those sourced from the Kenyan gene bank, smallholder farmers in Kenya and International Potato Centre (CIP) in Nairobi.

3.2 Materials and methods

3.2.1 Description of sites

The field experiments were conducted at two sites; Kenya Agricultural Research Institute (KARI)-Kiboko, and KARI-Thika, while the greenhouse experiment was conducted in KARI-Muguga. The KARI-Kiboko research station is located in Makueni county, 187 km east of Nairobi, at a latitude of 2°15' south and longitude of 37°45'E and altitude of 993 m asl. The research station is classified under agro-ecological zone five and receives mean annual rainfall of 560 mm with long-term annual average rainfall of 615 mm and is ideal for dry land research. The station receives bimodal rainfall with the more reliable short rains falling in late October to December (330 mm) and the poor long rains from March to May (230 mm). The annual mean maximum temperature is 30.6°C, while the annual mean minimum temperature is 17.4°C which translates to an annual mean temperature of 24°C. The soils are of rhodic ferrasols to ferric luvisols on the old peneplain and eutric fluvisol at the bottom of the river valley (Mwacharo et al., 2004). KARI-Thika is located 75 km north east of Nairobi, latitude 0°59' South, longitude 37°04' East, altitude 1548 m asl. The area receives bimodal mean rainfall of about 1000 mm annually with long rains of 142 mm falling March to May and the

short rains of 116 mm falling in October to December. The areas has minimum temperature of 13.7°C, maximum of 25.1°C, and mean annual temperature of 19.4°C (Ndegwa et al., 2009). The soils at Thika are well drained ferric luvisols.

KARI-Muguga is located 27 km north west of Nairobi, latitude 1°13' South, longitude 36°38' East, altitude 2096 m asl. The area receives bimodal mean rainfall of 900 to 1000 mm annually with long rains of 550 mm falling mid-March to June and the short rains of 400 mm falling in mid-October to December. The area has minimum temperature of 7°C and maximum of 20°C, which translate to 15°C. The area is classified as sub humid with a well-drained, very deep, dark reddish brown to dark red, friable clay soil classified as humic nitisols (UNESCO, 1977) or an oxycpaleustaf (USDA, 1975).

3.2.2 Sweetpotato germplasm

The germplasm consisted of 84 sweetpotato genotypes sourced from the gene bank of Kenya, the International Potato Centre (CIP), Nairobi and farmers' fields. The genotypes were selected on the basis of high yield, orange fleshed sweetpotato (OFSP), high dry matter, early maturity, drought tolerance, and sweetpotato virus disease (SPVD) resistance. The germplasm was multiplied in the greenhouse at KARI Muguga to increase the planting materials. The genotypes Marooko and Gatumbi were obtained from the National Gene Bank of Kenya (NGBK) and used as local checks.

3.2.3 Field evaluation

At KARI-Kiboko, the trial was planted in October 2010 when the rains had subsided and repeated for another season in April 2011. At KARI Thika the trial was planted in May 2011 after the rains had subsided and repeated in December 2011 (Fig. 3.1). A split plot design was used with irrigation as the main plot and clones as subplots arranged in a 14 x 6 alpha lattice replicated twice. The genotypes were planted on 25 cm high beds in single rows of 10 plants per plot at a spacing of 30 cm between plants and 90 cm between rows. Each row was separated by one meter planted with two plants of a clone with different vine and root skin colour, to ensure uniform competition within the rows. Distinct clones with coloured vines and roots were planted in four guard rows surrounding the outer rows of the experiment. Six tensiometers were installed in each replication, two at each of the following soil depths; 20 cm, 40 cm and 60 cm to monitor soil moisture content and determine when to irrigate. Vines used for planting were about 25 cm long and had 4-6 nodes. The vines were planted in a 60° slanting position and kept at field capacity soil moisture levels for four weeks until they were established. Thereafter, the drought stress environment received no irrigation water until harvesting while the irrigated environment received 35 mm equivalent irrigation water every time the tensiometer read 15 centibars. The amount of irrigation water was

collected and measured using artificial rain gauges and cumulative irrigation water quantified to mm of rainfall.

Soil analysis was conducted before planting to determine nutrient status of the trial site and moisture content (Table 3.1). Double ammonium phosphate fertiliser was applied during planting at the rate of 50 kg P₂O₅ ha⁻¹, while weeding was done by hand hoe twice in each experiment. The centrally placed six hills were used to collect data leaving two hills each side of the row.

Data on morphological traits were collected following IPGRI (bioversity) descriptors (CIP et al., 1991). Storage root harvesting was done 150 DAP using hand hoes and data collected on the six plants centrally placed in the rows. Data collected included:

- Number of storage roots (NSR) - a count of storage roots plant⁻¹
- Number of marketable storage roots (MSR) - a count of storage roots weighing between 100 – 500 g plant⁻¹
- Fresh root weight (FSR) - the weight of all storage roots at harvesting plant⁻¹
- Fresh vine weight plant⁻¹ (FVW) - the weight above ground biomass at harvesting plant⁻¹
- Fresh biomass (FB) - the sum of storage root and vine weight plant⁻¹
- Leaf chlorophyll content (CC)
- Harvest index (HI) - fresh storage root weight/fresh biomass
- Days to permanent wilting point (DPWP) under rapid box drought screening experiments.

Fresh root samples of 200 g and fresh vine samples of 300 g or the available were taken for determining dry matter. Drying of the samples was done in a forced air drying oven set at 40°C until a constant mass was attained and percent storage root dry matter content (%RDM), percent vine dry matter content (%VDM) were calculated. Drought sensitivity index (DSI) according to Fischer and Maurer (1978) rating the clones as, DSI 1=neutral, >1 sensitive, <1 tolerant, was determined.

3.2.4 Chlorophyll content determination

The chlorophyll content was determined using a chlorophyll meter (SPAD 502 plus: STSPAD502PLUS, Konica Minolta, Tokyo, Japan). The SPAD was calibrated by analysing the chlorophyll content of samples collected from some of the genotypes used. Three leaves were randomly sampled in each of the following randomly selected genotypes for calibration; 194515.15, A2, 441725, Resisto, and 1990621. For each leaf, two SPAD readings were taken at mid left and mid right of the selected leaves and 9 mm diameter discs cut using a

cork borer at each point. The chlorophyll in the discs was extracted in 4 ml of 0.1N HCl in Methanol (BDH) at 21°C in a dark room for 24 hours in a test tube. A blank sample with only the extraction solution was also included as a control. Absorbance of the extracts was measured using a WPA S105 spectrophotometer (Griffin and George Ltd. – WPA Scientific Instrument, located at Saffron Walden, England). The absorbance of the chlorophyll extracts was measured at 653 nm and chlorophyll content in mg cm^{-2} calculated as absorbance at 653 nm (A_{653})*24.88 (Mutui et al., 2001). A correlation scatter graph was generated using the SPAD measurements as x-axis and the chlorophyll extract absorbance at y-axis. The calibration equation fitted with the y-intercept set at zero was $Y = 0.0168X$, with $R^2 = 0.935$. Thus, chlorophyll content (mg cm^{-2}) was calculated as $Y = 0.168X * 24.88$. Where $Y =$ chlorophyll content in mg cm^{-2} , X is the SPAD reading and 24.88 is a constant.

3.2.5 Greenhouse evaluation

This experiment was conducted in the greenhouse at KARI Muguga between January and December 2011 (Fig. 3.1). Each of the 84 genotypes was planted in a box filled with sterilized soil comprised of forest soil, cattle manure, gravel of size one eighth of an inch, and NPK (17:17:17) fertiliser all at a ratio of 5:2:1:0.25. The soil was moistened and sterilized at 82.5°C in drums of 210 kg for 20 minutes, cooled for 21 days before use. The soil media was filled in to the boxes made of 15 x 0.45 x 0.45 m high density black polythene sheet supported by wooden pegs to a height of 0.4m (Fig. 3.1 b). The experiment was conducted using a RCBD design replicated four times and repeated two times. Prior to the beginning of the experiment, the growth media was watered to field capacity. Data on the number of days from establishment to permanent wilting point were counted. The growth media was watered to field capacity, indicated by a tensiometer reading of zero. Shoots of 10 cm were cut from each experimental genotype using a sterilized scalpel. Each cutting was planted to a depth of five cm, in upright position. The soil moisture was maintained at field capacity by putting more water every time the tensiometer reading dropped to 15 centibars, until it read zero again, carefully avoiding flooding. Water application was stopped 15 days after planting and observation of the plants done. Data on number of days from planting to permanent wilting point were taken for each plantlet (Laurie et al., 2004). Data on soil moisture stress using tensiometers and relative humidity, light intensity, maximum and minimum temperature were collected using a data logger (HOBO U12-012 – data logger temp/RH/Light/ext channel, Micro Precision Calibration Inc., 22835 Industrial Place Grass Valley, CA USA 95949).



Figure 3.1: (a) Field evaluation of 84 clones – drought and irrigated environments (b) Greenhouse evaluation of the 84 clones in box drought screening

3.2.6 Data analysis

The data was subjected to analysis of variance (ANOVA) to determine differences among genotypes and environments using SAS (2002), and means separated using least significant difference (LSD) at $p \leq 0.05$. The clones were ranked as follows; rank $y = \sum_{k=1}^n x$, where; y is the rank, x is the sum of genotype ranks from trait k to trait n for the traits measured, where k = rank in trait 1 on merit, and n = rank of the last trait. Thus, the best genotype in each trait scored one, while the worst scored 84, which indicates that, considering more than one trait, the best genotype had the least cumulative scores while the worst had the most cumulative scores.

3.3 Results

3.3.1 Weather conditions

At Kiboko research station, the rainy season occurred between September to December and February to May. Most of the rain occurred during October 2010 and May 2011 (Fig. 3.2). Percent relative humidity was around 80% during most of the year. Minimum temperature was about 16°C and maximum was about 32°C while the mean was 24°C (Fig. 3.2). At Thika research site, rainfall occurred from September to December 2011 and April to June 2012. The highest rainfall occurred in October 2011. Relative humidity ranged from 50-80%.

Minimum temperature was about 14°C, and maximum was about 26°C, while the mean was 20°C (Fig. 3.2).

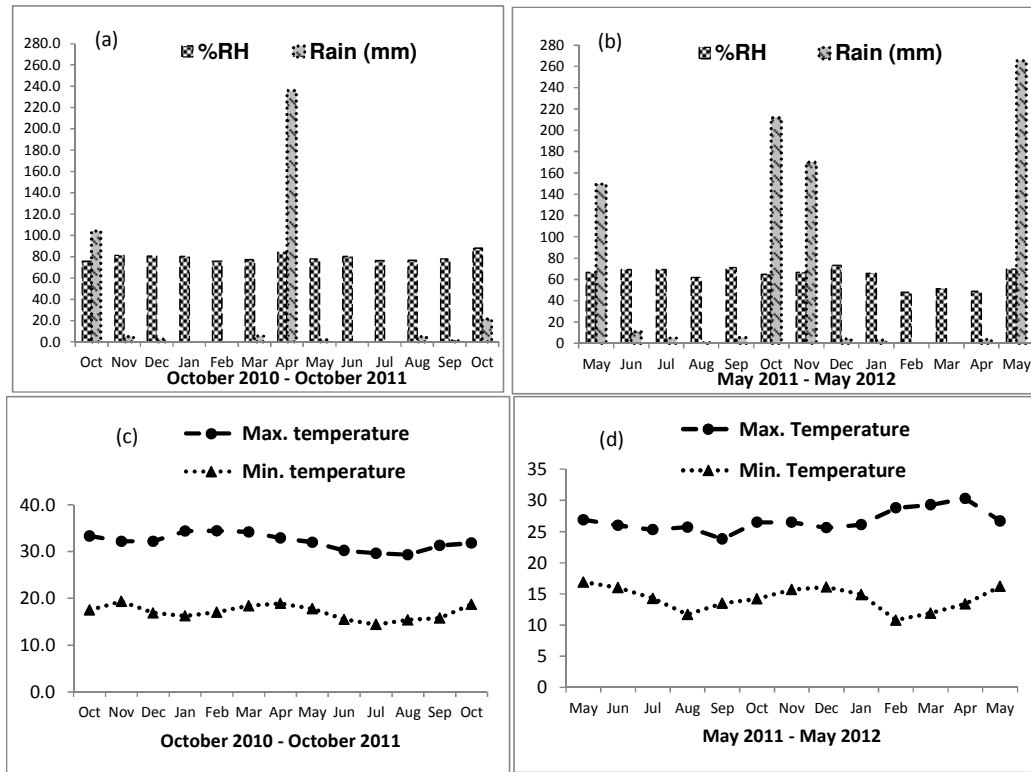


Figure 3.2: A graph showing; (a) and (b) - rainfall in mm and relative humidity (%), (c) and (d) - minimum and maximum temperature in °C for the two growing seasons in Kiboko, Makeni county (a and c) and Thika, Kiambu county (b and d) in Kenya, respectively.

On the greenhouse environmental conditions, the maximum temperature in the greenhouse ranged between 25-45°C (mean 35°C), while the minimum temperature ranged between 10-18°C (mean 14°C). Minimum relative humidity ranged between 20-70 (mean 45%) and the maximum between 80-99% (mean 89.5%). Minimum light intensity range was 2000-8000 (5000 lux) while maximum range was 5000-30000 (17,500 lux). The minimum dew point ranged 5-15°C (10°C) while the maximum ranged from 12-25°C (18.5°C) (Fig. 3.3).

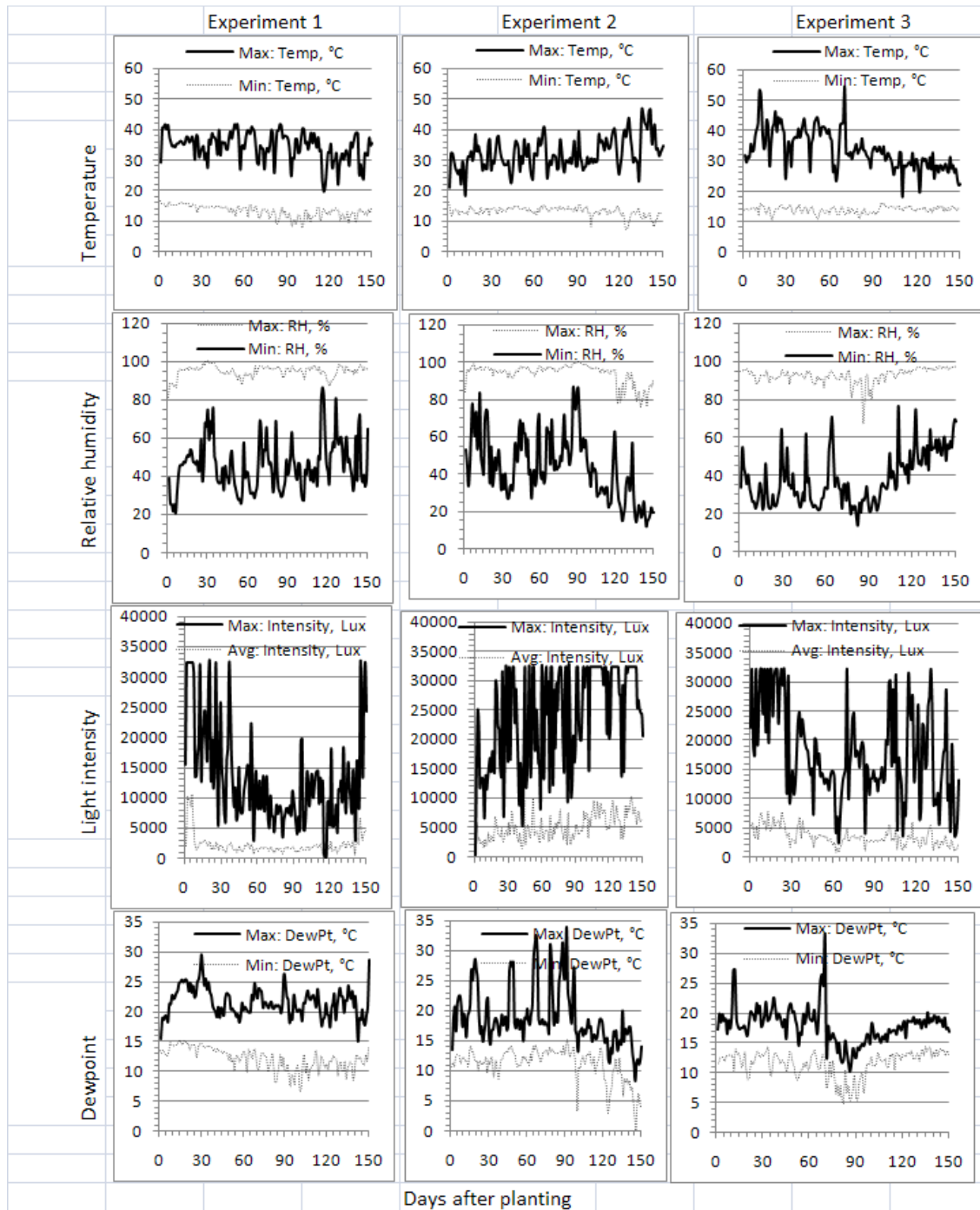


Figure 3.3: Temperature, relative humidity, light intensity and dew point during the box rapid drought evaluation study in the greenhouse at KARI Muguga, Kenya

3.3.2 Soil chemical properties

At Kiboko the soil had low %N and %organic C. The soil pH at Thika was slightly alkaline, and the amount of Na and Ca elements were high. Magnesium was low in the sterile soil, however, the rest of the minerals were adequate to high (Table 3.1).

Table 3.1: Chemical analysis of the macro and micro nutrients of soil samples from Kiboko and Thika sites

Parameter	Kiboko	Class	Thika	Class	^a Sterile	Class
pH	7.22	Slightly alkaline	8.18	Medium alkaline	6.98	neutral
%N	0.10	low	0.18	low	0.52	adequate
% Org. C	0.37	low	0.36	low	6.99	adequate
ppmP	52.33	high	74.59	high	132.75	adequate
ppmK	226.44	adequate	282.45	adequate	1658.60	high
ppmCa	1623.21	High	1825.93	High	2836.51	high
ppmMg	323.12	adequate	351.24	adequate	30.46	low
ppmNa	762.94	high	819.46	high	80.20	adequate
ppmFe	36.11	adequate	44.44	adequate	203.23	high
ppmZn	0.70	adequate	0.70	adequate	25.90	high
ppmCu	0.46	adequate	0.46	adequate	0.99	adequate
ppmMn	6.90	adequate	5.91	adequate	97.80	high

^asterile soil sterilised as described in section 3.2.5., at Kenya Plant Health Inspectorate Services station, at Muguga, Kenya

3.3.3 Results of field evaluation

Genotype (G), environment (E), and GE interaction effects were significant at $P \leq 0.05$ for all the traits observed except for %RDM and marketable fresh weight of storage roots (MFSR) (Table 3.2).

3.3.4 Mean performance of genotypes

There was a significant difference in the performance of the clones for all the traits evaluated. The clones also differed significantly under drought stress and no drought stress environments for all the traits observed except for NSR plant⁻¹ (Table 3.3).

3.3.5 Genotypes performance across environments

The best ranking 12 clones, had mean fresh storage root weight (FSR) of 0.84 kg plant⁻¹ and a harvest index of 0.77 and they all performed better than the local checks (Table 3.4; Appendix 1). The local checks, Gatumbi and Marooko, had FSR of 0.23 and 0.4 kg plant⁻¹, respectively. The mean performance of in the rest of the clones is shown in Table 3.4. The 12 poor performing genotypes had fresh storage root weight (FSR) of 0.20 kg plant⁻¹, and harvest index of 0.52 (Table 3.4; Appendix 1). Also, the mean performance for the rest of the clones is shown in Table 3.4.

Table 3.2: Mean squares for storage root yield and other traits of the 84 genotypes evaluated across the environments

Source	DF	FSR (kg plant ⁻¹)	NSR plant ⁻¹	%RDM	FB (Kg plant ⁻¹)	LCC (mgcm ⁻²)	MFSR (Kg plant ⁻¹)	HI
REP	1	0.028	0.0	6.1	0.015	0.015	6.06	0.015
Site	1	0.004	0.1	20.0	0.004	0.004	20.04	0.004
Site*REP	1	0.007	0.2	4.0	0.007	0.007	4.01	0.007
Env	1	85.71***	468.9***	0.8	233.9***	233.934***	0.85	233.9***
Env*REP	1	0.000	7.4	12.6	0.003	0.003	12.60	0.003
Genotype	83	0.907***	13.3***	32.4***	1.166***	1.166***	32.45***	1.1***
Genotype*REP	83	0.141***	2.8***	8.4	0.167***	0.167***	8.39ns	0.16***
Env*Genotype	83	0.615***	6.3***	7.4	0.755***	0.755***	7.35ns	0.75***
Environ*Genotype*Rep	83	0.085***	2.0***	7.6	0.104***	0.104***	7.57ns	0.104***
Site*Env	1	0.016	0.2	19.0	0.008	0.008	18.99	0.008
Site*Env*REP	1	0.052*	0.6	1.7	0.036	0.036	1.69	0.036
Site*Genotype	83	0.011	0.6	6.7	0.020	0.020	6.67	0.020
Site*Genotype*REP	83	0.016*	0.6	6.2	0.019	0.019	6.23	0.019
Site*Env*Genotype	83	0.011	0.9	8.5	0.020	0.020	8.48	0.020
Site*Env*Genotype*Rep	83	0.017**	0.9	4.8	0.018	0.018	4.79	0.018
R2		1.0	0.8	0.6	0.97	0.971	0.60	1.0
CV (%)		22.7	26.0	9.2	19.48	19.478	9.21	19.5

Site = Kiboko, Makueni county and Thika, Kiambu county, Kenya, Rep = replicate, Env = environment (irrigated and drought), ns = not significant, and *, **, ***, = significant at P≤0.05, P≤0.001, P≤0.0001 respectively, NSR = number of storage roots, FSR = fresh storage root weight, RDM = root dry matter, FB = fresh biomass weight, MFSR = marketable fresh storage root weight, HI = harvest index, CC = leaf chlorophyll content.

Table 3.3: Genotype performance under drought stress and no drought stress conditions for eight traits

Parameter	NSR plant ⁻¹	FSR(Kg plant ⁻¹)	% RDM	FB (Kg plant ⁻¹)	MFSR (Kg plant ⁻¹)	HI	^a DPWP	LCC (mgcm ⁻²)
Minimum	0.50	0.01	13.90	0.03	0.00	0.08	46	12.54
Mean	3.40	0.47	28.06	0.71	0.33	0.66	98	20.07
Maximum	8.00	1.76	36.23	2.41	1.76	0.99	65.1	29.19
E1(drought)	2.80	0.22	28.08	0.29	0.10	0.72	-	20.02
E2 (irrigated)	4.00	0.73	28.03	1.13	0.57	0.60	-	20.2
Site-Kiboko	4.00	0.51	29.9	0.77	0.36	0.68	-	19.10
Site-Thika	3.40	0.43	28.2	0.65	0.32	0.64	-	21.10
LSD _{0.05}	1.60	0.33	0.281	0.361	0.346	0.187	9.671	2.772

NSR = number of storage roots, FSR = fresh storage root weight, RDM = root dry matter, FB = fresh biomass weight, MFSR = marketable fresh storage root weight, HI = harvest index, ^aDPWP = days to permanent wilting point, evaluated in greenhouse therefore no data on environment (E) and sites, CC = leaf chlorophyll content.

The best three genotypes among the high ranking genotypes were 194555.7, 421066, and Chingova, which had FSR of 1.06, 1.05, and 0.94 kg plant⁻¹, respectively (Table 3.4; Appendix 1). Clones Kajamani, Kindolo, and K117, had the lowest yields of 0.11, 0.15, and 0.18 respectively (Table 3.4; Appendix 1).

3.3.6 Best performing genotypes under drought stress and no drought stress conditions

The means of the 84 genotypes were calculated by environment and ranked according to their performance for the traits observed and the best 12 genotypes in each environment identified (Table 3.5a; Appendices 2 and 3). The best three clones under no drought stress conditions were Chingova, Excel, and 420014 which had FSR of 1.56, 1.55 and 1.52 kgplant⁻¹ respectively. The best performing clones under no drought stress had a better performance than the local checks the same environment. The performance of the genotypes for the other traits is shown in table 3.5a. Genotypes 194555.7, W119, and Unawazambane06-01 performed best under the drought stress environment and had FSR of 0.58, 0.32, 0.3 kg plant⁻¹ respectively (Table 3.5 b; Appendix 2 and 3). Also, these clones performed better than the local checks. The performance of the other traits observed under drought stress environment is shown in Table 3.5b.

Table 3.4: Performance of sweetpotato clones across drought stress and no drought stress conditions

Genotype	FSR(kg plant ⁻¹)	% RDM	FB (kg plant ⁻¹)	MFSR (kg plant ⁻¹)	NSR plant ⁻¹	HI	CC mgcm ⁻²	Rank
Best performing genotypes								
194555.7	1.06	25.94	1.43	0.86	6.39	0.78	23.81	4
421066	1.05	28.09	1.36	0.48	1.86	0.76	21.39	3
Chingova	0.94	27.42	1.21	0.58	4.60	0.80	18.90	1
420014	0.91	28.57	1.23	0.78	3.53	0.79	21.87	2
Excel	0.90	26.52	1.13	0.73	4.92	0.80	19.46	11
1990621	0.87	28.39	1.17	0.41	4.41	0.79	21.52	8
189151.38	0.86	28.09	1.14	0.41	4.19	0.77	20.16	10
A56	0.84	27.79	1.02	0.47	4.02	0.84	18.40	12
Bosbok	0.69	30.15	0.95	0.52	4.90	0.70	19.42	7
Tanzania	0.66	29.19	0.89	0.60	4.75	0.75	19.40	5
Unawazambane06-01	0.65	28.90	0.87	0.48	5.17	0.78	18.04	6
W119	0.65	28.00	0.93	0.48	5.59	0.74	20.97	9
Mean	0.84	28.09	1.11	0.57	4.53	0.77	20.27	-
Least performing genotypes								
Polista	0.20	30.45	0.39	0.10	2.56	0.47	18.17	79
Okchio Dalani	0.26	26.77	0.50	0.21	2.77	0.58	21.40	73
Nyar Malo	0.24	27.18	0.45	0.16	2.55	0.56	19.17	81
Nyangangu	0.22	27.28	0.38	0.18	3.79	0.57	19.31	72
Namaswakhe	0.20	28.78	0.38	0.15	2.39	0.57	18.59	78
Maria-Angola	0.25	27.41	0.48	0.22	3.02	0.53	18.86	76
Mafuta	0.23	27.28	0.44	0.20	2.72	0.54	18.91	75
Kindolo	0.15	28.82	0.34	0.11	2.28	0.49	18.75	82
Kajamani	0.11	28.86	0.30	0.06	2.06	0.49	18.82	84
Kabut-Jolweny	0.21	29.66	0.47	0.18	2.71	0.52	20.97	74
K117	0.18	27.89	0.43	0.12	2.10	0.49	18.99	83
Jayalo	0.21	29.22	0.46	0.08	1.84	0.50	18.87	80
Mean	0.20	28.30	0.42	0.15	2.56	0.52	19.23	-
Performance of checks								
Gatumbi	0.23	27.28	0.44	0.20	2.72	0.54	21.4	25
Marooko	0.40	25.59	0.67	0.23	3.54	0.57	18.91	31
Mean	0.31	26.43	0.55	0.22	3.13	0.55	20.16	-
Overall mean	0.47	28.06	0.71	0.33	3.38	0.66	20.07	-
LSD _{0.05}	1.08	0.23	1.97	0.26	0.25	0.13	1.97	
CV%	26.10	35.50	9.30	19.40	24.50	15.60	15.60	

NSR = number of storage roots, FSR = fresh storage root weight, RDM = root dry matter, FB = fresh biomass weight, MFSR = marketable fresh storage root weight, HI = harvest index, LCC = leaf chlorophyll content, and rank = $\sum_{k=1}^n x$, where x is the sum of genotype rank in each trait measured, where k = rank in trait 1, and n = rank of the last trait. Thus, the best genotype in each trait scored one, while the worst scored 84, which indicates that, considering more than one trait, then the best genotype had the least cumulative scores while the worst had the most cumulative scores.

Table 3.5a: Best performing genotypes under no drought stress condition

Genotype	FSR(kg plant ⁻¹)	% RDM	FB (kg plant ⁻¹)	MFSR (kg plant ⁻¹)	NSR plant ⁻¹	HI	CC mg/cm ²	Rank
Chingova	1.56	26.85	2.01	1.03	5.24	0.78	19.11	1
Excel	1.55	26.03	1.95	1.36	5.53	0.80	19.49	2
420014	1.52	28.81	2.11	1.47	5.10	0.72	20.62	3
Gatumbi	1.26	26.50	1.52	1.19	3.80	0.83	20.49	4
Beauregard	1.50	25.92	2.04	1.45	4.25	0.74	21.03	5
A56	1.49	27.51	1.83	0.89	6.26	0.82	17.10	6
194555.7	1.54	27.71	2.20	1.43	6.57	0.70	23.41	7
189150.1	1.11	26.96	1.44	0.85	6.39	0.77	20.67	8
189151.38	1.46	28.50	1.94	0.76	5.86	0.76	17.93	9
420006	1.49	25.47	1.84	0.68	6.54	0.82	17.80	10
Tanzania	1.10	29.33	1.49	1.05	5.45	0.75	19.80	11
441725	1.02	25.86	1.36	0.96	5.32	0.76	21.08	12
Mean for genotypes	1.38	27.12	1.81	1.09	5.52	0.77	19.87	-
Checks								
Gatumbi	1.26	26.50	1.52	1.19	3.80	0.83	20.49	-
Marooko	0.85	30.35	1.43	0.51	3.49	0.61	20.66	-
Mean for checks	1.05	28.42	1.47	0.85	3.64	0.72	20.57	-
Overall Mean	4.0	28.0	1.1	0.6	0.6	4.0	20.0	
LSD _{0.05}	1.5	0.3	3.6	0.3	0.3	0.2	4.1	
CV%	26.6	26.1	9.3	20.3	38.2	18.3	14.8	

Note: The abbreviations of the traits measured and ranking are as indicated in Table 3.4

Table 3.5b: Best performing genotypes under drought stress conditions

Genotypes	FSR(kg plant ⁻¹)	% RDM	FB (kg plant ⁻¹)	MFSR (kg plant ⁻¹)	NSR plant ⁻¹	HI	CC mg/cm ²	Rank
194555.7	0.58	26.17	0.67	0.30	6.21	0.86	23.41	1
W119	0.32	27.84	0.39	0.22	5.86	0.81	21.27	2
Unawazambane06-01	0.30	28.25	0.37	0.18	4.98	0.81	17.44	3
KILUNGU	0.96	30.63	1.08	0.39	3.28	0.83	20.66	4
441725	0.27	27.68	0.29	0.18	4.18	0.91	21.08	5
Chingova	0.33	27.99	0.40	0.12	3.96	0.81	19.11	6
48 Gabagaba	0.48	30.12	0.61	0.34	2.32	0.77	20.93	7
Bosbok	0.25	29.57	0.42	0.15	5.06	0.64	18.57	8
Tanzania	0.21	29.05	0.28	0.15	4.06	0.76	19.80	9
Xiadla-xa-kau	0.24	28.78	0.33	0.17	3.59	0.72	22.73	10
Munyilia 3	0.37	28.57	0.47	0.23	2.83	0.77	19.29	11
189150.1	0.28	26.03	0.34	0.12	3.75	0.82	20.67	12
Mean for genotypes	0.38	28.39	0.47	0.21	4.17	0.79	20.41	
% reduction	72.5	-4.7	74.0	80.7	24.5	-2.6	-2.7	
Checks								
Marooko	0.36	30.17	0.42	0.26	1.51	0.84	20.66	-
Gatumbi	0.11	27.62	0.15	0.08	1.69	0.75	20.49	-
Mean for checks	0.23	28.89	0.29	0.17	1.60	0.79	20.57	-
Overall Mean	0.2	28.1	0.3	0.1	2.8	0.7	20.0	
LSD _{0.05}	1.4	0.2	3.6	0.2	0.1	0.2	3.7	
CV%	35.4	67.8	9.1	53.1	71.1	18.7	13.2	

Note: The abbreviations of the traits measured and rankings are as indicated in Table 3.4

3.3.7 Poor performing genotypes under drought stress and no drought stress conditions

The lowest ranked three clones under the no drought stress environment were Nyar-Malo, KSP 20, and Maria-Angola, which had FSR of 0.4, 0.5 and 0.38 kg plant⁻¹ respectively. These clones were ranked lower than the local checks (Table 3.6a; Appendix 2 and 3). The performance of the clones for the other traits is shown in table 3.5b. The lowest performing three genotypes under drought stress conditions were 420006, Wera, and Nyamilambo, which had FSR of 0.13, 0.09 and 0.1Kg plant⁻¹ respectively and performed lower than the checks. The performance of the best 12 clones under drought stress and no drought stress condition showed 24.1 - 74.1% reduction in FSR, FB, MFSR and NSR, but 4.5 - 47.4% increment in HI due to drought stress (Table 3.6b; Appendix 2 and 3).

Table 3.6a: Poor performing genotypes under no drought stress conditions

Genotype	FSR(Kg plant ⁻¹)	% RDM	FB (Kg plant ⁻¹)	MFSR (Kg plant ⁻¹)	NSR plant ⁻¹	HI	CC mgcm ⁻²	Rank
Nyar Malo	0.40	28.12	0.79	0.26	2.98	0.52	18.52	1
Ksp 20	0.15	27.80	0.40	0.14	4.50	0.39	20.42	2
Maria Angola	0.38	27.00	0.74	0.35	3.57	0.43	17.96	3
Kalamb Nyerere	0.27	27.29	0.56	0.20	4.22	0.47	18.47	4
Polista	0.35	29.93	0.68	0.18	3.28	0.52	17.95	5
Namaswakhe	0.27	29.51	0.59	0.22	2.43	0.44	18.59	6
Kilungu	0.28	29.72	0.67	0.28	3.46	0.42	20.66	7
Kabut Jolweny	0.22	28.32	0.63	0.22	3.22	0.36	22.04	8
Jayalo	0.12	28.48	0.52	0.09	1.31	0.24	18.36	9
Kindolo	0.12	28.89	0.41	0.09	3.07	0.29	19.94	10
K117	0.12	26.59	0.55	0.11	1.36	0.23	18.62	11
Kajamani	0.10	27.33	0.43	0.07	2.49	0.24	18.26	12
Mean	0.23	28.25	0.58	0.18	2.99	0.38	19.15	
<i>Performance of checks under no drought stress condition</i>								
Gatumbi	1.26	26.50	1.52	1.19	0.83	3.80	20.49	-
Marooko	0.85	30.35	1.43	0.51	0.61	3.49	20.66	-
Mean	1.05	28.42	1.47	0.85	0.72	3.64	20.57	-
Overall Mean	4.0	28.0	1.1	0.6	0.6	4.0	20.0	
LSD _{0.05}	1.5	0.3	3.6	0.3	0.3	0.2	4.1	
CV%	26.6	26.1	9.3	20.3	38.2	18.3	14.8	

Note: The abbreviations of the traits measured and ranking are as indicated in Table 3.4

Table 3.6b: Poor performing genotypes under drought stress conditions

Genotype	FSR(Kg plant ⁻¹)	% RDM	FB (Kg plant ⁻¹)	MFSR (Kg plant ⁻¹)	NSR plant ⁻¹	HI	CC mgcm ⁻²	Rank
420006	0.13	25.40	0.21	0.07	0.98	0.61	17.80	1
Wera	0.09	26.77	0.13	0.03	2.84	0.66	17.88	2
Nyamilambo	0.10	26.89	0.20	0.06	3.11	0.47	20.93	3
Okchio Dalani	0.10	25.97	0.17	0.07	2.23	0.64	21.58	4
Mulware 1	0.09	26.30	0.14	0.06	2.53	0.64	18.06	5
Nyangangu	0.08	27.37	0.14	0.03	3.15	0.56	18.21	6
Nyar Kamaa	0.09	27.20	0.20	0.05	2.46	0.43	19.46	7
Amina	0.06	28.63	0.11	0.05	1.39	0.58	17.34	8
Nduma	0.12	25.17	0.16	0.04	2.21	0.71	21.89	9
Nyar Kangonga	0.09	27.13	0.20	0.00	2.35	0.48	21.77	10
Polista	0.04	30.97	0.10	0.02	1.85	0.40	17.95	11
Nyar Malo	0.07	26.24	0.12	0.05	2.13	0.61	18.52	12
Mean	0.09	27.00	0.15	0.04	2.27	0.56	19.28	
Performance of checks under no drought stress condition								
Marooko	0.36	30.17	0.42	0.26	1.51	0.84	20.66	-
Gatumbi	0.11	27.62	0.15	0.08	1.69	0.75	20.49	-
Mean	0.23	28.89	0.29	0.17	1.60	0.79	20.57	-
% reduction	60.9	4.4	74.1	77.8	24.1	-47.4	-0.7	-
Overall mean	0.2	28.1	0.3	0.1	2.8	0.7	20.0	-
LSD _{0.05}	1.4	0.2	3.6	0.2	0.1	0.2	3.7	-
CV%	35.4	67.8	9.1	53.1	71.1	18.7	13.2	-

Note: The abbreviations of the traits measured are as indicated in Table 3.4

3.3.8 Days to permanent wilting point

The mean number of days to permanent wilting point (DPWP) of best 12 clones under drought stress was 73. The clones under drought stress environment with DPWP above 79 were W119, 441725, and Xiadla-xa-kau. Genotypes within the overall mean plus LSD_{0.05} value (73 +3 to +5.9) under drought stress were; Unawasambane06-1, Tanzania, Chingova, and 189150.1. Clone above the overall mean 73 DPWP by up to half the LSD value (by +0.1 to +3) under drought stress was 194555.7. The clone Chingova, Excel and 420014 were highest ranking under no drought stress environment while, Chingova, 420014, and 421066 were the highest ranking under overall environment evaluation (Table 3.7).

Table 3.7: The twelve best and poor performing sweetpotato clones across environments, under drought stress and, no drought stress environments and their days to permanent wilting point (DPWP) determined under rapid drought screening box experiments in greenhouse

Ranks	Across environments		Irrigated environment		Drought environment	
	Clone	DPWP	Clone	DPWP	Clone	DPWP
Highest performing clones						
1	Chingova	78	Chingova	78	194555.7	75
2	420014	77	Excel	66	W119	81
3	421066	70	420014	77	Unawazambane06-	76
4	194555.7	75	Gatumbi	72	KILUNGU	53
5	Tanzania	78	Beauregard	71	441725	81
6	Unawazambane06-01	76	A56	67	Chingova	78
7	Bosbok	67	194555.7	75	48 Gabagaba	66
8	1990621	67	189150.1	78	Bosbok	67
9	W119	81	189151.38	71	Tanzania	78
10	189151.38	71	420006	67	Xiadla-xa-kau	81
11	Excel	66	Tanzania	78	Munyilia 3	64
12	A56	67	441725	81	189150.1	78
	Mean	73		73		73
Lowest performing clones						
1	Kajamani	55	Nyar Malo	55	420006	67
2	K117	55	Ksp 20	67	Wera	65
3	Kindolo	55	Maria Angola	57	Nyamilambo	57
4	Nyar Malo	55	Kalamb Nyerere	62	Okchio Dalani	62
5	Jayalo	56	Polista	52	Mulware 1	62
6	Polista	52	Namaswakhe	61	Nyangangu	61
7	Namaswakhe	61	Kilungu	53	Nyar Kamaa	57
8	Maria-Angola	57	Kabut Jolweny	56	Amina	63
9	Mafuta	64	Jayalo	56	Nduma	57
10	Kabut-Jolweny	56	Kindolo	55	Nyar Kangonga	59
11	Okchio Dalani	62	K117	55	Polista	52
12	Nyangangu	61	Kajamani	55	Nyar Malo	55
	Mean	57		57		60
Checks						
1	Gatumbi	58				
2	Marooko	88				
	Mean	73				
	Overall mean	65				
	LSD0.05	6				
	CV%	11				

DPWP=days to permanent wilting point and rank = $\sum_{k=1}^n x$, where x is the sum of genotype rank in each trait measured, where k = rank in trait 1, and n = rank of the last trait. Thus, the best genotype in each trait scored one, while the worst scored 84 (all genotypes were 84), which indicates that, considering more than one trait, then the best genotype had the least cumulative scores while the worst had the most cumulative scores.

3.3.9 Drought susceptibility index for the best performing genotypes across the environments

Based on the total number of storage roots, all the twelve high yielding genotypes had DSI < 1 (Table 3.8; Appendix 3.4). The DSI calculated for genotypes Chingova, 441745, Xiadla-Xa-Kau and Bosbok was >1. Genotype 194555.7, Unawazambane06-01, 441725, Tanzania, Chingova, had DSI <1 under drought stress and no drought stress environments. The best performing clones under drought stress conditions were Kilungu, Munyilia-3, 48-Gabagaba and Marooko and had the lowest DSI (Table 3.8; Appendix 3.4).

Table 3.8: The DSI for the most productive genotypes across environments

DSI of the top ranked clones in drought stress environment				Clones with lowest DSI			
Clones	NSR plant ⁻¹	FB (kg plant ⁻¹)	MFSR (kg plant ⁻¹)	Clones	NSR plant ⁻¹	FB (kg plant ⁻¹)	MFSR (kg plant ⁻¹)
194555.7	0.93	0.82	0.98	Kilungu	0.96	0.11	0.15
W119	0.96	0.86	0.88	Jayalo	0.95	0.28	0.25
Unawazambane06-01	0.97	0.86	0.95	Munyilia 3	0.94	0.56	0.49
Kilungu	0.95	0.11	0.16	Kabut Jolweny	0.97	0.60	0.34
441725	0.97	0.92	1.10	K117	0.94	0.52	0.40
Chingova	0.96	0.94	1.01	48 Gabagaba	0.90	0.71	0.43
48 Gabagaba	0.89	0.69	0.47	K37	0.96	0.55	0.83
Marooko	0.92	0.83	0.60	Kindolo	0.98	0.47	0.36
Bosbok	0.97	0.85	1.04	Kamoko	0.96	0.65	0.56
Xiadla-Xa-Kau	0.96	0.85	1.06	Marooko	0.93	0.85	0.54
Tanzania	0.99	0.95	0.97	Saly Boro	0.96	0.81	0.71
Munyilia 3	0.93	0.54	0.54	Kajamani	0.99	0.70	0.48

DSI = drought sensitivity index, the rest of the abbreviations are as indicated in Table 3.4

3.4 Discussion

3.4.1 Weather and soil conditions

At both Kiboko and Thika, planting was done towards the end of the rainy season and irrigation water applied for the no drought stress environment. The temperatures were adequate for sweetpotato growth, though slightly higher in Kiboko than in Thika. The relative humidity was 80% at Kiboko indicating that the air was moist, which reduced the evapo-transpiration while in Thika, the relative humidity ranged from 50-80% indicating that the air was drier and thus depending on wind speed, sunlight intensity and cloud cover, there could have been more evapo-transpiration. However, due to lower temperatures at Thika, irrigation requirements of the crop seemed to be lower.

In the greenhouse the mean temperature (24.5°C), was suitable for sweetpotato growth. This is in agreement with the findings of Belehu (2003) who reported that root growth was optimum at temperature of 24°C. The maximum temperatures of 35°C attained could probably be due to greenhouse effect and this simulated the ideal situation of arid and semi-arid drought prone areas. The relative humidity ranged from 45-89.5%, which indicates evapo-transpiration was active largely all the time but at reduced rate as the relative humidity tended towards 100%. Mean light intensity largely ranged from 5000-17,500 lux which indicates that the light intensity was sufficient for evapo-transpiration and photosynthesis requirements of the sweetpotato, thus the light intensity was ideal for screening these genotypes for drought. Fluctuating cloud cover, and changing weather and seasons, which were uncontrollable, caused frequent lapses of the light intensity. Leghari et al. (2005) reported increased photosynthesis, leaf size, dry matter and yield of beans with increase of light intensity from 10,000 lux to 15,000 lux indicating that the light intensity in the greenhouse study was probably sufficient.

The mean dew point temperature was 14.25°C. This shows that there was dew in the greenhouse at temperature around 14.5°C, upon which the dew settled on the sweetpotato plants and cooled them and moistened the soil surface on the boxes. This may also suggest that the genotypes that had high yield under moisture stress regimes had positive response to cooling from the dew point dew or water.

Soils in both Kiboko and Thika had low %N, hence inorganic N was applied to correct the deficiency. The soil pH at Thika was slightly alkaline, and thus had higher amount of sodium (Na) and calcium (Ca) elements associated with alkalinity. However, their levels were not toxic and thus did not significantly affect crop growth. Magnesium availability was low but not to the level of negatively affecting the growth of the crop.

3.4.2 Performance of genotypes

The clones differed significantly for fresh storage root weight but they did not differ significantly for number of storage roots produced. This is probably because the moisture stress only hindered the bulking of the storage roots and not the number of storage roots produced. These experiments uncovered a wide range of minimum and maximum performance within clones and across environments for most of the traits observed indicating both phenotypic and genotypic diversity of the clones. The clones were comprised of local unimproved landraces, breeders' materials and improved clones and presumably represented a diverse set of genetic materials. Similar diversity was reported in evaluation

studies for yield of mustard seed under irrigated and drought environments (Chauhan et al., 2007).

Significant genotype x environment interaction (GEI) were observed for most of the traits an indication that genotypes varied from broad to specific adaption to the tested environments. Genotypes 194555.7, Unawazambane06-01, 441725, Tanzania, and Chingova ranked high (had high storage root yield), in both drought stress and no drought stress environment, and had DSI <1, which could suggest they are drought tolerant. The clones could also be used by farmers in dry areas with inadequate and unreliable rainfall to improve production. These findings are supported by those of Agili et al. (2012) who reported that clone 441725 had high yield and was stable in different sites in Kenya.

3.4.3 Genotype performance under irrigated and non-irrigated environment

These experiments demonstrated that drought stress suppressed the root size leading to smaller sized unmarketable storage roots. Thus production of sweetpotato for commercial purpose in areas with poor rainfall would require use of drought tolerant varieties. Furthermore, the results showed reduced biomass under drought stress, an indication that the photosynthesis was low which led to reduced vine growth and hence low vine biomass. The reduction in biomass observed was less in the drought tolerant clones. Comparing mean performance of the twelve best and twelve poor performing clones under drought and no drought environment; there was a 24.5-80% reduction in FSR, FB, MFSR and NSR. The results agree with the findings by Mall et al. (2012), who reported a yield reduction of 65-80% in rice grown under drought stress and no drought stress regimes. Genotypes Chingova, 194555.7, Tanzania and 441725 gave high yield and performed better than the local checks in both drought stress and no drought stress environments. These clones may be incorporated in breeding programmes for drought tolerance as donor parents.

3.4.4 Days to permanent wilting point

The clones with DPWP above 79 were W119, 441725, and Xiadla-xa-kau. These genotypes were rated as drought tolerant in both greenhouse and field screening. Agili et al. (2012), reported clone 441725 to be drought tolerant. Laurie et al. (2004) reported W119 as drought tolerant, while Recardo (2011) found Xiadla-xa-kau to perform better than other clones under drought stress. In this study, clone 441725 was also among the best in the no drought stress environment indicating it is stable and high yielding. These clones could be incorporated into crossing blocks designed to improve drought tolerance in sweetpotato breeding populations. Xiadla-xa-kau was not among the best in the overall mean production or best in production under no drought stress condition and therefore, its yielding ability still needs to be improved. However, W119 appeared among the highest under both drought

stress and no drought stress conditions, indicating it was an average yielder and probably its yielding ability needed to be improved.

Genotypes Chingova, Tanzania, and 189150.1 appeared among the highest yielding under no drought stress indicating that they probably were stable across environments. These genotypes could also be included in breeding programmes for drought and yield improvement. Clone Unawasamabneo6-1 only appeared among overall best clones across environments indicating its yielding ability was average and probably needed improvement. Clones that were above average by 0 to 3, under drought stress, may be described as neutral to drought tolerant. Among the twelve clones only 194555.7 appeared to be neutral to drought tolerance. This clone also appeared among the best in the no drought stress and overall mean performance across the environment, an indication it was high yielding. Thus clones 194555.7 and 441725, can be further evaluated for other important traits and if found good, promoted to farmers for boosting production.

Permanent wilting point (PWP) in plants occurs at soil moisture tension of -1.5 megapascals (Mpa). At PWP, soil water is held tight by soil capillary forces such that it is not available for plant use (Hillel, 1982; O'Geen, 2012). This shows that the plant under this drought stress selection pressure must devise a mechanism of survival. The results of this work reveal the ability of the individual genotypes to survive at PWP drought stress and beyond. Therefore the more the crop survives the more tolerant to drought it may be. These findings therefore, imply that days to permanent wilting point under rapid drought screening may have high discriminative power for identification of drought tolerant genotypes.

3.4.5 Drought susceptibility index for the best performing genotypes across the environments

The clones that took a few DPWP in the rapid drought screening experiment, had low yield across the environment and a DSI of >1 , an indication that they were drought susceptible. Additionally, these clones had lower HI because their yield was affected more by drought. DSI calculated using number of storage roots was in most cases < 1 , which showed that numbers of roots were not significantly affected by moisture stress especially if the stress occurred after establishment of the vines. Contrary, the high yielding clones typically took more days to permanent wilting point, had high HI and DSI <1 an indication that they are possibly drought tolerant. These results were similar to those by Chauhan et al. (2007) who based on DSI, identified high yielding genotypes with DSI <1 that could be used as donors for drought tolerance in a breeding programme. Therefore, genotypes that had DSI <1 in both environments in this study (194555.7, Unawazambane06-01, 441725, Tanzania, Chingova, Kilungu, Munyilia-3, 48-Gabagaba and Marooko), could be incorporated in a

breeding programme as donors for drought tolerance. This is also supported by Mall et al. (2012) who in their study emphasised the use of DSI as a useful tool for selecting parents for drought tolerant populations and also identifying genotypes suitable for commercial cultivation under different water regimes.

3.5 Conclusion

Genotypes 194555.7, 421066, Chingova, 420014, Excel, 199062.1, and Unawazambane06-01 performed well across environments. HI was higher in high yielding genotypes relative to poor yielding genotypes. Genotypes that took more days to permanent wilting point could also be drought tolerant. A wide range of mean minimum and maximum performance occurred within genotypes and across environments on all the traits because the clones comprised of local unimproved landraces, breeders' material and improved clones. Clones that performed well in both stress and non-stressed environments could be drought tolerant and stable across different rainfall zones and therefore, could be used to mitigate drought stress. In conclusion, the varieties that showed drought tolerance, may further be tested in multiple sites to validate their tolerance for use in drought areas, or their use as parents in breeding programmes aimed at improving drought tolerance.

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Appendix

Appendix 3.1: Mean performance of the 84 genotypes and their ranking across drought stress and no drought stress environments.

Rank	Genotype	NSR plant ⁻¹	FSR(kg plant ⁻¹)	% RDM	FB (kg plant ⁻¹)	MFSR (kg plant ⁻¹)	HI	DPWP	CC mgcm ⁻²
1	Chingova	4.60	0.94	27.42	1.21	0.58	0.80	78.25	18.90
2	420014	3.53	0.91	28.57	1.23	0.78	0.79	76.88	21.87
3	421066	1.86	1.05	28.09	1.36	0.48	0.76	69.62	21.39
4	194555.7	6.39	1.06	25.94	1.43	0.86	0.78	74.88	23.81
5	Tanzania Unawazambane06-	4.75	0.66	29.19	0.89	0.60	0.75	78.00	19.40
6	01	5.17	0.65	28.90	0.87	0.48	0.78	76.00	18.04
7	Bosbok	4.90	0.69	30.15	0.95	0.52	0.70	67.38	19.42
8	1990621	4.41	0.87	28.39	1.17	0.52	0.79	67.38	21.52
9	W119	5.59	0.65	28.00	0.93	0.52	0.74	81.25	20.97
10	189151.4	4.19	0.86	28.09	1.14	0.52	0.77	70.62	20.16
11	Excel	4.92	0.90	26.52	1.13	0.52	0.80	65.88	19.46
12	A56	4.02	0.84	27.79	1.02	0.52	0.84	67.25	18.40
13	189150.1	5.07	0.69	26.50	0.89	0.52	0.80	78.38	21.30
14	441725	4.76	0.64	26.77	0.83	0.52	0.84	81.38	20.71
15	A2	3.57	0.79	29.68	1.14	0.52	0.74	56.75	20.71
16	48 Gabagaba	2.93	0.72	29.81	1.05	0.52	0.70	66.25	21.79
17	422656	3.96	0.63	26.19	0.86	0.52	0.80	80.38	20.58
18	Lodha	2.97	0.79	27.22	1.11	0.52	0.76	67.88	20.96
19	Beauregard	2.80	0.87	26.75	1.18	0.52	0.73	71.25	21.47
20	Sinia	4.11	0.49	28.43	0.72	0.52	0.73	73.75	21.47
21	Nyatonge	2.59	0.69	30.02	0.92	0.52	0.73	66.75	20.16
22	Resisto	4.41	0.63	27.18	0.82	0.52	0.80	65.38	19.29
23	Xiadla-xa-kau	3.54	0.51	28.09	0.76	0.52	0.69	80.50	22.48
24	194573.9	2.85	0.81	28.15	1.18	0.52	0.72	66.50	21.41
25	194515.2	2.74	0.68	27.06	0.84	0.52	0.79	72.12	20.08
26	Canassumana	2.81	0.65	29.48	0.95	0.52	0.74	62.88	21.60
27	71 lo-323-1	4.15	0.58	28.16	0.81	0.52	0.71	66.50	21.39
28	Nyar buholo	4.93	0.42	27.69	0.59	0.52	0.76	81.50	20.45
29	Bulindo	3.82	0.58	27.48	0.80	0.52	0.77	72.25	19.08
30	19901513	3.72	0.68	27.40	1.00	0.52	0.70	65.38	22.68
31	Cheguna mowar	2.50	0.60	30.26	0.93	0.52	0.72	66.62	21.34
32	Bikira maria	2.78	0.75	25.17	0.95	0.52	0.78	75.25	21.47
33	420006	3.76	0.81	25.44	1.02	0.52	0.71	66.50	17.97
34	Kilungu	3.37	0.62	30.17	0.87	0.52	0.62	63.00	20.49
35	Mugande	3.96	0.45	30.74	0.68	0.52	0.69	60.88	20.41
36	105268-1	2.74	0.40	30.69	0.63	0.52	0.68	65.12	21.70
37	Munyilia 3	3.39	0.39	29.42	0.67	0.52	0.62	63.50	19.27
38	Gikanda	2.19	0.40	28.71	0.74	0.52	0.63	75.50	19.67

Rank	Genotype	NSR plant ⁻¹	FSR(kg plant ⁻¹)	% RDM	FB (kg plant ⁻¹)	MFSR (kg plant ⁻¹)	HI	DPWP	CC mgcm ⁻²
39	Ksp-28	3.92	0.38	29.99	0.64	0.52	0.60	61.38	20.11
40	Unknown 1	3.87	0.38	28.58	0.67	0.52	0.61	58.50	21.20
41	Amina	2.34	0.43	28.71	0.61	0.52	0.64	63.12	18.93
42	Nyaluolo	3.21	0.31	30.87	0.50	0.52	0.62	64.12	20.41
43	Tororo	4.31	0.26	30.68	0.40	0.52	0.67	64.88	17.78
44	Mwavuli	2.69	0.33	29.35	0.52	0.52	0.69	65.75	20.59
45	Wera	3.62	0.32	27.71	0.50	0.52	0.64	64.50	18.56
46	Yanshu 1	2.65	0.37	28.88	0.65	0.52	0.60	62.00	20.65
47	Spk 004	3.28	0.34	27.82	0.52	0.52	0.67	62.50	17.82
48	New kawogo	2.86	0.30	29.80	0.44	0.52	0.70	61.75	17.70
49	K37	3.64	0.34	28.92	0.60	0.52	0.61	62.38	20.96
50	Tis 70357	3.77	0.40	25.54	0.64	0.52	0.62	64.25	18.87
51	Sunjuki	2.64	0.32	28.37	0.43	0.52	0.74	72.25	17.12
52	Ondiek chilo	2.74	0.35	28.83	0.62	0.52	0.59	62.75	21.15
53	W-220	2.67	0.34	28.69	0.54	0.52	0.68	64.88	18.97
54	W217	3.03	0.40	26.01	0.64	0.52	0.68	64.62	20.65
55	Mafuta	4.59	0.36	25.82	0.64	0.52	0.61	61.50	21.10
56	Unknown	4.17	0.30	27.86	0.55	0.52	0.60	57.75	20.14
57	Utugu 2	3.56	0.30	26.69	0.51	0.52	0.63	63.75	19.46
58	Kamoko	2.69	0.31	29.77	0.58	0.52	0.53	57.50	20.69
59	Mulware 1	2.84	0.31	26.89	0.53	0.52	0.60	61.88	18.31
60	Nyar kangonga	3.15	0.31	27.83	0.54	0.52	0.53	58.50	22.18
61	Marooko	3.54	0.40	25.59	0.67	0.52	0.57	88.50	21.40
62	Saly boro	2.82	0.29	26.62	0.53	0.52	0.64	65.12	20.68
63	Miezi tatu	2.59	0.35	26.78	0.61	0.52	0.56	59.00	20.92
64	Naveto	3.11	0.33	25.60	0.65	0.52	0.56	58.75	21.13
65	Ksp 20	4.14	0.16	27.47	0.32	0.52	0.55	67.25	19.02
66	Mwei munene	2.40	0.28	28.87	0.45	0.52	0.68	59.12	18.01
67	Nyar kamaa	3.18	0.35	26.38	0.59	0.52	0.53	57.25	20.47
68	Kalamb nyerere	3.20	0.21	28.07	0.39	0.52	0.61	62.25	18.47
69	Nguroiwe	2.72	0.27	28.09	0.43	0.52	0.65	60.50	18.29
70	Nyamilambo	3.12	0.27	27.37	0.51	0.52	0.51	57.00	19.60
71	Unknown 2	2.91	0.27	27.33	0.46	0.52	0.64	57.00	19.52
72	Nyangangu	3.79	0.22	27.28	0.38	0.52	0.57	60.50	19.31
73	Kabut jolweny	2.71	0.21	29.66	0.47	0.52	0.52	56.38	20.97
74	Okchio dalani	2.77	0.26	26.77	0.50	0.52	0.58	62.12	21.40
75	Gatumbi	2.72	0.23	27.28	0.44	0.52	0.54	58.25	18.91
76	Maria angola	3.02	0.25	27.41	0.48	0.52	0.53	57.00	18.86
77	Nduma	2.55	0.29	25.97	0.53	0.52	0.62	57.00	21.27
78	Namaswakhe	2.39	0.20	28.78	0.38	0.52	0.57	61.25	18.59
79	Polista	2.56	0.20	30.45	0.39	0.52	0.47	52.00	18.17
80	Jayalo	1.84	0.21	29.22	0.46	0.52	0.50	56.25	18.87

Rank	Genotype	NSR plant ⁻¹	FSR(kg plant ⁻¹)	% RDM	FB (kg plant ⁻¹)	MFSR (kg plant ⁻¹)	HI	DPWP	CC mgcm ⁻²
81	Nyar malo	2.55	0.24	27.18	0.45	0.52	0.56	54.50	19.17
82	Kindolo	2.28	0.15	28.82	0.34	0.52	0.49	55.25	18.75
83	K117	2.10	0.18	27.89	0.43	0.52	0.49	54.62	18.99
84	Kajamani	2.06	0.11	28.86	0.30	0.52	0.49	54.50	18.82
	Mean	3.4	0.5	28.1	0.7	0.5	0.7	65.4	20.1
	LSD	1.5	0.3	0.3	0.4	0.3	0.2		2.8
	% CV	26.1	35.5	9.3	19.4	24.5	15.6		15.6

NSR= number of storage roots, FSR=fresh storage root weight, RDM= root dry matter, FB= fresh biomass weight, MFSR= marketable fresh storage root weight, HI= harvest index, DPWP=days to permanent wilting point, LCC= leaf chlorophyll content, and rank = $\sum_{k=1}^n x$, where x is the sum of genotype rank in each trait measured, where k = rank in trait 1, and n = rank of the last trait. Thus, the best genotype in each trait scored one, while the worst scored 84, which indicates that, considering more than one trait, then the best genotype had the least cumulative scores while the worst had the most cumulative scores.

Appendix 3.2: Mean performance of the 84 genotypes and their ranking in no drought stress environment.

Ranking	Genotype	FSR(kg plant ⁻¹)	% RDM	FB (kg plant ⁻¹)	MFSR (kg plant ⁻¹)	NSR plant ⁻¹	HI	CC mgcm ⁻²
1	Chingova	1.56	26.85	2.01	1.03	0.78	5.24	19.11
2	Excel	1.55	26.03	1.95	1.36	0.80	5.53	19.49
3	420014	1.52	28.81	2.11	1.47	0.72	5.10	20.62
4	Gatumbi	1.26	26.50	1.52	1.19	0.83	3.80	20.49
5	Beauregard	1.50	25.92	2.04	1.45	0.74	4.25	21.03
6	A56	1.49	27.51	1.83	0.89	0.82	6.26	17.10
7	194555.7	1.54	27.71	2.20	1.43	0.70	6.57	23.41
8	189150.1	1.11	26.96	1.44	0.85	0.77	6.39	20.67
9	189151.38	1.46	28.50	1.94	0.76	0.76	5.86	17.93
10	420006	1.49	25.47	1.84	0.68	0.82	6.54	17.80
11	Tanzania	1.10	29.33	1.49	1.05	0.75	5.45	19.80
12	441725	1.02	25.86	1.36	0.96	0.76	5.32	21.08
13	Bikira maria	1.19	24.57	1.49	0.72	0.80	4.17	22.60
14	Nyatonge	1.31	28.33	1.73	0.90	0.76	3.62	19.77
15	Lodha	1.33	27.17	1.92	0.97	0.70	4.16	21.33
16	Bosbok	1.12	30.74	1.49	0.89	0.75	4.73	18.57
17	1990621	1.31	28.84	1.84	0.80	0.72	6.13	22.07
18	Unawazambane06-01	1.01	29.55	1.36	0.77	0.74	5.37	17.44
19	422656	0.99	26.10	1.42	0.96	0.70	4.80	20.68
20	Resisto	1.03	28.54	1.35	0.76	0.77	4.62	18.39
21	W119	0.99	28.16	1.47	0.74	0.68	5.31	21.27
22	421066	1.08	27.45	1.62	0.94	0.64	2.11	20.39
23	Bulindo	0.96	26.38	1.34	0.51	0.72	4.59	18.38
24	71 lo-323-1	0.92	29.54	1.28	0.67	0.73	5.24	22.10
25	Xiadla-xa-kau	0.77	27.40	1.19	0.77	0.66	3.49	22.73
26	19901513	1.09	27.49	1.67	0.81	0.64	4.83	22.33
27	194573.9	1.18	27.74	1.82	0.58	0.65	3.96	21.49
28	A2	1.28	29.47	1.93	1.21	0.67	5.37	21.19
29	Sinia	0.77	28.79	1.17	0.77	0.66	4.19	23.48
30	Nyar buholo	0.66	27.73	0.94	0.50	0.71	4.49	19.38
31	Canassumana	0.98	29.16	1.52	0.81	0.65	3.50	22.06
32	Amina	0.79	28.79	1.13	0.79	0.70	3.29	17.34
33	48 Gabagaba	0.97	29.51	1.50	0.55	0.63	3.53	20.93
34	Marooko	0.85	30.35	1.43	0.51	0.61	3.49	20.66
35	105268-1	0.67	31.06	1.08	0.67	0.63	3.80	20.87
36	Sunjuki	0.51	29.10	0.67	0.35	0.79	3.46	17.93
37	Tis 70357	0.67	25.76	1.06	0.39	0.64	4.14	19.60
38	Spk 004	0.56	28.03	0.84	0.56	0.67	4.21	17.54
39	Gikanda	0.66	28.08	1.25	0.49	0.53	3.19	19.92
40	W217	0.61	25.44	1.03	0.42	0.62	2.89	21.20
41	Wera	0.55	28.65	0.88	0.55	0.63	4.38	17.88
42	Yanshu 1	0.59	28.88	1.05	0.59	0.58	2.61	22.24
43	New kawogo	0.49	29.95	0.73	0.48	0.68	2.96	18.28
44	Nyar kamaa	0.61	25.57	0.98	0.43	0.63	3.90	19.46
45	Ondiek chilo	0.58	28.26	1.05	0.44	0.56	2.81	21.49
46	Unknown 1	0.58	29.66	1.03	0.58	0.57	3.76	20.61
47	Utugu 2	0.53	27.33	0.90	0.44	0.59	2.80	19.02
48	W-220	0.52	28.35	0.88	0.37	0.60	3.15	17.67
49	Nyaluolo	0.47	30.95	0.76	0.47	0.61	3.00	21.02
50	Mulware 1	0.53	27.49	0.93	0.50	0.56	3.14	18.06
51	Miezi tatu	0.54	26.53	0.96	0.52	0.55	3.20	20.53
52	Nyar kangonga	0.53	28.52	0.89	0.50	0.59	3.95	21.77
53	Ksp-28	0.58	29.66	1.00	0.38	0.57	4.90	21.43
54	Cheguna mowar	0.62	25.70	1.00	0.37	0.60	3.76	21.12
55	Mwavuli	0.45	28.11	0.76	0.31	0.61	3.52	20.98

Ranking	Genotype	FSR(kg plant ⁻¹)	% RDM	FB (kg plant ⁻¹)	MFSR (kg plant ⁻¹)	NSR plant ⁻¹	HI	CC mgcm ⁻²
56	Tororo	0.39	30.74	0.63	0.26	0.62	4.43	16.89
57	Nguroiwe	0.45	28.25	0.74	0.27	0.61	2.59	19.57
58	Naveto	0.51	25.87	1.07	0.38	0.49	4.14	21.51
59	Mwei munene	0.45	29.26	0.77	0.28	0.59	2.48	17.17
60	194515.15	0.45	26.48	0.91	0.45	0.47	5.97	20.75
61	Nduma	0.47	26.78	0.90	0.39	0.55	2.89	21.89
62	Mugande	0.46	31.40	0.86	0.41	0.50	4.52	19.66
63	Munyilia 3	0.42	30.28	0.87	0.40	0.48	3.96	19.29
64	Nyamilambo	0.45	27.85	0.81	0.45	0.55	3.13	20.93
65	Okchio dalani	0.42	27.56	0.83	0.35	0.53	3.31	21.58
66	Unknown 2	0.45	24.97	0.80	0.32	0.57	2.55	19.01
67	Unknown	0.45	27.53	0.85	0.32	0.55	4.61	19.58
68	Nyangangu	0.36	27.19	0.61	0.32	0.59	4.42	18.21
69	Saly boro	0.38	27.54	0.80	0.26	0.49	2.84	21.69
70	Mafuta	0.35	26.59	0.71	0.35	0.46	3.37	18.53
71	Kamoko	0.36	30.14	0.80	0.36	0.44	3.44	21.82
72	K37	0.34	29.18	0.78	0.25	0.46	4.31	21.91
73	Nyar malo	0.40	28.12	0.79	0.26	0.52	2.98	18.52
74	Ksp 20	0.15	27.80	0.40	0.14	0.39	4.50	20.42
75	Maria angola	0.38	27.00	0.74	0.35	0.43	3.57	17.96
76	Kalamb nyerere	0.27	27.29	0.56	0.20	0.47	4.22	18.47
77	Polista	0.35	29.93	0.68	0.18	0.52	3.28	17.95
78	Namaswakhe	0.27	29.51	0.59	0.22	0.44	2.43	18.59
79	Kilungu	0.28	29.72	0.67	0.28	0.42	3.46	20.66
80	Kabut jolweny	0.22	28.32	0.63	0.22	0.36	3.22	22.04
81	Jayalo	0.12	28.48	0.52	0.09	0.24	1.31	18.36
82	Kindolo	0.12	28.89	0.41	0.09	0.29	3.07	19.94
83	K117	0.12	26.59	0.55	0.11	0.23	1.36	18.62
84	Kajamani	0.10	27.33	0.43	0.07	0.24	2.49	18.26
	Mean	0.73	28.04	1.13	0.62	0.61	4.03	20.01
	Lsd	1.51	0.32	3.60	0.33	0.31	0.22	4.13
	CV	26.60	26.12	9.32	20.31	38.23	18.32	14.81

Note: The abbreviations of the traits measured are as indicated in appendix 3.1

Appendix 3.3: Mean performance of the 84 genotypes and their ranking in no drought stress environments

Ranking	Genotype	FSR(kg plant ⁻¹)	% RDM	FB (kg plant ⁻¹)	MFSR (kg plant ⁻¹)	NSR plant ⁻¹	HI	CC mgcm ⁻²
1	194555.7	0.58	26.17	0.67	0.30	6.21	0.86	23.41
2	W119	0.32	27.84	0.39	0.22	5.86	0.81	21.27
3	Unawazambane06-01	0.30	28.25	0.37	0.18	4.98	0.81	17.44
4	Kilungu	0.96	30.63	1.08	0.39	3.28	0.83	20.66
5	441725	0.27	27.68	0.29	0.18	4.18	0.91	21.08
6	Chingova	0.33	27.99	0.40	0.12	3.96	0.81	19.11
7	48 Gabagaba	0.48	30.12	0.61	0.34	2.32	0.77	20.93
8	Marooko	0.36	30.17	0.42	0.26	1.51	0.84	20.66
9	Bosbok	0.25	29.57	0.42	0.15	5.06	0.64	18.57
10	Tanzania	0.21	29.05	0.28	0.15	4.06	0.76	19.80
11	Xiadla-xa-kau	0.24	28.78	0.33	0.17	3.59	0.72	22.73
12	Munyilia 3	0.37	28.57	0.47	0.23	2.83	0.77	19.29
13	189150.1	0.28	26.03	0.34	0.12	3.75	0.82	20.67
14	Mugande	0.45	30.08	0.49	0.04	3.39	0.89	19.66
15	422656	0.27	26.27	0.31	0.11	3.13	0.90	20.68
16	420014	0.30	28.34	0.35	0.09	1.96	0.86	20.62
17	Bulindo	0.21	28.58	0.26	0.14	3.06	0.81	18.38
18	Sinia	0.20	28.07	0.26	0.11	4.03	0.80	23.48
19	Canassumana	0.31	29.79	0.38	0.09	2.12	0.84	22.06
20	1990621	0.44	27.95	0.50	0.02	2.69	0.87	22.07
21	194573.9	0.44	28.56	0.54	0.09	1.73	0.79	21.49
22	421066	1.02	28.73	1.11	0.03	1.61	0.89	20.39
23	K37	0.34	28.66	0.43	0.07	2.98	0.77	21.91
24	A2	0.30	29.88	0.36	0.18	1.78	0.82	21.19
25	Excel	0.24	27.01	0.30	0.10	4.32	0.80	19.49
26	Nyar buholo	0.19	27.65	0.23	0.06	5.37	0.81	19.38
27	Resisto	0.23	25.80	0.28	0.12	4.19	0.84	18.39
28	Mwavuli	0.20	30.58	0.27	0.14	1.85	0.76	20.98
29	19901513	0.26	27.31	0.34	0.14	2.61	0.75	22.33
30	Lodha	0.25	27.27	0.30	0.14	1.78	0.83	21.33
31	189151.38	0.26	27.68	0.34	0.06	2.52	0.78	17.93
32	K117	0.24	29.18	0.32	0.14	2.83	0.76	18.62
33	Jayalo	0.29	29.97	0.40	0.07	2.37	0.76	18.36
34	Bikira maria	0.32	25.78	0.41	0.11	1.39	0.77	22.60
35	Ksp-28	0.19	30.33	0.29	0.12	2.95	0.64	21.43
36	Kabut jolweny	0.21	31.01	0.32	0.15	2.21	0.67	22.04
37	Ksp 20	0.17	27.13	0.24	0.12	3.79	0.72	20.42
38	Kamoko	0.25	29.40	0.37	0.18	1.95	0.62	21.82
39	Tororo	0.12	30.61	0.17	0.07	4.17	0.72	16.89
40	Saly boro	0.20	25.70	0.26	0.10	2.80	0.80	21.69
41	71 lo-323-1	0.23	26.78	0.33	0.06	3.07	0.70	22.10
42	Beauregard	0.25	27.58	0.33	0.09	1.34	0.73	21.03
43	Gikanda	0.15	29.34	0.22	0.11	1.19	0.73	19.92
44	Nyaluolo	0.15	30.79	0.24	0.05	3.41	0.64	21.02
45	Unknown 1	0.19	27.50	0.30	0.11	3.97	0.64	20.61
46	Unknown	0.16	28.19	0.25	0.12	3.73	0.66	19.58
47	A56	0.18	28.06	0.21	0.05	1.77	0.86	17.10
48	194515.15	0.28	25.16	0.37	0.03	3.21	0.75	20.75

Ranking	Genotype	FSR(kg plant ⁻¹)	% RDM	FB (kg plant ⁻¹)	MFSR (kg plant ⁻¹)	NSR plant ⁻¹	HI	CC mgcm ⁻²
49	Yanshu 1	0.16	28.87	0.26	0.08	2.68	0.63	22.24
50	W-220	0.15	29.04	0.20	0.06	2.18	0.77	17.67
51	Kalamb nyerere	0.16	28.86	0.21	0.05	2.19	0.75	18.47
52	W217	0.18	26.57	0.25	0.02	3.17	0.74	21.20
53	Kindolo	0.18	28.76	0.25	0.13	1.51	0.71	19.94
54	New kawogo	0.12	29.64	0.17	0.07	2.76	0.72	18.28
55	105268-1	0.12	30.31	0.17	0.05	1.67	0.74	20.87
56	Gatumbi	0.11	27.62	0.15	0.08	1.69	0.75	20.49
57	Cheguna mowar	0.17	25.48	0.34	0.10	3.31	0.54	21.12
58	Ondiek chilo	0.11	29.40	0.18	0.07	2.67	0.62	21.49
59	Tis 70357	0.13	25.31	0.21	0.08	3.41	0.61	19.60
60	Mwei munene	0.11	28.49	0.15	0.07	2.32	0.76	17.17
61	Spk 004	0.13	27.61	0.21	0.07	2.37	0.68	17.54
62	Namaswakhe	0.13	28.05	0.17	0.08	2.35	0.69	18.59
63	Sunjuki	0.13	27.65	0.20	0.02	1.82	0.70	17.93
64	Miezi tatu	0.15	27.03	0.27	0.11	1.99	0.57	20.53
65	Maria angola	0.12	27.83	0.21	0.09	2.48	0.62	17.96
66	Kajamani	0.13	30.38	0.18	0.04	1.63	0.73	18.26
67	Unknown 2	0.09	29.68	0.12	0.00	3.26	0.70	19.01
68	Nyatonge	0.08	29.70	0.11	0.04	1.57	0.70	19.77
69	Utugu 2	0.07	26.05	0.11	0.05	4.31	0.68	19.02
70	Naveto	0.14	25.32	0.23	0.08	2.08	0.64	21.51
71	Mafuta	0.10	27.97	0.18	0.05	2.06	0.62	18.53
72	Nguroiwe	0.09	27.93	0.12	0.04	2.85	0.67	19.57
73	420006	0.13	25.40	0.21	0.07	0.98	0.61	17.80
74	Wera	0.09	26.77	0.13	0.03	2.84	0.66	17.88
75	Nyamilambo	0.10	26.89	0.20	0.06	3.11	0.47	20.93
76	Okchio dalani	0.10	25.97	0.17	0.07	2.23	0.64	21.58
77	Mulware 1	0.09	26.30	0.14	0.06	2.53	0.64	18.06
78	Nyangangu	0.08	27.37	0.14	0.03	3.15	0.56	18.21
79	Nyar kamaa	0.09	27.20	0.20	0.05	2.46	0.43	19.46
80	Amina	0.06	28.63	0.11	0.05	1.39	0.58	17.34
81	Nduma	0.12	25.17	0.16	0.04	2.21	0.71	21.89
82	Nyar kangonga	0.09	27.13	0.20	0.00	2.35	0.48	21.77
83	Polista	0.04	30.97	0.10	0.02	1.85	0.40	17.95
84	Nyar malo	0.07	26.24	0.12	0.05	2.13	0.61	18.52
	Mean	0.21	28.13	0.31	0.12	2.81	0.72	20.01
	Lsd	1.42	0.21	3.61	0.22	0.10	0.21	3.70
	CV	35.42	67.80	9.12	53.13	71.11	18.71	13.21

Note: The abbreviations of the traits measured are as indicated in appendix 3.1

Appendix 3.4: Drought susceptibility index of the 84 genotypes and their ranking

Genotypes under drought	Ranking based on yield under drought	DSI based on NSR	DSI based on FSR	DSI based on fresh biomass	DSI based on MFR	Ranking based on the DSI's
194555.7	1	0.94	0.74	0.83	0.87	15
W119	2	0.97	0.81	0.87	0.78	20
Unawazambane06-01	3	0.98	0.84	0.87	0.84	25
Kilungu	4	0.96	0.08	0.11	0.14	1
441725	5	0.98	0.88	0.93	0.89	38
Chingova	6	0.97	0.94	0.95	0.97	54
48 Gabagaba	7	0.89	0.60	0.70	0.42	6
Marooko	8	0.93	0.69	0.84	0.53	10
Bosbok	9	0.98	0.92	0.86	0.92	34
Xiadla-xa-kau	10	0.96	0.83	0.86	0.86	21
Tanzania	11	0.99	0.96	0.96	0.94	62
Munyilia 3	12	0.94	0.14	0.55	0.48	3
189150.1	13	0.99	0.89	0.91	0.95	51
Mugande	14	0.93	0.03	0.51	1.00	16
422656	15	0.97	0.86	0.93	0.97	41
420014	16	0.97	0.96	0.99	1.03	63
Bulindo	17	0.99	0.93	0.96	0.80	46
Sinia	18	0.98	0.88	0.93	0.95	43
Canassumana	19	0.94	0.81	0.89	0.98	29
1990621	20	0.96	0.79	0.87	1.07	35
194573.9	21	0.92	0.75	0.84	0.92	17
421066	22	0.53	0.07	0.38	1.07	18
K37	23	0.95	0.01	0.54	0.81	7
A2	24	0.98	0.91	0.97	0.93	50
Excel	25	0.99	1.01	1.01	1.01	72
Resisto	26	0.98	0.92	0.94	0.92	44
Nyar buholo	27	0.99	0.84	0.90	0.96	45
Mwavuli	28	0.98	0.66	0.77	0.59	13
19901513	29	0.98	0.90	0.95	0.91	42
Lodha	30	0.97	0.97	1.00	0.94	58
189151.38	31	0.99	0.97	0.98	1.02	68
K117	32	0.94	0.49	0.51	0.39	4
Jayalo	33	0.94	0.10	0.28	0.24	2
Bikira maria	34	0.96	0.87	0.86	0.93	28
Ksp-28	35	0.99	0.80	0.84	0.74	23
Kabut jolweny	36	0.97	0.01	0.59	0.33	5
Ksp 20	37	0.99	0.25	0.48	0.16	14
Kamoko	38	0.96	0.36	0.64	0.55	9
Tororo	39	1.01	0.82	0.87	0.82	37
Saly boro	40	0.96	0.54	0.80	0.70	11
71 lo-323-1	41	0.99	0.89	0.88	1.00	53
Gikanda	42	0.98	0.91	0.98	0.86	48
Beauregard	43	0.97	0.99	1.00	1.03	67
Nyaluolo	44	0.98	0.81	0.82	0.98	33
Unknown 1	45	0.98	0.81	0.85	0.89	27
Unknown	46	1.00	0.76	0.85	0.70	26
A56	47	1.00	1.04	1.05	1.04	80
194515.15	48	0.99	0.46	0.70	1.03	32
Yanshu 1	49	0.97	0.87	0.90	0.95	36
W-220	50	0.98	0.85	0.92	0.93	39
Kalamb nyerere	51	0.99	0.48	0.74	0.85	22
W217	52	0.97	0.83	0.91	1.04	40
Kindolo	53	0.97	0.20	0.46	0.36	8
New kawogo	54	0.99	0.90	0.92	0.95	55

Genotypes under drought	Ranking based on yield under drought	DSI based on NSR	DSI based on FSR	DSI based on fresh biomass	DSI based on MFR	Ranking based on the DSI's
105268-1	55	1.00	0.97	1.00	1.01	74
Gatumbi	56	1.00	1.08	1.07	1.02	79
Cheguna mowar	57	0.99	0.85	0.79	0.81	24
Ondiek chilo	58	0.99	0.97	0.98	0.93	65
Tis 70357	59	1.00	0.96	0.95	0.88	60
Mwei munene	60	0.99	0.91	0.96	0.82	49
Spk 004	61	1.00	0.92	0.90	0.97	61
Namaswakhe	62	0.98	0.64	0.84	0.71	19
Sunjuki	63	1.00	0.89	0.84	1.05	57
Miezi tatu	64	0.98	0.85	0.86	0.87	31
Maria angola	65	1.00	0.80	0.85	0.81	30
Kajamani	66	0.98	0.48	0.69	0.47	12
Unknown 2	67	1.00	0.96	1.01	1.10	76
Nyatonge	68	1.01	1.12	1.11	1.05	84
Utugu 2	69	1.01	1.02	1.04	0.98	77
Naveto	70	1.00	0.86	0.94	0.86	47
Mafuta	71	1.00	0.84	0.89	0.95	52
Nguroiwe	72	1.00	0.96	0.99	0.93	66
420006	73	1.01	1.08	1.05	0.98	78
Wera	74	1.01	1.00	1.02	1.04	82
Okchio dalani	75	1.00	0.90	0.95	0.89	56
Nyamilambo	76	1.00	0.94	0.89	0.96	59
Mulware 1	77	1.00	0.99	1.01	0.96	73
Nyangangu	78	1.02	0.93	0.93	0.99	69
Nyar kamaa	79	1.01	1.01	0.94	0.97	71
Amina	80	1.01	1.09	1.08	1.03	83
Nduma	81	0.99	0.90	0.98	1.00	64
Nyar kangonga	82	1.01	0.98	0.92	1.10	75
Polista	83	1.02	1.05	1.02	1.00	81
Nyar malo	84	1.01	0.97	1.01	0.88	70

Note: The abbreviations of the traits measured are as indicated in appendix 3.1

Chapter 4

Genotype x Environment Interaction for Storage Root Yield in Sweetpotato under Managed Drought Stress Conditions in Kenya

Abstract

Most crops, including sweetpotato vary widely in yield performance across different agro-ecological environments. This study was set up to determine the genotype x environment interaction for storage root yield performance of 24 sweetpotato genotypes in eight environments; two locations - Kiboko and Thika, two moisture stress conditions - drought stress and no drought stress, and two years - 2011 and 2012 in Kenya. The experiments were laid out as a split plot design with two replications. Plots consisted of three rows each of 10 plants for each genotype, spaced at 0.9 m between rows and 0.30 m between plants. Planting was done in the dry season and controlled irrigation was applied to control moisture stress during the growth period. Data on fresh storage root yield (FSR) was collected, and drought susceptibility indices (DSI) and percentage yield reduction (YR) determined. Additive Main Effects and Multiplicative Interactions (AMMI) and genotype main effect by genotype-environment (GGE) interaction biplots and regression analyses were conducted using Genstat 14th edition to determine genotype x environment interaction effects. The environment, genotype main effects, and the genotype x environment interaction were all significant ($P < 0.001$). The DSI showed significant variation of genotypes in different environments. Highest yielding genotypes across the environments were 194555.7 (G7), Chingova (G14), Excel (G15), and 420014 (G10). Genotypes G7 and G14 had high storage root yield in both irrigated and non-irrigated environments. All the three methods of analyses (AMMI, GGE biplots and regression plots) indicated the most stable genotypes to be 441725 (G5), Unawazambane06-01 (G22) and 189150.1 (G2) and the least stable as Xiadla-Xa-Kau (G24). However, the most stable genotypes were not necessarily the highest yielding. Thus, genotypes G5, G22 and G2 may be used across environments, while genotypes G7 and G14 could be used in specific locations to boost production under unpredictable rainfall conditions. These genotypes (stable and high yielding) could be considered for drought screening breeding programmes to develop a new generation of drought tolerant sweetpotato varieties to meet changing climatic conditions.

Key words: biplot analysis; drought stress; genotype environment interaction; stability; storage root yield

4.1 Introduction

The ability of crop varieties to withstand drought stress varies across the world (Walters et al., 2002). Several factors including the micro and macro environment of a crop, growth stage, time and severity of drought affect the ability of the crop to tolerate drought stress (Boonjung and Fukai, 1996). Drought stress may occur during the initial crop growth stage, the reproductive stage or may be intermittent over the growth period of the crop (Mohammadi and Amri, 2013). A crop variety that withstands the fluctuating water stresses may be termed as stable and thus drought tolerant (Ekanayake, 1990).

Sweetpotato is an important root crop in the world and it has been reported to be drought tolerant. However the crop is sensitive to drought stress during establishment and storage root initiation periods (Ekanayake, 1990; Lewthwaite and Triggs, 2012). Drought at the storage root initiation stage causes small sized storage root formation thereby negatively affecting the crop yields (Ekanayake and Collins 2004; Pardales and Yamauchi, 2003). Sweetpotato storage root yield is a product of the number of plants per unit area, number of storage root per plant, and the weight of the storage roots, which may vary across environments. The number of plants per unit area depends on number of vines planted and the number that establish and survive to maturity. The number of the storage roots and their sizes depend on the genotype planted and its rooting structure which is influenced by prevailing environmental conditions (Lewthwaite and Triggs, 2012).

Large genotype (G) x Environment (E) interactions make identification of superior genotypes difficult (Sullivan et al., 2002). Thus, varieties need to be evaluated in different environments before they are released to determine their stability (Mohammadi and Amri, 2013). Drought resistance is generally controlled by quantitative traits influenced by the environment. Therefore, pre-release selection trials must be conducted in more than one season or location prior to release to determine their potential value (Mohammadi and Amri, 2013). The selected genotypes are further tested on a large scale to determine their stability and their commercial viability. The association of drought tolerance with morphological, physiological and chemical traits, all controlled by different genes, complicate environmental effects on genotype across locations (Lisar et al., 2012; Walters et al., 2002). Managing irrigation to simulate farmer's field conditions but allowing sufficient levels of water stress to distinguish drought and susceptible genotypes is a useful methodology employed to screen for and develop crops resistant to drought. Typically, soil moisture content is monitored using percent dry weight, tensiometers, or neutron probes (Amede et al., 2004). In the tropics, where rainfall is often bimodal and the rains begin and end in a defined time-frame, another useful strategy to evaluate drought tolerance incorporates delayed sowing after the onset of rains so the crop is challenged to yield during the ensuing dry period (Singh et al., 1994).

Drought alters sink-source relationship by affecting assimilate production, translocation and partitioning (Mundree et al., 2002). Translocation is less affected by water stress than photosynthesis and respiration (Boyer, 1976). Therefore, terminal drought exposes the ability of a genotype to translocate reserves to the sink (Ludlow and Muchow, 1990). Genotypes subjected to drought stress continually for some time and in different environments, express their ability to tolerate drought stress (Amede et al., 2004). If these genotypes are tested in multiple environments their stability may be determined through AMMI and GGE biplot analysis (Choukan, 2011; Sullivan et al., 2002; Yan et al., 2007). For example, in upland rain fed conditions, deep-rooted sweetpotato varieties that continue to grow by tapping water from deeper layers may be suitable. Also, genotypes with roots with the capacity to penetrate the hardpan layer of compacted soil at about 20-25 cm below the soil surface in low land areas are selected (Champoux et al., 1995; Ray et al., 1996). However, in Kenya there is no information on which sweetpotato genotypes are suitable for which agro-ecological zone.

Genotypes stable across environments in many cases may be drought tolerant (Lisar et al., 2012). Thus, it is vital for the breeder to establish the stability of varieties over different environmental conditions. Even though sweetpotato is regarded as drought tolerant, the crop loses a substantial amount of its potential yield in times of slight drought especially during the storage root bulking stage (Agili et al., 2012; Lewthwaite and Triggs, 2012). Moisture stress also triggers sweetpotato weevil infestation as weevils typically become more active during the onset of drought. Also, the cracks that develop in the soil as a result of drought enable weevils to penetrate in the soil and feed on the developing storage roots. This sequence of events can lead to total loss of the crop (Lewthwaite and Triggs, 2012).

Clearly, the determination of genotype by environment interaction effects on drought tolerance of sweetpotato varieties is essential prior to variety release and/or their use in a breeding program. As part of KARI's ongoing efforts to develop drought tolerant sweetpotatoes for Kenyan farmers, this study established a series of experiments and conducted AMMI, GGE biplot and regression analyses of 24 diverse sweetpotato genotypes across eight environments to determine their genotype x environment interaction effects for drought tolerance, and yield and quality characteristics.

4.2 Materials and methods

4.2.1 Plant materials

Twenty four genotypes of varying origins were used in this study. The genotypes were comprised of two local varieties (local checks; Nyatonge (G18) and Sinia (G20)), promising breeding lines, released varieties, and local landraces (Table 4.1). The genotypes were selected on the basis of their yielding ability and drought tolerance for possible inclusion into a crossing block focused on breeding for drought tolerance.

Table 4.1: The genotypes used in the study and their source

Genotype ID	Genotype name	Source	Status
G1	189151.38	Peru	CIP clone
G2	189150.1	Peru	CIP clone
G3	1990621	Peru	CIP clone
G4	422656	Peru	Breeders clone
G5	441725	Peru	Breeders clone
G6	194573.9	Peru	CIP clone
G7	194555.7	Peru	Breeders clone
G8	194515.15	Peru	CIP clone
G9	421066	Peru	CIP clone
G10	420014	Peru	CIP clone
G11	A56	South Africa	Breeders clone
G12	A2	South Africa	Breeders clone
G13	Beureguard	USA	Released clone
G14	Chingova	Mozambique	Improved clone
G15	Excel	Peru	USDA ARS germplasm release
G16	48 Gabagaba	Mozambique	Breeders clone
G17	Lodha	Kenya	Landrace
G18	Nyatonge (Check)	Kenya	Landrace
G19	Resisto	USA	Released variety
G20	Sinia (Check)	Kenya	landrace
G21	Tanzania	Uganda	Landrace
G22	Unawazambane06-01	Mozambique	Breeders cultivar
G23	W119	USA	USDA ARS germplasm release
G24	Xiadla-Xa-Kau	Mozambique	Breeders clone

4.2.2 Locations

The experiments were conducted at the two sites namely: Kenya Agricultural Research Institute (KARI)-Kiboko, and KARI-Thika. KARI-Kiboko research station is located at

Makueni county, 187 km east of Nairobi, at latitude 2°15', longitude 37°45'E and altitude 993 m asl. The research station is classified under agro-ecological zone five and receives mean annual rainfall of 548 mm with long-term annual average rainfall of 615 mm and is ideal for dry land research. The station receives bimodal rainfall with the more reliable short rains season falling in October to January (328 mm) and the less reliable rains season from March to May (233 mm). The annual mean maximum temperature is 30.6°C, while the annual mean minimum temperature is 17.4°C which translates to annual mean temperature of 24°C. The soils are of rhodic ferrasols to ferric luvisols on the old peneplain and eutric fluvisol at the bottom of the river valley (Mwacharo et al., 2004).

KARI-Thika is located 75 km north east of Nairobi, latitude 0°59' South, longitude 37°04' East, and altitude 1548 m asl. The area receives bimodal mean rainfall of about 1000 mm annually with long rains of 142 mm falling March to May and the short rains of 116mm falling in October to December. The areas has minimum temperature of 13.7°C, maximum of 25.1°C, and mean annual temperature of 19.4°C (Ndegwa et al., 2009).

4.2.3 Field evaluations

The experimental design was a split plot, laid in randomised complete block design (RCBD), where irrigation status was main plot and genotypes were the subplot. The experimental plots were three rows of 10 plants with 0.9 m between rows and 0.30 m between plants. The planting material was taken from presumably virus-free mother plants grown in greenhouses at KARI, Muguga. Two water regime levels, drought stress and no drought stress were tested (Table 4.2). Under no drought stress regime in the field, irrigation water was applied once the tensiometers read 15 cent bars which signify the permanent wilting point in most crops (O'Geen 2012; Table 4.3). Where no rainfall occurred during planting and up to a month after planting, such as E3 and E5, under drought stress regime, irrigation water was applied to avoid death of the plants. After establishment of the crop, plots under drought stress regime were not irrigated even when the tensiometer readings were beyond 15 cent bars to ensure persistent moisture stress, however, the occasional poor rainfall could reverse slightly the moisture stress (Table 4.3). Double ammonium phosphate fertilizer was applied at the rate of 50 kg P₂O₅ ha⁻¹ at planting. The experiments were planted late in the season to increase the probability of increased drought pressure in the life span of the crop. Data were collected from six centrally placed hills of every experimental plot. Harvesting was done at 150 days after planting (DAP). Data on number of storage roots, storage root fresh and dry matter, storage root yield per plot was taken. Also, storage root composite samples of 200 g (fresh weight) and vine composite samples of 500 g (fresh weight) were taken for

dry-matter determination. Table 4.2: Description of the test environments during the four cropping seasons at KARI Kiboko and Thika

Env	Site	Status	Planting dates	Harvesting dates	Soil type
E1	Kiboko	Rain fed	24/11/2010	24/04/2011	rhodic ferrasols
E2	Kiboko	Irrigated	24/11/2010	24/04/2011	rhodic ferrasols
E3	Thika	Rain fed	26/11/2010	26/04/2011	ferric luvisols
E4	Thika	Irrigated	26/11/2010	26/04/2011	ferric luvisols
E5	Kiboko	Rain fed	10/12/2011	10/05/2012	rhodic ferrasols
E6	Kiboko	Irrigated	10/12/2011	10/05/2012	rhodic ferrasols
E7	Thika	Rain fed	15/12/2011	15/05/2012	ferric luvisols
E8	Thika	Irrigated	15/12/2011	15/05/2012	ferric luvisols

Where: Env = environment

4.2.3 Tensiometer calibration

Six tensiometers were placed into 10 litre pots filled with sterile soil and watered to field capacity. The pots were allowed one hour for the water to infiltrate into the soil uniformly after which two samples from each pot were taken at tensiometer reading zero and moisture content determined. To do this, a five cm diameter by five cm height core sample was used to obtain soil samples from the pots containing the tensiometers. The amount of water in the core samples was gravimetrically determined and related to the tensiometer centibar readings to calibrate the soil moisture readings. Moisture loss was monitored using the tensiometers by taking two samples from each pot at readings; 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70 and 75 centbars and moisture loss determined. The data was used to calibrate the tensiometers readings taken from the field. A calibration curve of $Y = 0.1079x$ at $R^2 = 0.96$, was fitted on a scatter graph drawn using the data. The tensiometers were installed in the field at 30 cm deep in the soil during planting of the field experiment and used to monitor soil moisture status. Using the calibration curve fitted equation, the tensiometers readings were converted to moisture deficit in the field relative to field capacity (reading 0). Also, growing degree units (GDU) were estimated as $GDU = \frac{T_{max} + T_{min}}{2} - T_{base}$ using base temperature of 10°C (Wang, et al., 2003).

4.2.4 Statistical analysis

The data on storage root yield for all locations and seasons were combined to give a total of eight environments (locations x season x year) and analysed using AMMI and GGE biplots and regression analyses. A combined analysis of variance (ANOVA) for root yield data was done in GenStat 14th edition to determine the effects of environment (E) [combining the effects of season (S), location (L), and S x L interaction], genotype (G), and all possible interactions among the factors.

The mean values of genotypes for each experiment were used to analyse the relationships among genotypic yields under moisture stress and non-moisture stress environments. The model used was:

$$Y_{ij} = \mu + G_i + E_j + GE_{ij}$$

Where Y_{ij} is the corresponding variable of the i^{th} genotype in j^{th} environment (location), μ is the total mean, G_i is the main effect of i^{th} genotype, E_j is the main effect of j^{th} environment, GE_{ij} is the effect of genotype x environment interaction.

A drought stress index (DSI) was estimated as; $DSI = \left(1 - \frac{Y_s}{Y_p} / 1 - \frac{\bar{Y}_s}{\bar{Y}_p}\right)$, (Fischer and Maurer, 1978), where Y_s and Y_p are the storage root yield of a genotype under drought stress and no drought stress conditions, respectively.

AMMI was used to analyse and interpret genotype x environment interaction (Zobel et al., 1988). The AMMI model equation is as follows:

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^t \lambda_k \alpha_{ik} \gamma_{jk} + \epsilon_{ij}$$

Where; Y_{ij} is the cell mean in the i^{th} genotype and j^{th} environment, μ is the overall mean g_i and e_j are the main effects of genotype and environments, and ϵ_{ij} is the experimental error. Residuals of the ij^{th} cell, $Z_{ij} = Y_{ij} - Y_{i.} - Y_{.j} + Y_{form}$ a matrix Z. The least square estimate of the AMMI parameters λ_k is the singular value of the n^{th} PCA axis, α_{ik} and γ_{jk} are the scores for i^{th} genotype and j^{th} environment. The AMMI model was adjusted depending on the number of principal components (PC) considered. In this study two PC's were factored, therefore, the model was adjusted to $Y_{ij} = \mu + g_i + e_j + \lambda_1 \alpha_{i1} \gamma_{j1} + \lambda_2 \alpha_{i2} \gamma_{j2} + \epsilon_{ij}$ which considered the main effects in addition to IPCA1 and IPCA2 for non-additive variation (Gauch, 1992)

The GGE biplot analysis used the following model:

$$Y_{ij} - \mu - E_j = \lambda_1 \epsilon_1 \eta_{1j} + \lambda_2 \epsilon_2 \eta_{2j} + e_{ij}$$

where Y_{ij} is the corresponding variable of the i^{th} genotype in j^{th} environment (location), μ is the total mean, E_j is the main effect of j^{th} environment, λ_1 and λ_2 are singular values of principal components PC1 and PC2; ε_{i1} and ε_{i2} are eigen vectors in j^{th} environment (location) for PC1 and PC2 of i genotype in j environment. The GGE biplots were constructed by plotting the first two principal components (PC_1 and PC_2) derived from subjecting environment centred yield data to singular value decomposition (Yan et al. 2000). In the biplot, the best genotypes in each environment and groups of environments were identified through a polygon view (Yan et al., 2000) that was drawn by connecting genotypes that were furthest from the biplot origin such that all genotypes were enclosed within the polygon. Perpendicular lines were then drawn to each side of the polygon starting from the biplot origin.

The GGE biplot was also used to explore the interrelationships among environments by constructing lines (environment vectors) from the biplot origin to markers for the environments. The correlation coefficient between any two environments was approximated by the cosine of the angle between their vectors. Acute angles showed a positive correlation; obtuse angles showed a negative correlation and right angles no correlation (Yan and Kang 2003). The length of the vector described the discriminating ability of the environment (Yan et al., 2007; Choukan, 2011; Sibiya et al., 2013). Another line called the average environment axis (AEC) was also used to show the ranking of the genotypes by their mean yield and stability. The line passed through the biplot origin and another line perpendicular to it was drawn to represent the stability of the genotypes. According to Yan (2002), either direction away from the biplot origin on this axis, indicated greater GEI and reduced stability.

Genotypic stability was determined using linear regression model by Eberhart and Russell, (1966) :

$$Y_{ij} = \mu + biI_j + \delta_{ij} + \varepsilon_{ij}$$

where; Y_{ij} is the mean for the genotypes i at location j ; μ is the general mean for genotype i ; bi is the regression coefficient for the i^{th} genotype; I_j is the mean deviation from the overall mean for all genotypes at a particular location; δ_{ij} is the deviation from regression for the i^{th} genotype at the j^{th} location; and ε_{ij} is the mean experimental error.

4.3 Results

4.3.1 Climatic data

The amount of rainfall received during the first experiment (October 2010/February 2011) was 201.3 mm at Kiboko and 32.6 mm at Thika. During the second experiments (April 2011/August 2012, Kiboko received 8 mm and Thika 229 mm, and this was not sufficient for crop growth. Supplementary irrigation water was applied at both sites and seasons as follows; E1

(0 mm), E2 (280 mm), E3 (60 mm), E4 (340 mm), E5 (60 mm), E6 (360 mm), E7 (0 mm) and E8 (280 mm). Details of the supplementary irrigation water are shown in Table 4.3. The day degree units and relative humidity were higher in Kiboko (season one: 15.25 and season two: 13.15) than in Thika (season one: 9.7 and season two: 10.7) (Table 4.3).

Table 4.3: The temperature, rainfall, irrigation water and soil moisture loss of the test environments during the cropping seasons

Env	Min	Max	mean	DDU	R (mm)	I (mm)	%RH	SML 4WAP	SML harvesting
E1	17	33	25.3	15.4	201.0	0.0	78.9	3.4	573.5
E2	17	33	25.3	15.4	201.0	280.0	78.9	2.2	33.9
E3	14	26	16.2	9.7	32.6.0	60.0	67.5	2.2	449.6
E4	14	26	16.2	9.7	32.6	340.0	67.5	1.5	19.6
E5	16	31	23.2	13.2	8.0	60.0	77.9	3.4	551.4
E6	16	31	23.2	13.2	8.0	360.0	77.9	2.1	27.6
E7	13	28	20.7	10.7	229.0	0.0	57.6	2.4	412.7
E8	13	28	20.7	10.7	229.0	280.0	57.6	1.9	13.4

Env = environment as described in Table 4.2, max = maximum, DDU = day degree units, R = rainfall, I = irrigation water, %RH = % relative humidity, SML4WAP = soil moisture loss four weeks after planting

4.3.2 Combined AMMI analysis of variance

The AMMI analysis of variance for storage root yield revealed that genotype (G), environment (E) and genotype environment interaction (GEI) effects were significantly different ($P < 0.05$) (Table 4.4). The treatments (G and E) and GEI accounted for 95% of the total variation, with E accounting for the highest amount of variation (75.2%), followed by G (11.1%) and GEI (9%). The interaction principal component one (IPCA1) accounted for 77.7% while principal component two (IPCA2) accounted for 6.1% of the GEI variation sum of squares (Table 4.4).

Table 4.4: Source of variation, mean squares and significance, and their contribution to total variation of the genotypes

Source of variation	df	MS	% contribution to total variation	% contribution to GEI variation
Total	383	0.253	100.0	
Treatments (G,E,GEI)	191	0.487***	95.8	
Genotypes (G)	23	0.469***	11.1	
Environments (E)	7	10.418***	75.2	
Block	8	0.024ns	0.002	
Interactions (I)	161	0.057***	9.0	
IPCA1	29	0.247***	7.3	77.7
IPCA2	27	0.022ns	0.6	6.1
Residuals	105	0.014ns	1.5	
Error	184	0.021	4.0	

Where; *** = significant at $P < 0.001$, ns = not significant

4.3.3 Genotypic yield performance in the test environments

Genotype means indicated that storage root yield varied significantly among genotypes in each test environment (Table 4.5). The best three genotypes under drought stress environment were G7, G3, and G22; while, the best three genotypes under no drought stress environment were G14, G15, and G7. Genotypes G7, G14 G13, G15 and G10 did well in the drought stress and no drought stress environments. The checks used in this experiment, G18 and G20, performed much lower compared to the best clones (Table 4.5). The drought stress index (DSI), and percent yield reduction (%YR), confirmed that the responses of genotypes to drought stress differed with environments. Genotypes G8, G7, G22, G24, G23, G5, G9, and G10 had DSI scores < 1 (Table 4.5, Appendix 1).

Table 4.5: Storage root yield (kg plant⁻¹) of sweetpotato genotypes in the specific environments and their DSI values.

Genotype	Drought environment		Irrigated environment		Across environments		% YR	OY	DSI
	Kiboko	Thika	Kiboko	Thika	Drought	Irrigated			
G1	0.23	0.30	1.50	1.43	0.27	1.46	-81.81	0.87	1.08
G2	0.24	0.32	1.16	1.06	0.28	1.11	-74.90	0.70	0.99
G3	0.29	0.24	0.99	1.06	0.27	1.02	-74.02	0.65	0.87
G4	0.30	0.33	1.18	1.20	0.31	1.19	-73.62	0.75	0.95
G5	0.22	0.33	0.99	0.99	0.28	0.99	-72.11	0.64	0.98
G6	0.08	0.13	1.23	1.29	0.10	1.26	-91.90	0.68	1.22
G7	0.51	0.65	1.59	1.48	0.58	1.53	-62.31	1.06	0.82
G8	0.31	0.21	0.51	0.40	0.26	0.45	-42.60	0.36	0.49
G9	0.31	0.29	1.54	1.50	0.30	1.52	-80.42	0.91	0.97
G10	0.53	0.34	1.34	1.29	0.44	1.31	-66.81	0.88	1.06
G11	0.19	0.18	1.50	1.49	0.18	1.49	-87.90	0.84	1.16
G12	0.31	0.28	1.19	1.36	0.30	1.27	-76.72	0.79	1.01
G13	0.32	0.35	1.48	1.53	0.33	1.50	-78.01	0.92	1.03
G14	0.35	0.31	1.53	1.59	0.33	1.56	-78.91	0.95	1.05
G15	0.34	0.21	1.59	1.52	0.27	1.56	-82.42	0.92	1.09
G16	0.11	0.15	0.64	0.68	0.13	0.66	-79.90	0.40	1.06
G17	0.22	0.25	0.85	1.00	0.23	0.93	-74.81	0.58	0.99
G18	0.28	0.20	0.94	0.97	0.24	0.96	-75.10	0.60	0.99
G19	0.30	0.24	1.01	1.05	0.27	1.03	-74.20	0.65	0.98
G20	0.47	0.18	0.98	1.04	0.33	1.01	-67.73	0.67	0.97
G21	0.28	0.21	1.15	1.06	0.25	1.10	-77.61	0.68	1.03
G22	0.35	0.34	1.11	0.91	0.34	1.01	-65.92	0.68	0.85
G23	0.26	0.37	1.01	0.97	0.32	0.99	-68.10	0.66	0.89
G24	0.23	0.25	0.77	0.92	0.24	0.84	-71.91	0.54	0.92
Mean	0.29	0.28	1.15	1.16	0.28	1.16	74.14		0.98
LSD	0.07	0.06	0.06	0.05	0.05	0.06	5.16		0.06
%CV	21.90	19.60	20.30	17.70	43.40	13.30	17.30		17.30

Where; %YR = percent yield reduction, OY = Overall mean yield, DSI = drought stress index

The AMMI analysis ranked genotypes G7, G14, G3, G15, G10, G20, G22, G23, G13 and G11, as the best across the environments. Among them; G7 and G14 were superior in performance across the environment (Table 4.6). Environment E5 had the lowest IPCA

score, which, indicated that GEI was low in that environment confirmed by the low variance of 0.03. Environment E6 had the highest IPCA scores and also high variance, while E5 had the lowest variance. In this study, E6 was the highest yielding site (no drought stress) but unstable, while E5 was lowest yielding but stable site (drought stress) (Table 4.6).

Table 4.6 Genotype performance for storage root yield (kg plant⁻¹) and ranking of the first four AMMI selections in each test environment

Env.	mean	variance	IPCA 1 effects	IPCA 2 effects	IPCA Score	Rank			
						1	2	3	4
E1	0.32	0.03	0.51	-0.37	0.47	G7	G20	G3	G22
E2	1.14	0.11	-0.47	-0.13	-0.47	G15	G14	G10	G7
E3	0.27	0.03	0.50	-0.13	0.50	G7	G3	G20	G22
E4	1.17	0.10	-0.50	0.38	-0.50	G14	G15	G7	G10
E5	0.28	0.02	0.16	0.01	0.46	G7	G3	G14	G23
E6	1.17	0.21	0.50	0.03	-0.52	G14	G7	A56	G13
E7	0.28	0.11	0.47	0.23	0.5	G7	G3	G14	G23
E8	1.15	0.10	-0.48	-0.28	-0.48	G15	G10	G14	G13

Env = environment as described in Table 4.2

4.3.4 AMMI GE and IPCA scores biplot

An AMMI biplot was drawn with IPCA scores of genotypes and environment against their respective means (Fig. 4.2). In the biplot, genotypes with IPCA scores close to zero were G12, G13, G1, G2, G22 and G5. Genotypes with a negative IPCA score such as G8 did well under the environments with negative IPCA scores such as E3 and vice versa. The stable high yielding genotypes were G1, G10, and G13 while the least stable genotypes included G24 and G8 (Fig. 4.2).

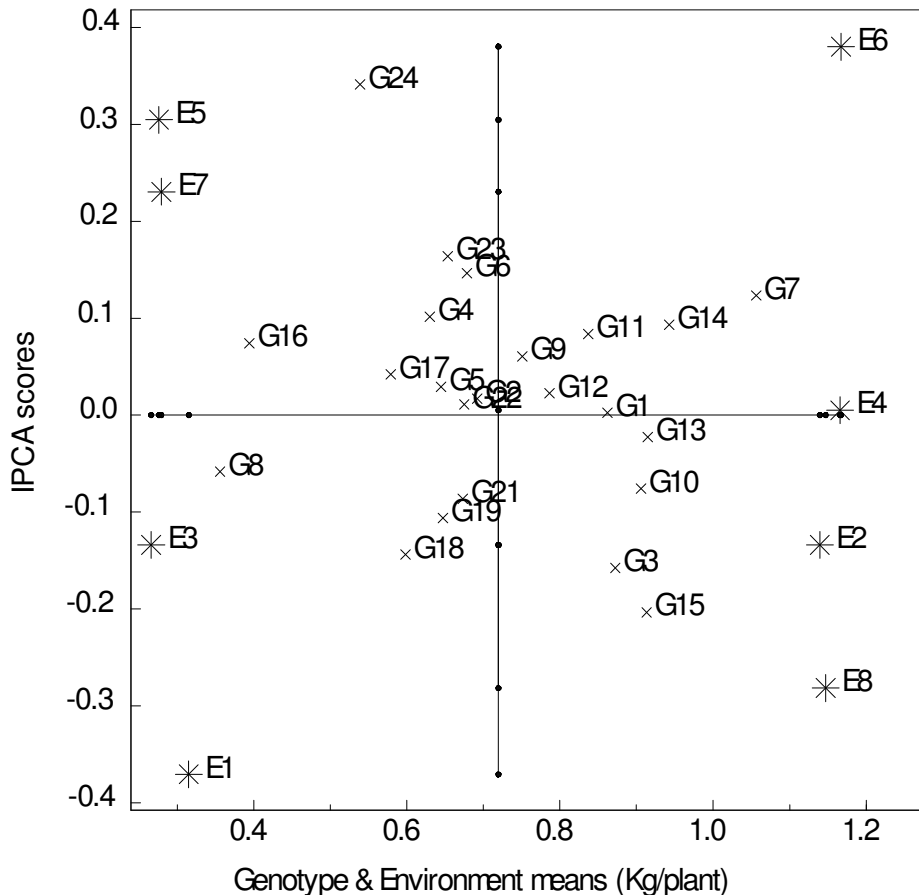


Figure 4.2: Genotype and environment IPCA2 scores and means based on storage root yield for the eight test environments. The genotypes and environments are as given in Tables 4.1 and 4.2, respectively.

4.3.5 GGE biplot analysis

The two PCs in the GGE biplot explained 90.80% of the total GGE variation, where PC1 = 82.99%, and PC2 = 7.81% (Fig. 4.3). Yield and stability of genotypes was estimated using the average environment coordinates (AEC) method (Yan, 2001; Yan and Hunt, 2001). From the polygon view, genotypes G7, G14, G15 and G11 were high yielding while G8, G16 and G24 were low yielding. The rays (continuous lines from centre) of the biplot divided the plot into seven sections, with the eight environments appearing in three sectors (Fig. 4.3). The environments were divided into three mega environments (Fig. 4.3).

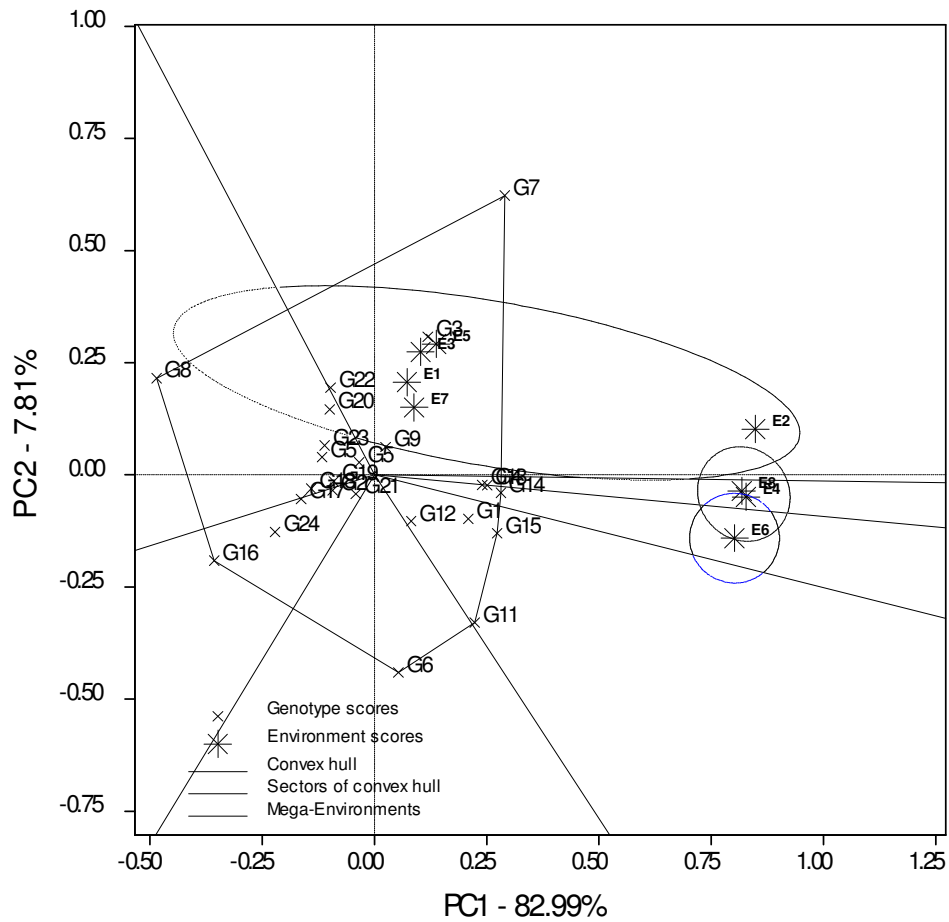


Figure 4.3: Polygon view of the GGE biplot based on the storage root yield for eight environments. The genotypes and environments are as given in Tables 4.1 and 4.2, respectively

4.3.6 Ranking GGE biplot

GGE biplot analysis also enabled visual assessment of yield performance of PC1 and PC2 of the genotypes for the all environments as presented in a circle (Fig. 4.4). From the circular view, genotypes with the highest nominal yield were G7, G3, G9, G22, G20, G1, and G4, and the lowest were G16, G11, G6, and G8.

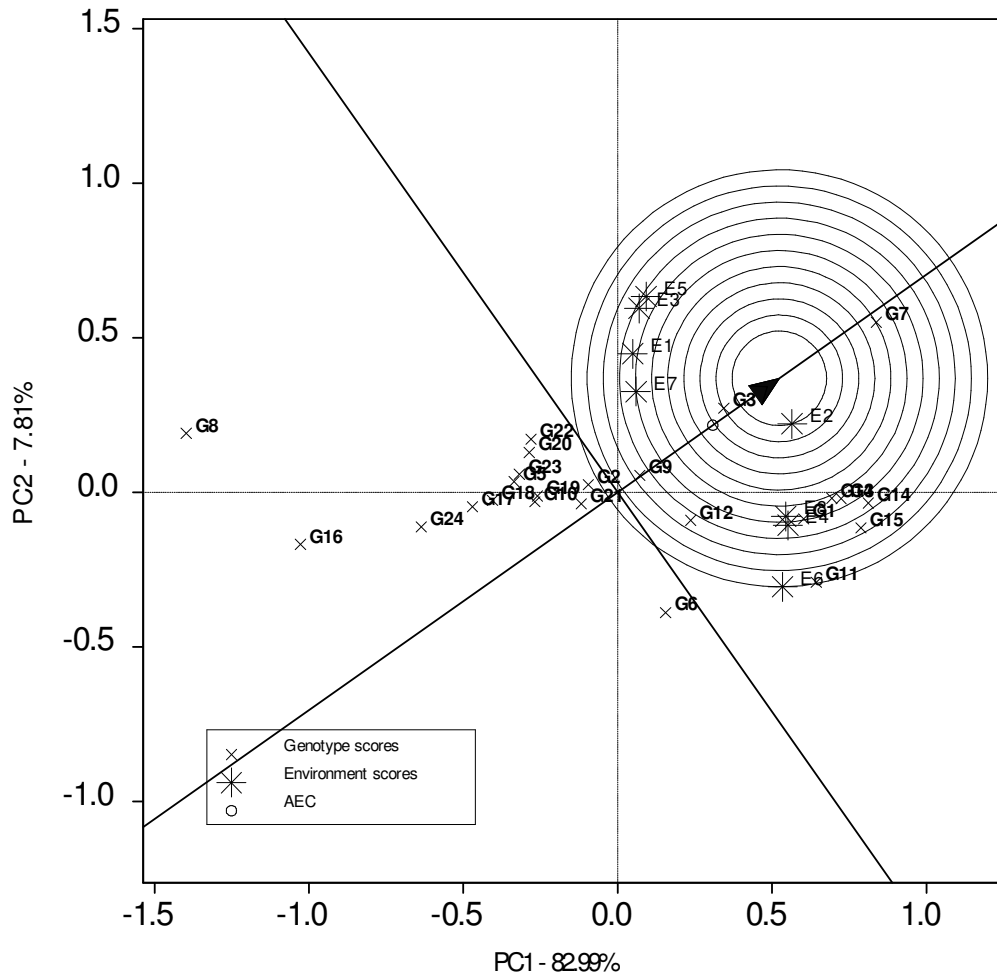


Figure 4.4: Circular view of the GGE biplot based on the storage root yield for eight environments

4.3.7 Relationship between environments

The inter-relationship among environments was plotted in a GGE biplot and all environments had positive PC1. The angles between them revealed that the environments were divided into two groups, drought stress (E1, E3, E4 and E5 and no drought stress (E8, E2, E6, E7) (Fig., 4.5). The length of the environment vector also approximated the standard deviation within each environment and drought stress environments were distinctively apart from no drought stress environments. The most discriminative environments were the no drought stress and the least were the drought stress. The angle between the average environment coordinate line and the environment vector determined the stability of the environment; in this study, the most stable environment were E5 and E6 (Fig., 4.5).

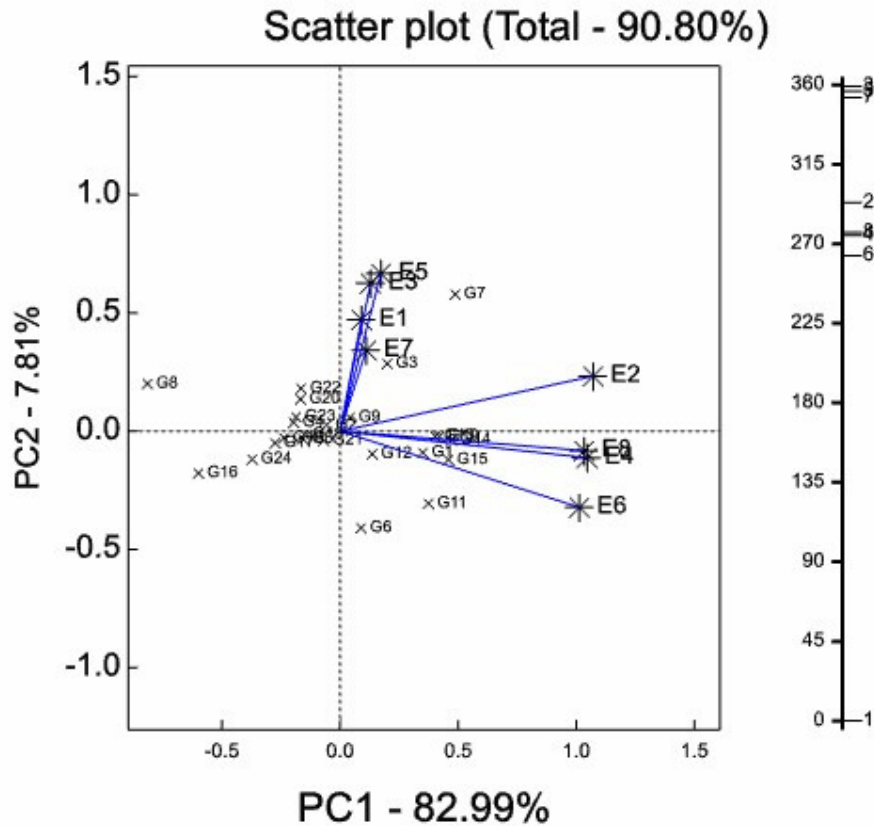


Figure 4.5: Environment focused scaling GGE biplot based on the storage root yield for eight environments, with 360° positioning scale based on PC1 indicated on the right

4.3.8 Regression analysis

Genotypes close to the regression curve were G13 (A56), G12 (A2), G5 (194573.9), G9 (441725), G4 (194555.7), G24 (Xiadla-Xa-Kau) and G10 (199062.1). Genotypes G7 (421066), G6 (420066), G11 (48 Gabagaba), G3 (194515.15) and G16 (Excel) were further away from the regression line (Fig. 4.6).

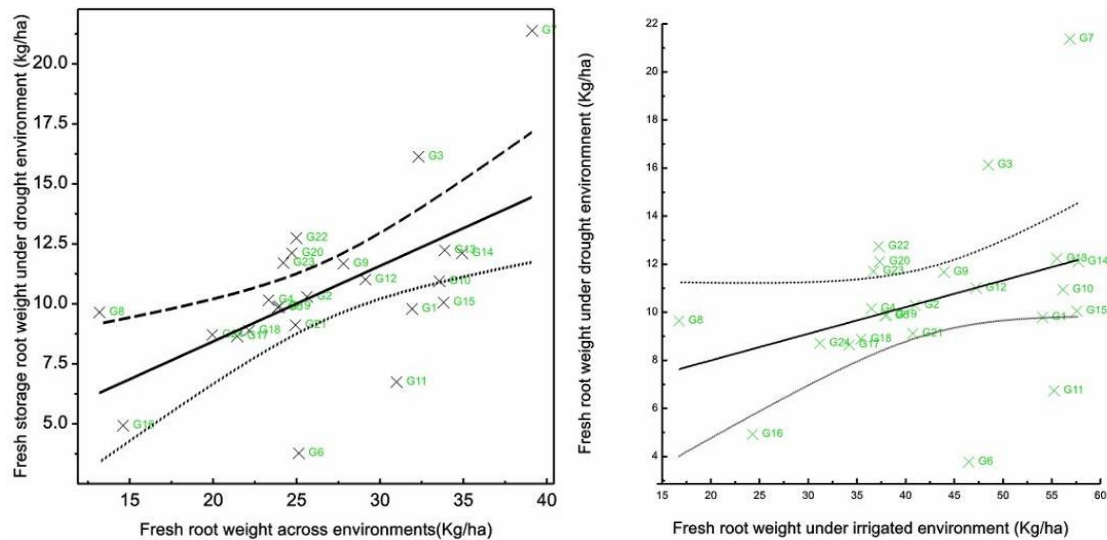


Figure 4.6: Graphs showing the regression of fresh storage root weight under drought with (a) fresh root weight across environments and (b) Fresh root weight under irrigated environment

4.4 Discussion

4.4.1 Climatic data

The rainfall received was not sufficient for sweetpotato growth indicating the environments were fit for the drought screening study. Also, the mean day degrees units for Kiboko were 14.4°C and Thika was 10.2°C indicating that, the minimum daily temperature approximated to 20°C (Table 4.2) which is relatively good for sweetpotato growth although not optimal. Mohammadi and Amri (2013) in their work reported that, rainfall and temperature were the main environmental factors that had greater impact on GEI occurrence.

4.4.2 AMMI analysis on genotype performance across environments

In this study, the AMMI2 model ($G + E + \text{IPCA1} + \text{IPCA2}$) accounted for 94.2% of the total variation suggesting that the model fitted well.

Genotypes G7 and G14 had high root yield across the eight environments tested, an indication that they were stable and widely adapted. In crop breeding programmes genotypes are tested across varied sites and locations to determine their yield performance and scope of adaptation (Bantayehu, 2009). Moreover, AMMI IPCA scores indicated the stability of the environments in terms of genotypes evaluated. Environment E5 had the lowest IPCA score, and low variance an indication that it was the best site for the evaluation of the genotypes for drought stress. This was in contrast to E6 that had the highest IPCA scores and variance, indicating the site had high discrimination for the

genotypes and would be good to screen genotypes for specific adaptation. Favourable test environments have large IPCA1 scores and near zero IPCA2 scores (Kaya et al., 2006). Environments E5 and E6 are located at Kiboko, which is a site for drought screening experiments. These findings are in agreement with Bantayehu (2009) who reported that genotypes had small deviation from the mean in stable environments unlike in unstable environments. He also grouped the experimental sites into high yielding with high GEI and low GEI.

There were large differences in root yield, mostly due to differences in environment and genotype effects. The genotypes with high yields under no drought stress condition which had DSI scores <1 could be ranked as drought tolerant. Some of the genotypes with high yields under no drought stress also tended to yield well under drought stress conditions over the four cropping seasons. Additionally, the ranking of genotypes based on DSI, showed that the responses of genotypes to drought stress are not consistent over years. Thus, the DSI indicator was able to discriminate different genotypes at each cropping season, depending on the type of drought stress that occurred and the development stage of the crop. Therefore, cultivars for drought tolerance need to be evaluated across environments to select for drought tolerance. This also suggests that breeding for specific adaptation in drought tolerance may be required. Lewthwaite and Triggs (2012) conducted similar work using twelve sweetpotato cultivars in new Zealand and reported three responses due to drought stress. In their study some clones had significant yield reduction, others had no change, while others, interestingly, had increased yields. This implies that, selecting for drought tolerance in breeding programmes, require diverse screening sites. However, high discriminating sites may be used to select site specific tolerant cultivars.

4.4.3 AMMI GE and IPCA scores biplot

Genotypes with positive IPCA 1 scores in the AMMI biplot (Fig. 4.2) were high yielding; while those on the left side were low yielding. Nominal yield on the X-axis is indicative of genotype adaptability, and allows evaluation of genetic responses to yield stability and adaptation based on IPCA scores (Mohammadi and Amri, 2013). The AMMI biplot revealed genotypes that performed better in one environment than in another, which implies that there was a specific interaction between genotypes and environments. Genotypes with IPCA values near zero demonstrated broader adaptability, while genotypes with IPCA1 values far from zero could be suitable for the environment with IPCA1 values of the same sign. Therefore, assessment of individual genotype performances was related to their positions relative to X and Y axis. The best genotypes were considered to be those that have high yield with stable

performance in most environments. Of the six high yielding genotypes (G7, G14, G13, G15, G10, G3), genotype G7 was the highest yielding across the environments.

4.4.4 GGE biplot analysis

A polygon view of the GGE biplot revealed the highest yielding genotypes for each environment and clustered the environments. According to Kaya et al. (2006), a succinct summary of genotype performance on different environments in multi environment yield trial can be demonstrated by a display of GGE polygon view biplot. In this study, the rays (continuous lines from the centre) of the biplot divided the plot into seven sections, with the eight environments appearing in three sectors. According to Yan et al. (2007), when different environments fall into different sectors, it implies that they have different high yielding cultivars (susceptible or tolerant) for those sectors and it shows crossover GEI suggesting that the test environments could be divided into mega-environments. In this study, the environments fell in three interacting mega environments indicating significant crossover interaction. The cultivars far from the origin of the polygon had high yield in the environments close to them, and the cultivars close to the origin were more stable across the environments. According to Yan et al. (2000), genotypes within the polygon, especially those located near the plot origin, were less responsive than the vertex genotypes. The environments were divided in three mega environments clustered into two groups of the optimal environments and the moisture stressed environments.

Sullivan et al. (2002) evaluated three varieties of red raspberry (Heritage, Autumn Bliss and Redwing) in 17 year x location environments using GGE biplot analysis and grouped the environments into 2 mega environments on the basis of the performance of the varieties Autumn Bliss and Redwing. They also found environmental variability was responsible for within and between genotype variations. Choukan (2011) performed AMMI and GGE biplot analysis on 14 inbred lines of maize in five diverse locations on basis of grain yield, and identified the most suitable inbred for each environment. The environments were then grouped into three mega-environments and the most discriminative environments to the genotypes as well as the most and the least responsive maize inbred lines were determined.

4.4.5 GGE ranking biplot for stability and yield

The GGE biplot analysis also enabled visual assessment of genotype performance, where average values of PC1 and PC2 of the genotypes for the all environments were presented in a ranking GGE biplot. In the GGE biplot, performance of different genotypes was revealed by the relations of the genotypes and the average environment coordinate (AEC) axis whereby, genotypes in the direction of the arrow of AEC are high yielding. The line which

passes through the circle and the origin of the plot is called the average environment axis (AEA) (Yan, 2001; Yan and Hunt, 2001). The line, which is perpendicular to the AEA line and passes through the origin, is called the average ordinate environment (AOE). This line divides the genotypes into those with higher yield than average (to the right of it) and into those with lower yield than average (on its left side). By projecting the genotypes on AEA axis, the genotypes are ranked by yield, where the yield increases in the direction of the arrow. In this study, the highest nominal yield had genotypes G7, G3, G9, G24, G20, G1, and G4, and the lowest were G16, G11, G6, and G8. Stability of the genotypes depends on their distances from the AE abscissa. Genotypes closer to abscissa are more stable than others. In this study genotypes G2, G5 and G22 were stable. Agili et al. (2012) reported genotype G5 was stable across varying moisture regimes. The circular representation of GGE biplot also enables identification of an ideal genotype. In GGE biplots, ideal genotypes are expected to have high mean productivity (PC1) and more stability (PC2 near zero) (Mohammadi and Amri, 2013). Thus, an “ideal” genotype is one that has the highest yield across test environments and ranks the highest in all test environments (Kaya et al., 2006). Although, such an “ideal” genotype may not exist in reality, it can be used as a reference for genotype evaluation. The closest to the “ideal” genotype in this study was G3. Moreover, genotypes located closer to the “ideal” genotype (G3) were also more desirable.

4.4.6 Relationship among test environments using GGE biplots

All the environments had positive PC1 scores indicating high drought tolerance scores and good drought tolerance discriminative ability. The environments could be grouped into two based on drought tolerance expression and discrimination groups of the genotypes; E2, E4, E6, E8 and E1, E3, E5, E7. The second group was close to zero and comprised of environments under drought stress indicating that under such conditions, drought tolerance discrimination was poorer than under no drought stress environment. Genotypes with disproportionately large positive interactions in some environments and large negative interactions in others have crossover GEI (Kaya et al., 2006). The cosine of the angle between the environment vectors is related to their correlation coefficient; whereby the smaller the angle between them, the higher the correlation (Choukan, 2011). In this study, the inter-relationship between environments revealed that the environments were divided into two groups, drought stress (E1, E3, E5 and E7 and no drought stress (E2, E4, E6, E8) (These environments are described in Table 4.2).

The length of the environment vector also approximates the standard deviation within each environment and is a measure of the discriminating ability of the environment. The most discriminative environments were the no droughts stress and the least were drought stress

in this study. The angle between the average environment coordinate line and the environment vector determines whether the environment is stable (representative or not) (Choukan, 2011). Environments located furthest from the biplot origin were the most discriminating of the cultivars. Thus, of the eight environments, E2 had highest drought tolerant expression discrimination (high positive PC1 scores, longest vector) than the others. It appears, therefore, that one site under no drought stress and another site under no drought stress either in Kiboko or Thika could be used for preliminary drought screening after which multisite trials can be conducted.

4.4.7 Regression analysis

Genotypes close to the regression curve (G13, G9 and G10) were stable; however genotypes further away from the regression (G7, G6 and G16) were unstable.

4.4.8 Comparison of yield and stability of genotypes using the different methods used

The genotypes that performed well in both drought and no drought environment based on mean yield analysis (G7, G14, G13, G10, G15) also, did well in the AMMI biplot analysis, however, among them, only G7 and G10 had DSI <1. Local check G20 had DSI <1 and performed well under AMMI biplot analysis. Based on AMMI biplot analysis genotypes G10 and G13 were stable and high yielding while G24 and G8 which had DSI <1 were unstable and low yielding. The GGE biplot showed G1 and G13 as stable similar to AMMI biplot while G8 and G24 unstable similar to AMMI biplot. Ranking by GGE biplot indicated that G7, G3, G22, G20 and G1 as among the highest yielding genotypes similar in AMMI and GGE biplot analysis. Also, based on ranking by GGE biplot, G8 and G16 ranked lowest similar in GGE and AMMI biplots. Genotypes G10, G12 and G13 appeared stable based on AMMI, GGE biplots and regression analysis. However, the comparison of the yield and stability of genotypes between various methodologies used in this study showed that drought tolerant genotypes were not necessarily high yielding or stable. Furthermore, high yielding genotypes were not necessarily drought tolerant or stable. Moreover, there were slight disparities in discriminating genotype stability and performance between the AMMI, GGE biplots and regression across environments which may be attributed to their different procedures and formulae for their plotting and computation.

4.5 Conclusion

Rainfall was low in all the locations and seasons and thus the sites were suitable for screening for drought tolerance. In Kiboko the day degrees were higher than in Thika while the relative humidity was higher in Kiboko than in Thika, a situation that seemed to have equalized evapo-transpiration in both sites. The combined ANOVA showed that

environmental effects contributed to the highest variation of 72.5%, an indication that screening the genotypes for GxE effects was vital. The GGE and AMMI biplot clearly showed that some genotypes had high yields in particular environments (specific interaction) between genotypes and environments while others had high yields across environments (stable genotypes). This implies the genotypes varied in their ability for drought tolerance. Clones revealed as stable under the AMMI biplot also were found stable under regression e.g. G10 and G13 as well the unstable G8. The GGE polygon view and ranking GGE biplots indicated the stable but low yielding clones e.g. the high yielding unstable clones were G7, G11, while stable high yielding were G10 and G13. Thus, evaluation programme for drought tolerance genotypes need to factor in evaluation across environments while selecting drought tolerance clones for wide or narrow environments. The biplots also indicated the stability levels of the cultivars and the environment. AMMI and GGE biplots are necessary in describing the test sites and the genotype performance across tests sites. This implies that, selecting for drought tolerance in breeding programmes, require diverse screening sites. However particular sites can be used to select site-specific tolerant cultivars.

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Appendix 1. AMMI genotype storage root yield mean estimates (kg plant⁻¹) in the eight environments

Genotype (G)/Environment (E)	E1	E2	E3	E4	E5	E6	E7	E8	mean	Superiority ¹	Rank ¹
G7	0.56	1.50	0.54	1.55	0.61	1.60	0.60	1.49	1.06	0.01	2.75
G14	0.31	1.53	0.29	1.58	0.36	1.61	0.35	1.52	0.94	0.03	5.62
G13	0.36	1.48	0.31	1.51	0.32	1.51	0.33	1.50	0.91	0.04	5.88
G10	0.35	1.51	0.28	1.53	0.27	1.50	0.28	1.53	0.91	0.04	7.62
G15	0.37	1.56	0.28	1.57	0.21	1.49	0.23	1.60	0.91	0.05	8.75
G3	0.53	1.31	0.44	1.32	0.38	1.26	0.40	1.35	0.87	0.05	6.62
G1	0.29	1.44	0.24	1.48	0.26	1.48	0.27	1.45	0.86	0.05	9.75
G11	0.17	1.46	0.15	1.51	0.21	1.54	0.20	1.46	0.84	0.06	13.12
G12	0.32	1.26	0.27	1.29	0.30	1.30	0.30	1.26	0.79	0.08	10.00
G9	0.32	1.16	0.29	1.20	0.33	1.22	0.32	1.16	0.75	0.08	9.75
G2	0.30	1.09	0.26	1.12	0.27	1.13	0.28	1.09	0.69	0.11	12.88
G6	0.07	1.22	0.06	1.27	0.14	1.33	0.13	1.21	0.68	0.11	16.75
G21	0.31	1.10	0.24	1.11	0.21	1.08	0.22	1.12	0.67	0.12	14.38
G22	0.38	0.99	0.33	1.01	0.33	1.02	0.34	1.00	0.67	0.13	11.12
G5	0.29	1.01	0.25	1.03	0.26	1.05	0.27	1.01	0.64	0.13	14.38
G19	0.34	1.03	0.27	1.04	0.22	1.00	0.24	1.05	0.65	0.13	14.12
G23	0.29	0.96	0.28	1.00	0.35	1.07	0.34	0.94	0.65	0.14	13.25
G20	0.54	1.05	0.38	1.01	0.18	0.84	0.22	1.13	0.67	0.14	14.50
4G4	0.27	0.96	0.24	1.00	0.29	1.04	0.29	0.95	0.63	0.14	14.38
G18	0.33	0.96	0.24	0.96	0.19	0.91	0.20	0.99	0.60	0.16	17.88
G17	0.25	0.91	0.21	0.93	0.23	0.95	0.24	0.91	0.58	0.17	17.12
G24	0.14	0.79	0.17	0.85	0.32	0.98	0.30	0.74	0.54	0.21	18.00
G16	0.14	0.64	0.11	0.66	0.14	0.69	0.14	0.63	0.39	0.31	22.75
G8	0.33	0.46	0.26	0.45	0.22	0.43	0.23	0.46	0.36	0.38	18.62

¹The lower the superiority and ranks score the greater the yield across environments, the environments are described in Table 4.2. The superiority and ranks scores are generated by the analysis software on command in GenStat (Payne et al., 2012).

Chapter 5

Mechanisms of Tolerance to Drought Stress in Sweetpotato

Abstract

Drought is a major yield reducing factor in sweetpotato and breeding for drought tolerant varieties requires knowledge of the mechanisms of drought tolerance. This study was conducted to more closely evaluate the effects of drought on a set of sweetpotato genotypes assessed as highly, moderately and not drought tolerant based on their prior performance in the field. The experiments were conducted at Kenya Agricultural Research Institute (KARI) Muguga, Kenya, in a greenhouse during 2012 and 2013. The studies were laid out in a split plot design, with watering regimes as the main plot and genotypes as subplots in a randomised complete block design (RCBD), replicated three times. The watering regimes were; drought stress started at 30, 60, and 90 days after planting (DAP) and no water stress over the growth period. Data on growth and yield characteristics were recorded and analysed in Genstat 14th edition. Significant differences ($P=0.05$) were observed in the fresh weight of pencil roots (FPR) plant⁻¹, fresh vine weight (FV) plant⁻¹, and fresh storage root weight (FSR) plant⁻¹ among the genotypes and between watering regimes. Fresh storage root yield was significantly lower at regime 1 (30) and regime 2 (60). The genotype x watering regime (GE) interaction was significant for number of vine branches (NB), pencil roots index (PRI), total length of vines branches (VL), and vine tip pubescence (VTP). The drought tolerant genotypes (194555.7 and Unawazambane06-1) produced significantly more fresh storage root yield (FSR) and number of storage roots (NSR) compared to the non-tolerant genotypes (Excel and A56). The number of branches (NB) increased with reduction of drought stress; however, more tolerant cultivars had reduced NB. In addition, the difference in number of pencil roots (NPR), FSR, and %RDM between drought stress at 90 DAP and the control was not significant. Drought stressed genotypes had shorter VL, reduced chlorophyll content (CC) and reduced leaf size (LS). Vine tip pubescence (VTP) and mature leaf pubescence (MLP) increased with drought stress and also with drought tolerant genotypes. These findings suggested that assimilates were being channelled to the storage roots from vines and leaves as a survival mechanism. The reduced vine branches on drought tolerant genotypes minimised evapo-transpiration suggesting that vine structure may be an important mechanism for drought tolerance. Drought stress that occurred within 90 days (30 and 60 days regimes) after planting led to the proliferation of pencil roots, as a response to moisture stress. Therefore, the first three months are the critical period when moisture stress will significantly affect the sweetpotato storage root yield.

Key words: Drought tolerance mechanisms, vine biomass, drought tolerance, storage roots, pencil roots, moisture stress, genotypes

5.1 Introduction

Drought is a major abiotic stress in sub-Saharan Africa. Growing environments which initially did not experience drought episodes are now encountering drought due to poor unreliable and erratic rainfalls (Reddy et al., 2009). Moreover, the majority of farmers in sub-Saharan Africa do not have the resources to irrigate their farms. Most farmers do small scale farming where irrigation is not economically feasible. Thus farmers tend to plant crops that are perceived as drought tolerant such as sweetpotato, cowpeas and sorghum (Chapman and Augé, 1994). The yield of these perceived drought tolerant crops, which until now still consists of unimproved varieties and/or landraces, however is still decreased considerably due to drought stress. Thus, a mitigation intervention is required to reduce the impact of drought stress. One such mitigation would be breeding improved drought tolerant varieties (Reddy et al., 2009). To assist this breeding intervention, breeders need to understand the mechanisms of drought tolerance in the crop being improved.

The response of crops to drought in most cases is summed up by evaluating the yield of genotypes under drought stress (Makihara et al., 1999). Different parameters are measured to determine whether a genotype is drought tolerant or not. These include days to maturity (DTM), an indicator of whether the clone is capable of escaping drought, and growth and productivity characteristics such as yield, plant vigour, and drought sensitivity index (DSI) (Fischer and Maurer, 1978). Sweetpotato is generally recognized as a drought tolerant crop and it may tolerate drought through its ability to adjust its plant structure and metabolism. These developmental adjustments include broad genotypic variability for root length and density, biomass accumulation, translocation efficiency, stomatal regulation and soil moisture content mining and conservation.

There are many factors that influence the storage root yield of sweetpotato under drought stress. Rooting and vine growth structure influence the number of storage roots and their sizes which is further influenced by drought stress. This may be explained by alteration of sink-source relationships, which affect assimilate production, translocation and partitioning, and thus influencing the size and number of roots and thus yield (Anjum et al., 2011). Sweetpotato is sensitive to drought stress during the establishment and storage root initiation stages (Ekanayake, 1990). Moderate drought stress is estimated at 60% of the potential evapo-transpiration (Ekanayake, 1990). However, the responses to drought of sweetpotato at a specific stage of its growth have not been reported. Drought tolerant

sweetpotato varieties would minimize the risk of crop failure in absence of sufficient rains and irrigation to resource poor, and food insecure farmers. However, breeding for the drought tolerant varieties of sweetpotato will require knowledge of the crop's drought response mechanisms. Therefore, the objective of this study was to determine the mechanisms of drought tolerance in a set of sweetpotato genotypes assessed as highly, moderately and not drought tolerant based on their prior performance in the field.

5.2 Materials and method

5.2.1 Plant materials and experimental site

The study was conducted in a greenhouse at the National Agricultural Research Centre, KARI-Muguga between January 2012 and March 2013. Eight sweetpotato genotypes that included two drought tolerant clones (194555.7 (G3) and Unawazambane06-1 (G7)), two semi-drought tolerant (199062.1 (G3) and Resisto (G2)), two drought susceptible cultivars (Excel (G4) and A56 (G8)), and two controls (drought tolerant 441725 (G1) and drought susceptible Nyar buholo (G6)) were used in this study. Irrigation treatments comprised: regime 1 - stress started 30 DAP until harvesting, regime 2 - stress started 60 DAP until harvesting, regime 3 - stress started 90 DAP until harvesting and regime 4 - soil moisture maintained at field capacity until 2 weeks before harvesting (control). Pots of 10 kg were filled with sterile soil which contained macro and micro nutrients as indicated in Table 5.1. Two tensiometers were fitted into two pots of each irrigation regime at 30-40 cm depth such that at least each of the eight cultivars had moisture monitoring tensiometers. The pots were also fitted with drippers connected to the drip line with a control that allowed water to run for one and half hours into the growth media to attain field capacity moisture. Sweetpotato vines of each genotype and about 25 cm long were planted in the pots. Each genotype was planted in a pot replicated four times per block using a split-plot design, with each irrigation line assigned one irrigation regime (main plot) and each sweetpotato genotype (subplot) with three blocks. The drippers released water at the rate of two litres per hour. Water for regime four (control) was applied twice a week or when the pot tensiometers read 15 centbars. Irrigation was done in two splits; 30 minutes in the morning and 30 minutes in the evening, to allow uniform water infiltration (Table 5.1). Weather conditions in the greenhouse were monitored using data loggers (HOBO U12-012 – data logger temp/RH/Light/ext channel, Micro Precision Calibration Inc., 22835 Industrial Place Grass Valley, CA USA 95949).

Table 5.1: Amount of irrigation water (litres) applied for various treatment regimes

Regime	During planting pot ⁻¹	2-30 DAP	31-60 DAP	61-90 DAP	91-120 DAP	121-150 DAP	Total water applied
1	3	16	0	4	4	0	27
2	3	16	16	0	0	0	35
3	3	16	16	16	0	0	51
4 (control)	3	16	16	16	16	8	75

DAP = days after planting

Data on fresh pencil roots (roots that would otherwise develop to storage roots but does not because of unfavourable condition) weight in g plant⁻¹ (FPR), fresh vine weight in g plant⁻¹ (FV), fresh storage root weight gplant⁻¹ (FSR), were recorded. Counts were also done for number of storage roots plant⁻¹ (NSR), branches plant⁻¹ (NB), and pencil roots plant⁻¹ (NP). The length of all pencil roots in m plant⁻¹ (PL), vine branches in m plant⁻¹ (VBL), basal vine length in m (VL), and basal vine diameter in mm (VD) were also measured 15 days after moisture stress was initiated (DAMSI) and at 45 DAMSI. Leaf length and leaf width of 10 marked leaves in cm plant⁻¹ (LL+ LD) was also measured 15 DAMSI and at 45 DAMSI. Chlorophyll content (CC) in µgcm⁻², scores of vine tip pubescence (VTP) and mature leaf pubescence (MLP) (scores 1 = least; 7 = highest) were taken 45 DAMSI while at regime R4 (control) was taken at 135 days after planting. Root samples were dried in a forced draught oven set at 40°C until a constant mass was attained and percent root dry matter (%RDM) generated. Harvest index (HI), pencil root index (PRI), and root length index (RLI) were estimated as follows:

$$HI = \frac{\text{weight of storage roots}}{\text{Weight of storage roots plus weight of pencil roots and vine}}$$

$$PRI = \frac{\text{weight of pencil roots}}{\text{Weight of pencil and storage roots plus weight of vine}}$$

$$RLI = \frac{\text{Length of pencil roots}}{\text{Length of storage roots plus length of vine branches}}$$

The temperature in °C, percent relative humidity, light intensity in lux and dew point °C was monitored using data logger, while soil moisture content was monitored using tensiometers.

5.2.2 Data analysis

Data were subjected to analysis of variance (ANOVA) using Genstat 14th edition (Payne et al., 2012) under split plot design commands to determine differences among genotypes. Treatment means were separated using LSD at p<0.05.

5.3 Results

5.3.1 Weather conditions

The maximum temperature ranged between 25-45°C (mean 35°C), while the minimum temperature ranged between 10-18°C (mean 14°C). Minimum relative humidity ranged between 20-70 (mean 45%) and maximum range was 80-99% (mean 89.5%). Minimum light intensity was 2000-8000 (mean 5000 lux) while maximum range was 5000-30000 (mean 17,500 lux). The minimum dew point ranged 5-15°C (mean 10°C) and maximum ranged from 12-25°C (mean 18.5°C) (Fig. 3.3 in chapter 3 of this thesis)

5.3.2 Soil chemical analysis

The major soil nutrients, N, P, and K were adequate. The pH was neutral while magnesium was low. Also, the minor nutrient elements were high (Table 5.2).

5.3.3 Analysis of variance for yield traits

The clones showed significant ($p \leq 0.001$) genotype (G), and environment (E) effects in all the traits studied. Genotype x environment interaction (GEI) was only significant for fresh weight of pencil roots (FPR) and percent storage root dry matter (%RDM) (Table 5.3).

Table 5.2: Amounts of macro and micro nutrients in the sterile soil used for planting the sweetpotato genotypes

macro nutrients	quantity	status	micro nutrients	quantity	status
%N	0.524	adequate	ppmMg	30.46	low
% Org. C	6.99	adequate	ppmNa	80.20	adequate
ppmP	132.75	adequate	ppmFe	203.23	high
ppmK	1658.60	high	ppmZn	25.90	high
ppmCa	2836.51	high	ppmCu	0.99	adequate
pH	6.98	neutral	ppmMn	97.81	high

Table 5.3: Combined analysis of variance for yield-related agronomic traits of eight sweetpotato genotypes tested under different watering regimes

Source	df	Mean squares					
		PRI	%RDM	HI	FSR	FPR	FV
Block	2	25.1	1.0	18.8	3516.2	219.5	1740.2
Regime (E)	3	8882.2***	1832.2***	1258.1***	595660.0***	6410.4***	525796.1***
Residual	6	5.3	17.7	17.4	2538.1	200.1	559.3
Genotype (G)	7	2288.1***	98.0***	728.4***	77197.2***	4876.4***	37503.0***
GE	21	380.3*	38.1*	313.4*	2281.3ns	893.5ns	5757.1ns
Residual	56	27.9	14.5	59.1	2384.2	453.9	3347.0
CV%	-	53.3	15.5	25.4	41.1	43.4	45.3

df = degrees of freedom, PRI = weight of pencil roots/weight of pencil roots plus storage roots and fresh vine weight in %, %RDM = percent root dry matter, HI = harvest index, FSR = fresh storage root weight in g plant⁻¹, FPR = fresh pencil root weight in g plant⁻¹, FV = fresh vine weight in g plant⁻¹

5.3.4 Genotype performance for yield traits

Water regime R1 had the lowest FSR (98.9), FV (242.7) and HI (43.4) but highest %RDM (36.9), and PRI (30.7). Regime R3 and R4 had similar FSR; 270.8, 286.6 g plant⁻¹, respectively, but both regimes differed significantly in FV, RDM, FPR, PRI and HI (Fig. 5.1a and b).

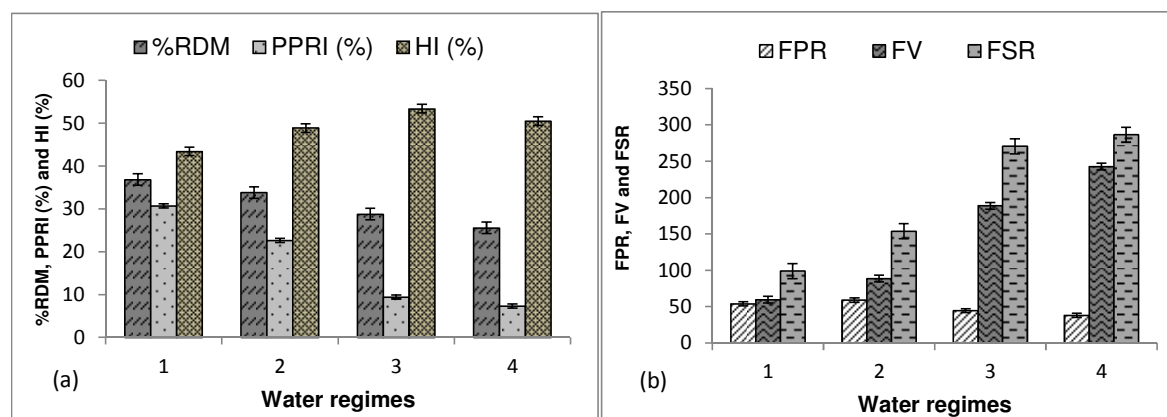


Figure 5.1: The effect of water regimes on selected traits: (a) percent root dry matter (%RDM), pencil roots index plant⁻¹ in % (PRI), and harvest index (HI) in %, (b) fresh weight of pencil roots in g plant⁻¹ (FPR), fresh weight of vines in g plant⁻¹ (FV) and fresh storage root weight in g plant⁻¹, fresh weight of storage roots in g plant⁻¹ (FSR). LSD_{0.05} bars are shown. The water regimes are as described in Table 5.1

Checks G1 and G6 and the drought tolerant genotypes G3 and G7 showed increased %RDM and their %RDM was only different from that of clone G5. Clone G5 had the lowest

%RDM (28.41) and FPR (47.91). The drought tolerant genotypes G3 and G7 had the highest FSR (262.93, 248.42), FV (186.52, 177.72) and HI (54.45 and 53.7) but, lowest FPR (33.13, 35.43), PRI (7.84, 9.11). Clones G6 and G8, which were drought susceptible had lowest FSR (142.82, 149.32) and HI (43.34, 43.73), while G4 had the lowest FV (97.54) (Table 5.4).

5.3.5 Performance of genotypes on the growth traits

Analysis of variance for the growth traits showed significant differences ($p \leq 0.001$) of genotype and moisture regimes effects. The interaction effects were significantly different at $p \leq 0.05$ on number of branches, total length of pencil roots, and total length of vines among the genotypes (Table 5.5).

Table 5.4: Genotype performance on yield traits

Genotypes	Status	RDM(%)	PRI (%)	HI (%)	FPR	FV	FSR
G1	T (CK)	31.73	12.12	50.09	41.44	162.07	199.34
G2	IT	31.37	15.24	52.99	49.59	159.61	221.99
G3	T	31.24	7.84	54.45	33.13	186.52	262.93
G4	IT	29.35	28.47	45.45	61.18	97.54	162.93
G5	S	28.41	16.51	48.66	47.91	145.09	232.61
G6	S (CK)	33.41	25.39	43.34	63.13	114.74	142.82
G7	T	32.51	9.11	53.74	35.43	177.72	248.42
G8	S	32.15	25.45	43.73	59.29	116.28	149.32
LSD _{0.05}	-	1.72	2.49	3.63	10.06	27.32	23.05

Genotypes were G1 = 441725, G2 = Resisto, G3 = 194555.7, G4 = Excel, G5 = 1990621, G6 = Nyar buholo, G7 = Unawazambane06-01, and G8 = A56, T = drought tolerance in the field, IT = moderately drought tolerant, S = drought susceptible, CK check, the abbreviations for the traits are as described in Fig. 5.1.

Table 5.5: Combined analysis of variance for growth-related agronomic traits of eight sweetpotato genotypes tested under different watering regimes

Source	d.f	Mean squares				
		NSR	NB	VL	LRV (m)	%RLI
Block	2	0.14	10.1	29.28	65.9	30.4
Regime	3	133.6***	514.4***	1147***	434.06*	29715.7***
Residual	6	1.15	10.9	15.86	44	143
Genotype	7	60.7***	93.3***	277***	1227.0***	545.5***
GE	21	0.92ns	16.32*	58*	99.5*	445.4*
Residual	56	0.71	7.77	8.51	31.2	109
Total	287					
CV%		38.2	51.5	16.5	24.1	23.9

NSR = number of storage roots plant⁻¹, NB = number of branches plant⁻¹, VL = vine braches plant⁻¹ in m, **LRV** = estimated total length of roots plus the length of all vine braches plant⁻¹ in m, %RLI = percent length of total roots LRV plant⁻¹ in m.

Water regime R1 had the longest root plus vine length (RVL) (27.2), followed by R2 (23.6). Regime R3 and R4 had similar RVL; 21.3 and 21.8 respectively. Regime R1 had the highest root length index (% RLI) (82.4), while regime R4 had the least (44.4) (Figure 5.2).

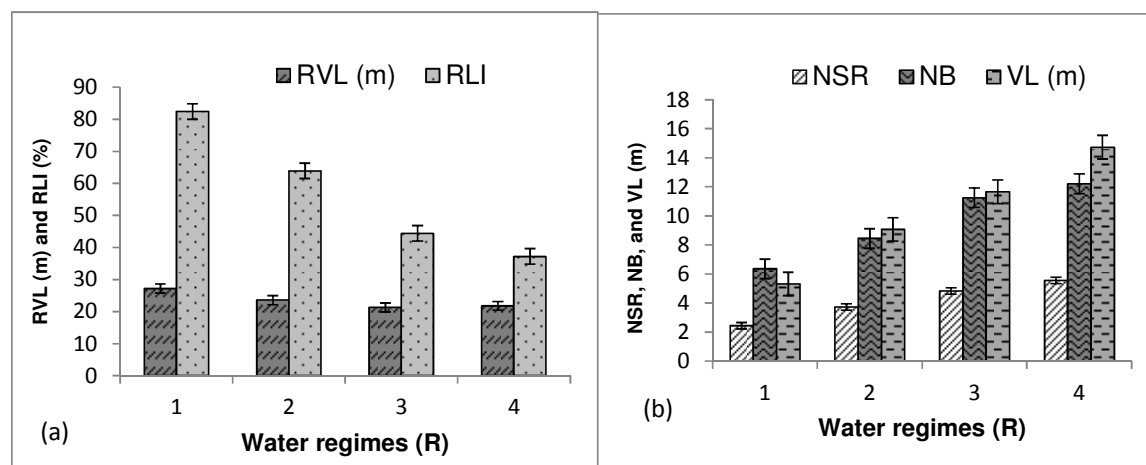


Figure 5.2: The effect of water regimes on (a) roots length plus length of vine branches in m plant⁻¹ (RVL) and percent root length index plant⁻¹ (RLI), (b) the total number of storage roots plant⁻¹ (NSR), number of branches plant⁻¹ (NB), and total length of vine braches plant⁻¹ in m (VL). LSD_{0.05} bars are shown.

Genotype G4 had the lowest RLI (53.2%), while genotype G7 had the highest RLI (64.9%). Genotypes G4 and G8 had the lowest number of storage roots while G3 and G7 had the

highest. Genotypes G3 and G1 had the lowest number of branches (NB) while G2 and G8 had the highest. Genotype G3 and G5 had highest number of vine branches while G4 and G6 had the lowest. Genotypes G4 and G8 had the lowest root vine length while genotype G3 and G5 had the longest (Table 5.6).

Table 5.6: Performance of genotypes for growth-related traits under different moisture regimes across environments

Genotypes	Status	RVL (m)	% RL	NSR	NB	VL (m)
G1	T (CK)	24.60	57.30	3.88	7.82	10.79
G2	IT	28.50	59.90	4.38	11.40	11.58
G3	T	30.10	54.20	6.12	7.38	13.33
G4	IT	13.20	53.20	2.68	10.30	5.26
G5	S	23.40	53.80	5.10	10.60	13.69
G6	S (CK)	20.40	56.70	2.57	8.85	8.56
G7	T	30.50	64.90	5.24	8.62	8.60
G8	S	18.50	55.90	3.12	11.60	9.75
LSD _{0.05}	-	5.40	10.02	0.40	1.32	1.38

T = drought tolerance in the field, IT = moderately drought tolerant, S = drought susceptible, CK check, the abbreviations for the traits are as described in Fig. 5.2., and the genotypes are as described in Table 5.4

5.3.6 Performance of the genotypes on drought stress traits

Genotype and moisture regimes were highly significantly different at $p \leq 0.001$ for all traits recorded. However, the interaction effect was only significant at $p \leq 0.05$ for vine tip pubescence (Table 5.7).

Table 5.7: Mean squares for drought stress traits

Source of variation	d.f.	BVL	VID	Leaf size (LL+LD)/2	CC	VTP	MLP
Block	2	2360.001	0.002	1.321	23.496	0.056	0.003
Regime (E)	3	26583.012***	1.351***	660.301***	178.703***	0.760***	0.470***
Residual	6	702.031	0.004	0.703	3.446	0.021	0.003
Genotype (G)	7	14640.021***	0.582***	25.702***	58.004***	1.149***	0.110***
GE	21	467.004	0.003	1.822	6.961	0.105	0.009*
Residual	56	307.022	0.003	1.551	4.968	0.015	0.004
Total	287	1073.031	0.006	2.240	6.421	0.075	0.022
CV%	-	36.702	10.410	12.301	11.004	13.802	38.201

BVL= basal vine length plant⁻¹ in m, VID = mean internode diameter of 10 randomly selected internodes plant⁻¹ in cm, Leaf size (LL+ LD) = the mean of sum of length and width of randomly selected 5 leaves plant⁻¹. CC = leaf chlorophyll content plant⁻¹ in μgcm^{-2} , VTP = vine tip pubescence (scores 1 = least 7 = highest), MLP = mature leaf pubescence (scores 1 = least 7 = highest). VTP and MLP scores were transformed by $\log_{10}(x+1)$, where x is the score.

Water regime R4 had the highest basal vine length (53.5 cm), vine diameter (0.44 cm), leaf size (10.27 cm) and chlorophyll content (24.55). Regime R1 had the lowest change in basal vine length (10 cm), vine diameter (0.15 cm), and leaf size (3.28 cm) and also the lowest chlorophyll content (21.0). Vine tip pubescence was highest for regime R1 and lowest under regime R4 and the same was observed for mature leaf pubescence. Drought stress reduced chlorophyll (CC) in leaves (Fig. 5.3a). Drought stress (R1, R2, and R3) reduced basal vine length and vine internode diameter (Fig. 5.3b).

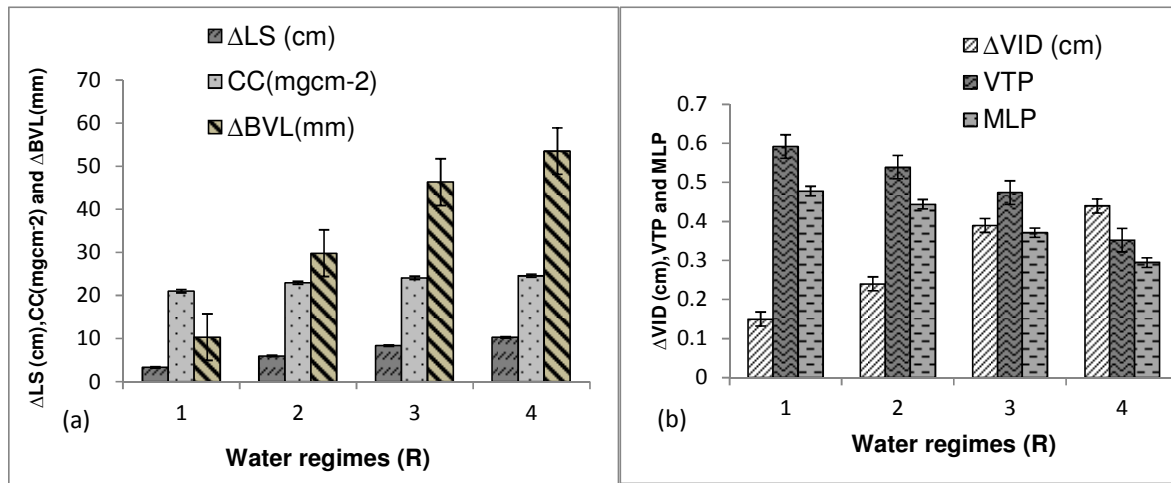


Figure 5.3: The effect of water regimes on selected traits: (a) change in size of randomly selected 10 leaves plant⁻¹ in cm (Δ LS), chlorophyll content (CC) in five randomly selected leaves plant⁻¹ in mgcm² (Δ CC), change of basal vine length plant⁻¹ in cm (Δ BVL), (b) change in diameter of randomly selected 10 vine internodes plant⁻¹ in cm (Δ VID), vine tip pubescence plant⁻¹ (VTP) and mature leaf pubescence plant⁻¹ (MLP). VTP and MLP scores with 0 = no pubescence, and 7 = the highest pubescence, were transformed by $\text{Log}_{10}(x+1)$. $\text{LSD}_{0.05}$ bars are shown.

Clone G8 had the least leaf expansion while clone G4 and G5 had the highest leaf expansion. Clone G1 and G6 had the lowest chlorophyll content while clone G3 and G5 had the highest. Clone G5 had the highest basal vine length while clone G4 had the lowest. Clone G3 had the highest vine diameter. Genotype G8 had the lowest vine internode diameter (0.14). Clone G4 had the least vine tip pubescence while clone G5 had the highest pubescence. Clone G5 had the highest mature leaf pubescence while clone G4 had the least mature leaf pubescence (Table 5.7).

Table 5.7: Genotype performance on drought related traits

Genotypes (G)	Status	Δ BVL (cm)	Δ VID(mm)	Δ LS (cm)	CC(mg cm ²)	VTP	MLP
G1	T (CK)	26.00	0.23	6.64	21.62	0.40	0.35
G2	IT	44.00	0.24	7.42	23.61	0.61	0.38
G3	T	55.10	0.49	7.12	24.57	0.63	0.46
G4	IT	7.80	0.24	8.13	22.25	0.20	0.36
G5	S	63.60	0.44	7.73	24.67	0.72	0.47
G6	S (CK)	22.20	0.23	6.51	21.70	0.33	0.37
G7	T	46.60	0.43	6.71	24.19	0.62	0.45
G8	S	14.40	0.14	5.40	22.52	0.42	0.33
$\text{LSD}_{0.05}$	-	8.27	0.03	0.59	1.05	0.06	0.03

T - drought tolerance in the field, IT - moderately drought tolerant, S - drought susceptible, CK check, the traits are as described in Fig. 5.3 and the genotypes are as described in Table 5.4

5.4 Discussion

5.4.1 Weather conditions and soil analysis

The mean minimum maximum temperature range was 14°C-35°C. The low temperatures mainly at night were largely within the minimum for growth of the crop since, the basal temperature for accumulation of DDU's in most crops including sweetpotato is 10°C. Tarun et al (2010) reported in *Brassica juncea* that growing days degrees (heat units) accounted for 60-70% of the variation in seed yield and oil content. In this study, the high maximum temperatures above 35°C were probably due to greenhouse effect, which simulated the ideal situation of arid and semiarid drought prone areas. The mean minimum and maximum relative humidity ranged from 45 - 89.5%, which indicates evapo-transpiration was largely active. At relative humidity of 100%, the air can no longer hold all the water vapour and thus condenses back as dew, usually referred as dew point

The light intensity ranged from 5000-17,500 lux, on average, which indicates the light intensity was sufficient for evapo-transpiration and photosynthesis of sweetpotato. Leghari et al. (2005) reported increased photosynthesis, leaf size, dry matter and yield of beans as light intensity increased from 10,000 lux to 15,000. Kumura (1965) reported that soybean photosynthesis increases rapidly up to 15,000 lux and increases with reducing rate up to 25,000 lux. The light intensity was good for the drought screening experiment. The fluctuations of the light intensity were due to fluctuating cloud cover, and changing weather and seasons, which were uncontrollable but similar to a field situation.

The mean minimum maximum dew point ranged 10-18.5°C. Lawrence (2005) reported that dew point temperature of 13.71-13.51°C was equivalent to 90% relative humidity while 4.66-5.00°C was equivalent to 50% relative humidity, which agrees with this study (Fig. 5.1). Thus in the greenhouse study, at dew point, dew settled on the sweetpotato plants and cooled them and moistened the soil surface on the pots reducing the severity of the moisture stress. This may also indicate that the genotypes that had high yield under moisture stress regimes had better cooling and utilisation ability of the water (dew) at dew points.

The major nutrients, N, P, and K were adequate indicating there were no side effects of nutrient deficiencies in the experiment. The pH was neutral while magnesium was low indicating the high minor nutrient elements though high, were not toxic to the plants. Also, the micro elements, might have chelated the magnesium making it unavailable and hence why it was low. But in general, the plant growth observed in this experiment was good.

5.4.2 Genotype performance for yield traits

Percent storage root dry matter increased with drought stress probably due to cell dehydration. However, the dry matter was relatively high in drought stressed genotypes, which may indicate that these clones accumulated solutes in cells to balance turgor pressure as a way of regulating stomatal opening and hence water loss through evapo-transpiration. Probably also, the storage roots of the drought tolerant clones had substantial amount of the water in the vacuoles for transpiration which in turn accumulated more starch in the cytoplasm, hence higher storage root yields. More underdeveloped roots (pencil roots) were found in the drought stressed regimes, an indication that the clones channelled assimilates to the fibrous root in search of water in deeper parts of the soil. There were no significant differences in stress after 90 DAP and to some extent 60 DAP and the control in RDM, FSR, NB, and RVL an indication that the first two to three months is the critical period when drought stress can significantly affect the sweetpotato storage root yield. This is supported by work in Malawi, where five sweetpotato cultivars were evaluated on residual moisture during dry season and the results showed, the most drought tolerant genotype had the highest root yield of 18.25 t ha⁻¹, while the least tolerant cultivar had root yields of 9.65 t ha⁻¹. (Mkandawire et al., 2008)

The sweetpotato storage roots also may act as a conduit of water and nutrients from the soil to the above ground parts of the plant while serving as the storage organ of the photosynthates, and thus, its ability to regulate solute concentration is vital. Probably, continued drought stress in sweetpotato interferes with the filling of storage roots with assimilates especially if the drought stress occurs in the first three months after planting, resulting in lignified pencil roots which are not edible and will not develop into storage roots. However, this may be another form of drought stress tolerant mechanism that does not benefit the grower. Similar results were reported in wheat where drought stress reduced the yield but the reduction was lower in resistant genotypes relative to susceptible genotypes (Jaleel et al., 2009; Abd El-Moneim et al., 2010). In another study Shigwedha et al. (2004) reported that high storage root yield was attributed to drought tolerance. The length of the pencil roots was found to be longer on genotypes under moisture stress than genotypes under no moisture stress, showing that sweetpotato responds to moisture stress by increasing the length of the roots in search of water in deeper parts of the soil.

5.4.3 Performance of genotypes for the growth traits

Clones grown under drought stress regimes (R1, R2, and R3) had small sized and fewer storage roots an indication that sweetpotato responds to drought by reducing the number of storage roots as well as their size. The length of the pencil roots was longer on genotypes under drought stress indicating sweetpotato responds to drought stress by increasing the

length of fibrous roots. The number of vine branches was reduced in drought tolerant genotypes compared to the control line, suggesting that reduced branching may also represent a mechanism of drought tolerance in sweetpotato. Reduced branching may have minimised the leaf area which in turn reduced water transpiration as drought stress gradually turned severe. Moreover, the length of the branches was also shorter under drought stress. Studies on wheat also reported variability among six genotypes for the developmental traits (Lazar et al., 1995).

5.4.4 Performance of the genotypes for moisture stress traits

Drought tolerant genotypes had increased shoot and mature leaf pubescence which suggests that drought tolerance in sweetpotato may be associated with pubescence, which reduces evapo-transpiration in the leaves sparing some water for metabolism. This could also be the reason for improved yield in drought tolerant genotypes. Newell et al. (1994) found lower moisture loss, higher variable fluorescence, and higher fluorescence quenching under drought stress for drought tolerant cultivars. The chlorophyll content (CC) in non-drought tolerant genotypes was reduced compared to tolerant types and CC content was also reduced in the drought stress regimes indicating moisture stress reduces CC in leaves. This phenomenon could reduce assimilate formation and result in lower storage root yields. Compared to the drought susceptible lines, the drought tolerant cultivars still retained some level of CC indicating that retention of leaves and CC on the leaves is a mechanism of drought tolerance in sweetpotato.

Drought stress also led to reduced growth of vines in terms of internode length, diameter and vine length. This is in agreement with the findings of Saraswati et al. (2004) who screened 15 clones of sweetpotato for drought in the greenhouse and found that plant biomass, main stem length, internode diameter, internode length, leaf number, leaf area and root weight decreased in response to water stress. Also, Maluf et al. (1983) reported high positive correlation of vine length and number of internodes per vine ($r=0.72$).

5.5 Conclusion

Drought tolerant genotypes had increased root yield while number of storage roots, and vine branches, reduced with increase of drought stress. Moreover, drought tolerant cultivars had reduced vine branches, an indication that the vine structure of sweetpotato is vital for reduced evapo-transpiration and thus is a mechanism for drought stress survival. Shoot and mature leaf pubescence increased with moisture with the drought tolerant genotypes revealing pubescence as one mechanism to reduce drought stress. Drought stress after 90 DAP (R3) did not cause significant difference with non-stress regime (control) in root dry

matter and fresh storage root weight (FSR). In summary, this work showed mechanisms such as reduced numbers and sizes of storage root, proliferation of pencil fibrous roots, reduced vine branching, prolonged fibrous roots, increased shoot, mature leaf pubescence and ability to retain chlorophyll content under moisture stress, were probably the drought tolerance mechanism used by the sweetpotato clones evaluated.

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Chapter 6

Combining Ability and Heterosis for Yield and Drought Tolerance Traits under Managed Drought Stress in Sweetpotato

Abstract

Drought is one of sweetpotato production constraints in sub Saharan Africa. There is limited information on the genetics of sweetpotato yield under managed drought stress conditions in Kenya. Two studies were conducted using 15 F1 sweetpotato families (G1-G15) generated using a half-diallel mating scheme of six parents. The first experiment was conducted in the field at the Kenya Agricultural Research Institute (KARI) Kiboko research station. The experiment was laid out in a split plot design involving two replicates under drought stress and no drought stress conditions and repeated three times between January 2012 and June 2013. Drought tolerance was validated in a second greenhouse experiment using a rapid drought screening method under randomized complete block design (RCBD) replicated five times at KARI Muguga. General combining ability (GCA) and specific combining ability (SCA) effects for root yield in both drought stressed and no drought stress environments were significant ($P \leq 0.05$). Families G2, G5, G7, G8, G10, G12 and G15 had high fresh storage root yield (FSR) under the drought stressed ($5.42-6.82 \text{ t ha}^{-1}$) and none drought stressed ($39.5-63 \text{ t ha}^{-1}$) environments and higher number of days to permanent wilting point (DPWP) (79-91 days) and drought susceptibility index (DSI) of 0.9-1 compared to the other families. Crosses G2, G15 and G12 had progenies with the highest total biomass ($10.1-10.5 \text{ t ha}^{-1}$) under drought stress, while G15, G12 and G5 had highest biomass ($55.8-68.9 \text{ t ha}^{-1}$) under the no drought stress environment. Crosses G15, G5 and G7 had the highest significant ($P \leq 0.05$) SCA effects for FSR yield under drought stress while under no drought stress G15, G7, and G12 had the highest significant SCA effects for FSR yield. Crosses G15, G5 and G2 had the highest significant ($P \leq 0.05$) SCA effects under drought stress while crosses G12, G7, and G2 had the highest significant SCA effects under no drought stress for FSR. The mean GCA/SCA ratio was 0.67 under drought stress and 0.54 under no drought stress indicating additive gene effects were more important than non-additive gene effects for FSR, total fresh biomass (BIO), harvest index (HI), marketable number of storage roots (MNR) and percent storage root dry matter (%RDM). Progeny 8 from family G4, 5 and 8 from G15, showed the highest mid and best parent heterosis (117% and 269.6%) for FSR yield in both environments. Progeny 6 and 7 from cross G10 had the highest mid and best parent heterosis (164.8% to 233.6%) for fresh total biomass yield under no drought stress environment. Based on the overall results of these experiments families G8 (P2xP3), G10

(P2xP1), G12 (P2xP5) and G15 (P1xP5) seemed to have improved drought tolerance and could be used in recurrent selection to develop drought tolerant cultivars.

Key words: Combining ability; days to permanent wilting point; drought tolerance; gene effects; heterosis; sweetpotato

6.1 Introduction

Sweetpotato is an important crop in sub-Saharan Africa (Laurie et al., 2004). Drought is the main abiotic constraint occurring in large parts of this region (Anjum et al., 2011). In Kenya, over 80% of the land experiences drought and this drastically reduces crop yields (Jaetzold et al., 2006). This raises the need for crop improvement programmes in the region to address drought tolerance.

Understanding the mode of gene action is vital in any crop improvement programme (Acquaah, 2007). Sweetpotato, *Ipomoea batatas* (L.) Lam. is hypothesized to be an autohexaploid ($2n=6x=90$) and the species exhibits complex segregation ratios in crosses (Kriegner, et al 2003.). Inheritance of some traits may be simple and follow Mendelian segregation ratios when a single dominant gene is present, but the majority of the characteristics of importance in sweetpotato are inherited quantitatively (Jones et al., 1987). However, even when a trait is simply inherited segregation in this complex polyploid typically results in a continuous distribution due to allele dosage effects (Falconer and Mackay, 1996).

Diallel mating designs are commonly used to determine gene action for quantitative traits (Hayman, 1954; Hallauer et al., 2010). Two parameters which are normally calculated from such studies include general combining ability (GCA) and specific combining ability (SCA). GCA is the average performance of a parent genotype over several cross combinations and is associated with additive gene effects, while specific combining ability (SCA) reveal the average performance of crosses that perform better and is typically associated with non-additive gene effects (dominance) (Shiri et al., 2010; Darvishzadeh et al., 2011). Stuber (1980) indicated that an evaluation of crosses with at least five parents in a half diallel gives reliable estimates of GCA and SCA. Various diallel mating methods have been extensively used in crop plants. In this study, the diallel mating design method II (parents, F1's, no reciprocals) was used (Griffing, 1956).

Although studies to understand the mode of gene action of inheritance of important traits in sweetpotato have been conducted, none has been reported for drought tolerance. Collins (1977) reported dominant additive gene action for the control of fusarium wilt in sweetpotato,

Mwanga et al (2002) reported additive gene action as dominant for SPVD resistance, Chiona (2010) reported additive gene action in the inheritance of β -carotene. The objective of this study was to determine the inheritance of drought tolerance in sweetpotato and provide insights into the type of gene action controlling sweetpotato storage root yield under managed drought stress conditions. This information is required to begin a breeding program for drought stress tolerance in sweetpotato.

6.2 Materials and methods

6.2.1 Experimental sites

The experiments were conducted at Kenya Agricultural Research Institute (KARI) Kiboko and in greenhouse at KARI-Muguga Research station. Descriptions of these experimental sites are as in section 3.2.1 of this thesis.

6.2.2 Plant materials and crosses

Twenty-four sweetpotato clones were selected during an earlier field-based drought evaluation trial (see chapter three of this thesis). The clones consisted of eight drought tolerant, eight moderately drought tolerant and eight drought susceptible genotypes (Appendix 6.1). During flowering, the clones were pollinated in a diallel mating design to generate F1's (Griffings method II). Crosses in all possible combinations (excluding selfs) were made between 2010 and 2011 at the KARI-Muguga Research station. A total of six parents that had over 20 seeds per cross were selected and the full diallel reduced to a 6 x 6 half diallel. The F1 seed from the crosses of the selected parents were collected at maturity. The seeds were hand scarified and germinated in 5 x 5 x 10 cm sized pots in 3 x 5 cell polystyrene seedling trays, filled with sterile soil and placed on benches in the screen house. The seeds took 4-8 days to germinate. Two months after germination, the seedlings were transplanted into 3 litre plastic pots filled with sterile soil and placed in the greenhouse for multiplication and preservation. Multiplication was done in the greenhouse for 3 months (Fig. 6.1). Twenty cuttings from each parent and 20 F1 seedlings from each cross (family) were obtained for use in this study.



Figure 6.1: Photographs showing (a) no drought stress experiment (b) moderately drought stressed (c) severe drought stress (d) and (e) storage roots harvested from no drought stress plots (f) and (g) rapid drought screening box experiments in greenhouse and planting materials bulking

Table 6.1: Characteristics of sweetpotato clones selected for this study

ID	Parental name	Origin/ Source	Maturity class	Root flesh colour	Fresh root yield t ha ⁻¹	Drought tolerance
P1	1990621	Peru	Medium	Orange	14.3	T
P2	Resisto	USA	Medium	Yellow	16.5	I
P3	Bosbok	South Africa	Medium	Orange	19.5	I
P4	A56	South Africa	Medium	Cream	18.7	S
P5	Excel	USA/Peru	Medium	Light yellow orange	20.1	S
P6	W119	USA	Medium	Deep orange	15.9	T

Where; ID = identification of parents, P = Parent, Medium 120 days on average for maturity T = tolerance to drought, I = semi-tolerant, S = susceptible.

6.2.3 Field experiment

The experimental design used was a split plot with water regime as whole plot and F1 families and parents, as subplots and replicated twice. The experiment was conducted during dry season to enable moisture stress on the plants. In drought stress water regime, soil moisture was maintained optimal until establishment (after one month) after which water application was stopped. On the other hand, water was applied throughout the growth period after planting the genotypes, in the no drought stress regime. At planting, vegetative plant cuttings of about 25 cm long with 4-6 nodes were taken from each parental and F1 plant. The cuttings were inserted 20-30 cm in a 60° slanting position on 25 cm high rows at an intra-row plant spacing of 30 cm and 90 cm spacing between rows. Each experimental plot consisted of 20 plants of each genotype for a total of 300 plots (15 families, 20 sibs per family). Double ammonium phosphate fertiliser was applied at the rate of 50 kg of P₂O₅ ha⁻¹ at planting. The experiment was repeated three times during March 2012 to August 2013. Weeding of the plots was done as required. Morphological data was collected following IBPGR (bioversity) descriptors (CIP, AVDRC, and IBPGR, 1991). The plots were harvested five months after planting time using hand hoes.

Data were recorded on the following traits (Fig. 6.1):

- number of plants harvested per cross
- fresh root yield per cross (FR)
- fresh vine weight per cross(FV)
- number of storage roots per cross (NSR)

- number of marketable storage roots (NMSR)
- total fresh biomass per cross (FB)
- days to permanent wilting point per cross (DPWP)

Samples of vines and roots were obtained and dried in a forced air oven for 72 hours at 40°C and then used to calculate the dry matter. All data were recorded on individual plant basis over the 20 hills.

6.2.4 Screen house experiment

This experiment was conducted in the greenhouse at KARI-Muguga using 20 F1 plants from each of the 15 families. Shoots of 10 cm were cut from each test plant using a sterilised scalpel. The cuttings were planted in a box filled with sterile soil media using RCBD design replicated five times. The box type and dimensions, the composition and filling in of the sterile soil are as described in section 3.2.5 chapter three of this thesis. Each cutting was planted to a depth of five cm. The cuttings were sown at an inter- and intra-row spacing of 15 cm. The growth media was watered to field capacity, as indicated by a zero tensiometer reading. The soil moisture was maintained at field capacity by putting more water every time the tensiometer reading dropped to 15 centibars, until it read zero again, carefully avoiding flooding. Water application was stopped 15 days after. The plots were observed daily and days to permanent wilting point were recorded for each plantlet. Weather data on light intensity, and relative maximum and minimum temperature were collected using data logger and soil moisture stress using tensiometers. The experiment was repeated three times during the period April 2012 and December 2012.

6.2.5 Ranking the clones

The clones were ranked as follows; rank $y = \sum_{k=1}^n x$, where; y is the rank, x is the sum of genotype ranks from trait k to trait n in the traits measured, where k = rank in trait 1 on merit, and n = rank of the last trait. Thus, the best genotype in each trait scored one, while the worst scored 21, which indicates that, considering more than one trait, the best genotype had the least cumulative scores while the worst had the most cumulative scores.

6.2.6 Statistical analysis

Analysis of variance was conducted using SAS 9.2.1 and the Diallel SAS05 procedure developed by Zhang et al. (2005) encoding Griffing's Model I (fixed genotypes), Method II (parents, F1's, no reciprocals) diallel analysis. GCA and SCA effects were computed using Griffing's model (1956) as follows: $Y_{ij} = \mu + g_i + g_j + s_{ij} + \epsilon_{ij}$. Where, Y_{ij} = Average value of the progeny derived from the crossing of i^{th} female parent with j^{th} male parent, μ = Overall mean,

g_i = the GCA effects of the i^{th} female parent, g_j = the GCA effects of the j^{th} male parent, s_{ij} = the SCA effects for the cross between the i^{th} female parent and the j^{th} male parent and ϵ_{ij} = experimental error with ij^{th} genotype in the k^{th} environment. The relative importance of GCA and SCA were estimated using the general predicted ratio (GPR) for the traits observed (Baker, 1978). Ratios close to one indicate additive effects in the inheritance of the trait are important while ratios close to zero indicate dominance effects are important in the inheritance. The GCA/SCA ratio formula is as follows; $GCA/SCA = (2MS_{GCA})/(2MS_{GCA} + MS_{SCA})$ (Baker, 1978). The heterosis estimates were calculated on the basis of mid parent and best parent. Mid parent heterosis was calculated as $H_{F_1} = X_{F_1} - 1/2(X_{P_1} + X_{P_2})$, where X_{P_1} = yield of parent one, X_{P_2} = yield of parent two and X_{F_1} is the yield of progeny one, while best parent heterosis was calculated as $H_{F_1} = X_{F_1} - (X_B)$, where X_{F_1} is the yield of progeny one, X_B is the yield of best parent (Sleper and Poehlman, 2006).

6.3 Results

6.3.1 Analysis of variance

Under the drought stress treatment, environment (E) and genotype (G) effects on fresh root yield of the genotypes were significant but their interaction (GE) effect was only significant for fresh total biomass (BIO) and harvest index (HI) (Table 6.2). The GCA and SCA effects for all traits were significant. However, the GCA and SCA interaction with environment effect was only significant for BIO (Table 6.2). All the GCA/SCA ratios were more than 0.5 except for total fresh biomass (BIO) and marketable number of roots (MNR) which had 0.4 and 0.27, respectively (Table 6.2).

Table 6.2: Combined analysis of variance for five agronomic traits and GCA/SCA ratios for the F1 progenies and their parents under drought environment

Source	df	Mean Squares				
		FSR	BIO	HI	MNR	%RDM
Environment (E)	2	2.67*	65.32***	0.18***	936.60**	1.08 ns
Replication	3	3.18**	2.04	0.02*	807.90**	0.18 ns
Genotype (G)	20	9.66***	20.28***	0.05***	1792.30***	50.02***
G x E	40	0.49 ns	6.93***	0.02***	66.1 ns	0.20 ns
GCA	5	10.15***	8.15**	0.06***	423.50*	77.55**
SCA	15	10.19***	24.65***	0.09***	2235.00**	
GCA*E	10	0.76ns	6.93***	0.01 ns	90.50 ns	0.34 ns
SCA*E	30	0.50 ns	7.78***	0.02**	68.50ns	0.20 ns
Error	60	0.70	1.61	0.01	182.90	0.63
GCA/SCA ratio		0.67	0.40	0.57	0.27	0.76
R2		0.84	0.87	0.80	0.79	0.98

*, **, ***, and ns indicates data significant at $P \leq 0.05$, $P \leq 0.01$, $P \leq 0.001$ and data not significant at $P > 0.05$ respectively, df = degrees of freedom, FSR = fresh root weight in tha^{-1} , Bio = fresh total biomass weight in tha^{-1} , HI = harvest index, MNR = marketable number of storage roots in thousands ha^{-1} , %RDM = percent root dry matter under drought, GCA = general combining ability, and SCA = specific combining ability

Under the no drought stress treatment, the environment (E) and genotype (G) effects on fresh root yield of the genotypes were significant but their interaction (GE) effect was not significant (Table 6.3). GCA and SCA effects on all traits were significant; however, GCA and SCA interaction with environment effect was not significant (Table 6.3). All the GCA/SCA ratios were more than 0.5 (Table 6.3).

Table 6.3: Combined analysis of variance for five agronomic traits and GCA/SCA ratios for the F1 progenies and their parents under no drought stress environment

Source	df	Mean Squares				
		FSR	BIO	HI	MNR	%RDM
Environment (E)	2	2425.01***	2983.21***	0.026**	1226.20 ns	1.08 ns
Replication	3	306.91**	330.45**	0.024***	9499.40***	0.18 ns
Genotype (G)	20	842.17***	822.91***	0.022***	1235.40*	50.02***
G x E	40	12.16 ns	12.19 ns	0.002 ns	153.10 ns	0.20 ns
GCA	5	559.67***	497.49***	0.022**	1143.20*	77.55**
SCA	15	965.31***	941.26***	0.023**	1234.90*	
GCA*E	10	6.56 ns	6.16 ns	0.002 ns	192.70 ns	0.34 ns
SCA*E	30	14.83 ns	14.58 ns	0.002 ns	167.00 ns	0.20 ns
Error	60	47.03	48.94	0.003	580.30	0.63
GCA/SCA ratio		0.54	0.51	0.66	0.65	0.76
R2		0.89	0.90	0.86	0.63	0.98

The abbreviations are as described in Table 6.2

6.3.2 Performance of F1's and parents under drought and no drought stress environment

Parental crosses with DSI of ≤ 1 were G7, G8, G10, G12, and G15 and were ranked as drought tolerant. Genotypes that had DSI between 0.9-1 were classified as semi-tolerant (ST) while genotypes with DSI above one were susceptible (Table 6.4).

Table 6.4: Drought susceptibility index and classification of F1 crosses and parents under managed drought and no drought stress conditions

Parental crosses		DSI	Drought susceptibility	Female flesh colour
F1 families				
G1	A56 x Resisto	1.01	S	Cream=11D
G2	A56 x W119	0.99	ST	Cream=11D
G3	A56 x1990621	1.03	S	Cream=11D
G4	A56 x Bosbok	1.04	S	Cream=11D
G5	A56 x Excel	0.99	ST	Cream=11D
G6	Resisto x W119	1.03	S	yellow orange=16D
G7	Resisto x 1990621	0.95	T	yellow orange=16D
G8	Resisto x Bosbok	0.98	T	yellow orange=16D
G9	Resisto x Excel	1.00	ST	yellow orange=16D
G10	W119 x 1990621	0.91	T	deep orange=30D
G11	W119 x Bosbok	1.02	S	deep orange=30D
G12	W119 x Excel	0.89	T	deep orange=30D
G13	1990621 x Bosbok	1.02	S	Intermediate orange= 29A
G14	1990621 x Excel	1.03	S	Intermediate orange= 29A
G15	Bosbok x Excel	0.95	T	Intermediate orange= 29A
Parents				
P1	1990621	0.99	ST	Intermediate orange= 29A
P2	Resisto	0.96	T	yellow orange=16D)
P3	Bosbok	1.04	S	Intermediate orange= 29A
P4	A56	1.02	S	Cream=11D
P5	Excel	0.99	ST	pale yellow orange=28D
P6	W119	0.94	T	deep orange=30D
Mean	-	0.99	-	-

DSI = Drought susceptible index, T = tolerant, ST = semi-tolerant, S = susceptible LSD_{0.05} = least significance difference at P≤0.05, %CV = percent coefficient of variation. The female flesh colour were described according to Burgos, et al, 2009.

Under drought environment, genotypes from families G10, G12, G7, G5, and G15, had the highest storage root yield (6.01-6.82 t ha⁻¹) (Table 6.5). Progenies G2, G15 and G12 had the highest total biomass (10.1-10.5 t ha⁻¹). Progenies from G10, G12 and G7 families had the highest harvest index (0.66-0.71). Progenies from families G12, G10 and G13 had the highest number of marketable storage roots (32-41.4 thousands ha⁻¹). The parents' storage root yield ranged between 3.2-5.2 t ha⁻¹, of which the highest to the lowest were P6>P2>P1>P4>P3>P5 (Table 6.5). Parent P6 had the highest total biomass (12.35 t ha⁻¹). Parent P1 had the highest HI (0.46). Parent P3 had the highest number of marketable roots (71.5 thousand ha⁻¹) (Table 6.5).

Table 6.5: The storage root yield ($t\ ha^{-1}$) of F1's and parents tested under drought stress environments

Parental crosses		FSR	Bio	Hi	MNR	%RDM
F1 families						
G1	A56 x Resisto	3.81	8.03	0.48	19.80	28.90
G2	A56 x W119	5.62	10.30	0.55	23.70	30.40
G3	A56 x1990621	3.85	7.17	0.54	25.20	31.20
G4	A56 x Bosbok	4.45	8.43	0.53	19.60	26.40
G5	A56 x Excel	6.01	9.67	0.62	30.00	30.60
G6	Resisto x W119	2.30	5.08	0.45	27.90	28.20
G7	Resisto x 1990621	6.15	9.28	0.66	25.10	30.50
G8	Resisto x Bosbok	5.42	9.72	0.56	31.80	27.50
G9	Resisto x Excel	3.47	7.41	0.47	27.20	26.10
G10	W119 x 1990621	6.82	9.56	0.71	33.70	33.60
G11	W119 x Bosbok	2.19	5.59	0.39	30.30	23.50
G12	W119 x Excel	6.65	10.10	0.66	41.40	26.40
G13	1990621 x Bosbok	4.98	7.96	0.63	32.00	24.20
G14	1990621 x Excel	5.17	8.56	0.60	24.30	34.50
G15	Bosbok x Excel	6.06	10.50	0.58	30.80	27.80
Parents						
P1	1990621	4.52	9.79	0.46	61.20	26.50
P2	Resisto	4.67	10.30	0.45	50.00	26.50
P3	Bosbok	3.45	10.90	0.32	71.50	27.10
P4	A56	3.69	10.80	0.34	63.60	28.20
P5	Excel	3.21	11.50	0.28	70.40	27.60
P6	W119	5.20	12.35	0.42	61.80	26.60
Mean	-	4.79	9.19	0.57	19.08	28.20
L.S.D _{0.05}	-	1.81	2.55	0.16	14.57	0.83
CV%	-	18.90	13.90	14.20	19.10	2.82

FSR = fresh root weight in tha^{-1} , Bio = fresh total biomass weight in tha^{-1} , HI = Harvest index, MNR = marketable number of storage roots in thousands ha^{-1} , %RDM = percent root dry matter, LSD_{0.05} = least significance difference at $P \leq 0.05$, %CV = percent coefficient of variation

Under no drought stress environment, parental crosses G15, G8, G5, G10 and G2 had the highest storage root yield ($45.6-63.2\ t\ ha^{-1}$). Genotypes G15, G12 and G5 had highest biomass ($65.8-78.9\ t\ ha^{-1}$). Genotypes G8, G15 and G5 had the highest HI (0.74-0.81). Genotypes G14, G10 and G12 had the highest number of marketable roots ($92-102.7$ thousand roots ha^{-1}) (Table 6.6). The parents' storage root yield ranged $23.4-37\ t\ ha^{-1}$ and the highest yielding to the lowest were $P5 > P1 > P4 > P3 > P2 > P6$ (Table 6.6). Parent P1 had the highest biomass (58.2), while P5 had the highest HI (0.67). Parent P5 had the highest number of marketable roots (73.4 thousand ha^{-1}) (Table 6.6).

Table 6.6: The storage root yield ($t\ ha^{-1}$) of F1 crosses and parents tested across environments under no drought stress environments

Parental crosses		FSR	Bio	Hi	MNR	%RDM
<i>F1 families</i>						
G1	A56 x Resisto	29.20	48.50	0.60	48.60	28.90
G2	A56 x W119	45.60	62.40	0.73	84.10	29.80
G3	A56 x 1990621	39.50	54.30	0.73	84.00	28.40
G4	A56 x Bosbok	26.30	44.90	0.59	68.70	24.80
G5	A56 x Excel	48.70	65.80	0.74	78.80	29.50
G6	Resisto x W119	21.80	40.60	0.54	70.50	26.20
G7	Resisto x 1990621	45.30	61.90	0.73	83.20	30.10
G8	Resisto x Bosbok	49.40	61.30	0.81	91.90	26.80
G9	Resisto x Excel	18.30	35.40	0.52	66.30	24.20
G10	W119 x 1990621	46.80	65.70	0.71	93.20	32.40
G11	W119 x Bosbok	19.70	38.00	0.52	77.00	20.90
G12	W119 x Excel	26.30	66.50	0.40	92.00	25.20
G13	1990621 x Bosbok	23.30	39.30	0.59	73.00	22.10
G14	1990621 x Excel	33.90	50.80	0.67	102.70	32.40
G15	Bosbok x Excel	63.20	78.90	0.80	88.10	27.70
<i>Parents</i>						
P1	1990621	35.30	58.20	0.61	57.90	26.60
P2	Resisto	27.20	47.00	0.58	52.70	26.50
P3	Bosbok	28.70	51.50	0.56	69.90	27.20
P4	A56	34.00	51.60	0.66	62.80	28.20
P5	Excel	37.00	55.30	0.67	73.40	27.60
P6	W119	23.40	47.70	0.49	60.10	26.70
Mean	-	34.43	42.18	0.80	75.19	27.20
L.S.D _{0.05}	-	15.40	15.78	0.12	63.35	0.91
CV%	-	22.40	18.70	7.60	42.20	2.90

FSR = fresh root weight in tha^{-1} , Bio = fresh total biomass weight in tha^{-1} , HI = Harvest index, MNR = marketable number of storage roots in thousand sha^{-1} , %RDM = percent root dry matter, LSD_{0.05} = least significance difference at $P \leq 0.05$, %CV = percent coefficient of variation

6.3.3 Combining ability effects

6.3.3.1 Combining ability effects under drought stress environment

Under drought environment, parent P6 had positive and significant GCA effects for storage root yield (Table 6.7). The GCA effects for this parent, for all the other traits were significant and positive. Parents P1, P3, P4 and P5 had negative significant storage root SCA effects. Parent P4 had significant positive GCA effects for HI (0.06) and %RDM (1.684). The order of GCA effects of the parents on storage root yield were P6>P2>P1>P5>P3>P4 (Table 6.7).

Parental crosses G15 and G7 had the highest significant SCA effects (1.46-2.17) under drought stress on fresh storage roots. Families G15, G5 and G12 had the highest significant SCA effects (0.14–0.2) for harvest index. SCA effects for marketable number of roots on all progenies were negative, of which families G8, G10, and G13, had the least negative effects (-0.5 to -3.6) (Table 6.7).

Table 6.7: GCA and SCA for root yield traits ($t\ ha^{-1}$) under drought stress environments

SCA effects	Crosses	FSR	BIO	HI	MNR	%RDM
G1	A56 x Resisto	-0.45	-0.43	-0.05	-6.80	0.09
G2	A56 x W119	1.16***	1.28	0.01	-9.10*	1.41***
G3	A56 x1990621	-1.37***	-1.71*	-0.03	-4.71	0.26
G4	A56 x Bosbok	-0.13	-0.58	0.06	-12.72**	-0.59*
G5	A56 x Excel	1.46**	-1.67	0.16*	-40.60***	0.51
G6	Resisto x W119	-1.64***	-3.16***	-0.02	-4.91	0.81**
G7	Resisto x 1990621	1.46***	1.15	0.09*	-4.82	1.90***
G8	Resisto x Bosbok	1.38***	1.46*	0.05	-0.50	3.77***
G9	Resisto x Excel	-2.32***	-4.23**	0.01	-29.91***	-2.30***
G10	W119 x 1990621	1.17***	0.91	0.10*	-2.31	-3.60***
G11	W119 x Bosbok	-2.05***	-3.19***	-0.07	-8.22*	2.90***
G12	W119 x Excel	0.26*	-3.04*	0.14*	-21.31**	-1.30**
G13	1990621 x Bosbok	-0.02	-0.72	0.04	-3.60	-0.88
G14	1990621 x Excel	-0.35	-2.13	0.12	-40.73***	9.27***
G15	Bosbok x Excel	2.17***	-1.13	0.20**	-42.10***	-2.11***
GCA effects for parents						
P1	1990621	-0.02	0.16	0.00	-3.70*	0.892***
P2	Resisto	0.41**	-0.59	-0.03	-3.72*	-0.433**
P3	Bosbok	-0.35**	-0.07	-0.04*	2.51	-0.273*
P4	A56	-0.54***	-0.18	0.06**	-0.43	1.684***
P5	Excel	-0.23*	-0.04	-0.01	2.01	-2.324***
P6	W119	0.73***	0.73*	0.03	3.41*	0.454**

FSR = fresh root weight in $t\ ha^{-1}$, Bio = fresh total biomass weight in $t\ ha^{-1}$, HI = Harvest index, MNR = marketable number of storage roots in thousands ha^{-1} , %RDM = percent root dry matter, and *, **, ***, = significant at $P\leq 0.05$, $P\leq 0.001$, $P\leq 0.0001$ respectively

6.3.3.2 Combining ability effects under no drought stress environment

Parent W119 had positive and significant GCA effects for storage root yield (Table 6.8). The GCA effects of this parent, for all the other traits were significant and positive. Parent P2, had negative significant storage root GCA effects under storage root yield. Parent P4 had significant positive GCA effects for HI (0.02) and %RDM (1.39). Parent P1 had a significant positive GCA effects on %RDM. The order of GCA effects of the parents on storage root yield from highest to lowest were P6>P2>P1>P5>P3>P4, of which parents P2, and P6 had significant GCA effects (Table 6.8)

Progenies G15, and G7 had the highest significant SCA effects (16.32-20.99) on fresh storage root (Table 6.8). SCA effects for progenies G15, G7, and G10 on fresh total biomass were significant. Families G12, G7, and G2 had the highest significant SCA effects (0.08 – 0.12) on harvest index.

Table 6.8: The SCA and GCA effects based on the root yield of the progenies and parents on 6 traits under no drought stress

SCA effects	Crosses	FSR	BIO	HI	MNR	%RDM
G1	A56 x Resisto	-0.92	-0.74	-0.02	-14.2*	0.79**
G2	A56 x W119	10.48*	8.75**	0.08***	10.6	1.92***
G3	A56 x1990621	-6.9*	-5.85	-0.05*	7.81	-
G4	A56 x Bosbok	-7.92**	-7.54*	-0.03	-3.32	1.27***
G5	A56 x Excel	6.05	8.42	0.01	3.61	-
G6	Resisto x W119	-9.05**	-9.26**	-0.04*	-0.60	0.55***
G7	Resisto x 1990621	16.32***	15.54***	0.09***	9.31	1.58***
G8	Resisto x Bosbok	9.51**	12.67**	0.01	22.20**	2.05***
G9	Resisto x Excel	-21.33***	-21.35**	-0.13**	-1,01	4.16***
G10	W119 x 1990621	14.80***	15.01***	0.05*	8.61	-
G11	W119 x Bosbok	-15.23***	-15.06***	-0.08***	-3.30	4.20***
G12	W119 x Excel	16.22**	13.52*	0.12**	27.81*	1.84***
G13	1990621 x Bosbok	-9.72**	-10.33**	-0.04*	-10.20	-
G14	1990621 x Excel	2.54	3.79	0.01	43.61**	2.95***
G15	Bosbok x Excel	20.99***	20.95**	0.02	12.71	-2.35**
						2.38***
GCA effects for Parents						
P1	1990621	-0.33	0.15	0.00	-6.11*	0.99***
P2	Resisto	-1.52**	-3.66**	-0.04***	-8.40**	-0.13
P3	Bosbok	6.44	0.68	-0.01	2.21	-
P4	A56	4.53	-2.73**	0.02*	5.12	0.40***
P5	Excel	-0.44	-0.45	0.00	0.81	1.39***
P6	W119	0.39***	6.01***	0.03**	6.31*	-
						2.36***
						0.51***

Note: Abbreviations are as indicated in Table6.7

6.3.4 Performance of F1's and their parents on number of days to permanent wilting point (DPWP)

The number of days to permanent wilting point (DPWP) of seven parental crosses, G15, G7, G12, G8, G10, G2 and G5 ranged from 79 to 91 (Table 6.9). The mean yield of those seven crosses ranged from 25.46 - 34.62. Parent P3 and P6 had yields of 16.06 and 14.32 t ha⁻¹ respectively. The best parental crosses together with their FSR yields in t ha⁻¹ under drought stress were G15 (34.62), G8 (27.43), G5 (27.34), G10 (26.80) and G7 (25.71) and their DPWP were 91, 79 and 90 respectively. The highest yielding family under drought stress was G15 and was also the highest yielding under no drought stress. However, the second highest ranking parental cross (G8) under no drought stress ranked 7th under drought stress environment while the fourth ranking under no drought stress (P4) ranked first under drought (Table 6.9). The parents DPWP under no drought stress from highest to lowest were P6>P2>P1>P3>P4=P4 and parents P1, P3 and P6 had significant GCA effects. When ranked together with the progenies, parent P54 and P1 ranked 8th and 9th under no drought stress environment but ranked 19th and 112th under drought environment respectively. The highest ranking parent under drought stress was P6 which ranked 8th but 17th under no drought stress. The highest ranking crosses under drought stress which also ranked high under no drought stress were crosses involving parents P3, P5 and P4.

Table 6.9: Performance of F1 and their parents on days to permanent wilting point (DPWP)

Parental crosses		DPWP	SCA effects	^a Yield (t ha ⁻¹)	ⁱ Rank	^d Rank
G1	A56 x Resisto	68	-2.71**	16.52	12	15
G2	A56 x W119	81	8.31***	25.59	5	6
G3	A56 x1990621	72	0.40	21.70	7	14
G4	A56 x Bosbok	67	- 5.32***	15.38	15	13
G5	A56 x Excel	79	13.31***	27.34	3	5
G6	Resisto x W119	63	-13.30***	12.06	19	20
G7	Resisto x 1990621	90	15.31***	25.71	6	3
G8	Resisto x Bosbok	85	10.11***	27.43	2	7
G9	Resisto x Excel	70	-1.20	10.90	21	17
G10	W119 x 1990621	83	5.30***	26.80	4	1
G11	W119 x Bosbok	67	-10.51***	10.96	20	21
G12	W119 x Excel	87	7.02***	16.46	16	2
G13	1990621 x Bosbok	67	-9.31***	14.15	18	10
G14	1990621 x Excel	71	0.30	19.55	11	9
G15	Bosbok x Excel	91	13.10***	34.62	1	4
Parents		GCA effects				
P1	1990621	70	0.91***	19.91	9	12
P2	Resisto	78	1.30	15.93	14	11
P3	Bosbok	69	-0.80***	16.06	13	18
P4	A56	60	-3.90	18.82	10	16
P5	Excel	60	0.61	20.12	8	19
P6	W119	80	1.82**	14.32	17	8
Mean	-	74	-	19.54	-	-
LSD _{0.05}	-	4.12	-	3.16	-	-
% CV	-	2.83	-	7.01	-	-

DPWP = days to permanent wilting point, SCA = specific combining ability, ^a = Mean yield across the drought and irrigated environment, ^d = Drought environment, ⁱ = irrigated environment, rank1 = the highest fresh storage root yield, rank 21 = the lowest storage root yield, LSD_{0.05} = least significance difference at P≤0.05, %CV = percent coefficient of variation, and *, **, ***, = significant at P≤0.05, P≤0.001, P≤0.0001 respectively, ranking as described in section 6.2.5.

6.3.5 Heterosis

6.3.5.1 Heterosis under drought stress environment

All the F1 clones were ranked based on their performance for the traits measured and the top 35 were identified and their heterosis calculated. Clones G8-8 and G15-8 and G15-5, showed the highest mid parent (269.6, 184.5 and 196.3) and best parent (223.4, 117.8, and 126.9) heterosis on fresh storage root yield under drought stress. Clone G7-10 had the

highest mid parent (75.8) and best best-parent (81.4) heterosis on the basis of fresh total biomass yield (Table 6.10). Female parents P2 and P6 had each 12 progenies out of the 35 heterotic crosses while male parents P3 and P1 had 17 and 9 of the 35 heterotic progenies respectively.

6.3.5.2 Heterosis under no drought stress environment

Clone G4-9, G4-10 and G4-6, showed the highest mid parent (247.6, 233.7, and 231.5) and best parent (209.2, 199.6, and 194.9) heterosis on fresh storage root yield. Clone G4-9, G4-10 and G7-5 had the highest mid parent (164.6, 153.8, and 153.6) and best parent (233.6, 110.3, and 112.3) heterosis on the basis of fresh total biomass yield (Table 6.11).

Table 6.10: Heterosis for the best 35 F1 recombinants identified based on performance of all F1 crosses on storage root weight and total fresh biomass under drought environment

Cross	Family	Clone ID	Rank	Fresh storage root weight		Total fresh biomass	
				MH	BH	MH	BH
Excel x Bosbok	G15	10	1	177.1	112.2	19.6	15.8
Excel x Bosbok	G15	9	2	173.1	109.1	16.5	12.8
Excel x Bosbok	G15	8	3	184.5	117.8	6.1	2.7
Excel x Bosbok	G15	5	4	196.3	126.9	-2.1	-5.2
Excel x Bosbok	G15	4	5	168.2	105.3	3.0	-0.2
Excel x Bosbok	G15	1	6	151.0	92.2	-62.7	-63.9
1990621 x Excel	G14	6	7	117.6	66.6	12.3	20.3
1990621 x Excel	G14	2	8	140.8	84.4	-19.5	-13.8
W119 x Bosbok	G11	9	9	126.1	108.4	11.6	16.8
W119 x Bosbok	G11	4	10	104.1	88.1	25.8	31.8
W119 x Bosbok	G11	3	11	96.6	81.3	-7.2	-2.8
W119 x Bosbok	G11	2	12	99.0	83.4	-7.9	-3.6
W119 x Bosbok	G11	1	13	98.6	83.1	-22.9	-19.3
W119 x Excel	G12	2	14	4.1	21.9	30.5	35.5
W119 x 1990621	G10	8	15	99.0	83.4	7.5	25.4
W119 x 1990621	G10	7	16	129.6	100.9	-11.0	-14.3
W119 x 1990621	G10	6	17	125.0	96.9	12.8	8.6
W119 x 1990621	G10	5	18	128.5	110.6	9.1	27.3
W119 x 1990621	G10	3	19	96.9	81.6	15.9	35.3
W119 x 1990621	G10	2	20	137.1	107.5	-16.8	-19.9
Resisto x Bosbok	G8	5	21	3.5	14.1	43.3	46.8
Resisto x Bosbok	G8	1	22	60.0	42.5	-53.4	-56.3
Resisto x Excel	G9	9	23	142.4	103.6	-45.9	-44.0
Resisto x Excel	G9	7	24	140.5	102.0	39.4	44.5
Resisto x Excel	G9	4	25	135.2	97.6	-8.1	-4.8
Resisto x 1990621	G7	10	26	107.7	85.0	75.8	81.4
Resisto x 1990621	G7	5	27	124.2	99.7	15.4	19.1
Resisto x 1990621	G7	2	28	114.0	90.6	9.8	13.3
Resisto x W119	G6	7	29	-5.4	-8.9	-25.2	-32.8
Resisto x W119	G6	6	30	23.1	25.9	36.8	43.2
Resisto x W119	G6	3	31	22.7	25.6	31.2	38.2
A56 x Bosbok	G4	10	32	84.1	69.7	-5.4	10.4
A56 x Bosbok	G4	9	33	116.6	99.7	-9.0	6.2
Resisto x Bosbok	G8	8	34	269.6	223.4	-12.1	-15.4
A56 x Bosbok	G4	6	35	88.1	73.4	15.9	35.3

MH = mid parent heterosis, BH = best parent heterosis, ID = identification number for the progeny of the cross

Table 6.11: Heterosis for the best 35 F1 recombinants identified based on performance of all F1 crosses on storage root weight and total fresh biomass under no drought stress environment

Genotype identity				Fresh storage root weight		Total fresh biomass	
Cross	Family	Clone ID	Rank	MH	BH	MH	BH
Excel x Bosbok	G15	10	1	139.3	131.8	105.3	94.2
Excel x Bosbok	G15	9	2	145.0	137.3	113.1	101.6
Excel x Bosbok	G15	8	3	91.7	85.6	67.0	58.0
Excel x Bosbok	G15	5	4	198.4	189.0	149.0	135.6
Excel x Bosbok	G15	4	5	193.4	184.2	145.9	132.7
Excel x Bosbok	G15	1	6	179.1	170.3	134.6	122.0
1990621 x Excel	G14	6	7	12.3	-14.1	16.5	-8.1
1990621 x Excel	G14	2	8	13.0	-13.6	14.6	-9.6
W119 x Bosbok	G11	9	9	120.1	80.1	81.6	62.0
W119 x Bosbok	G11	4	10	111.0	72.7	66.1	48.2
W119 x Bosbok	G11	3	11	114.2	75.3	71.1	52.7
W119 x Bosbok	G11	2	12	134.8	92.2	84.9	65.0
W119 x Bosbok	G11	1	13	145.7	101.1	89.8	69.3
W119 x Excel	G12	2	14	4.3	12.4	-5.2	1.2
W119 x 1990621	G10	8	15	215.4	180.5	146.4	210.7
W119 x 1990621	G10	7	16	101.4	90.2	84.6	74.6
W119 x 1990621	G10	6	17	82.5	72.4	64.0	55.2
W119 x 1990621	G10	5	18	187.5	155.7	124.0	182.4
W119 x 1990621	G10	3	19	222.8	187.2	147.0	211.5
W119 x 1990621	G10	2	20	81.4	71.3	64.7	55.8
Resisto x Bosbok	G8	5	21	10.2	24.0	12.3	22.6
Resisto x Bosbok	G8	1	22	-14.0	-27.2	-20.5	-29.9
Resisto x Excel	G9	9	23	79.7	56.3	82.1	69.1
Resisto x Excel	G9	7	24	84.3	60.3	75.3	62.8
Resisto x Excel	G9	4	25	74.8	52.0	63.4	51.7
Resisto x 1990621	G7	10	26	185.7	145.2	132.7	94.8
Resisto x 1990621	G7	5	27	210.9	166.8	153.6	112.3
Resisto x 1990621	G7	2	28	188.3	147.5	139.1	100.1
Resisto x W119	G6	7	29	20.9	16.1	3.5	4.8
Resisto x W119	G6	6	30	-11.1	-6.7	3.8	2.6
Resisto x W119	G6	3	31	-14.9	-10.3	-7.5	-8.9
A56 x Bosbok	G4	10	32	233.7	196.9	153.8	110.3
A56 x Bosbok	G4	9	33	247.6	209.2	164.6	233.6
Resisto x Bosbok	G8	8	34	82.5	72.3	63.7	54.9
A56 x Bosbok	G4	6	35	231.5	194.9	148.5	213.4

Note: the abbreviations are as described in Table 6.9

6.4 Discussion

6.4.1 Performance of F1's and parents under drought and irrigated environment

The significant mean squares for families on fresh root weight, biomass, harvest index, marketable number of roots, and percent root dry matter indicated the genetic variation among the parents and their crosses. This significant variation shows that varieties tolerant to drought and with desired agronomic attributes may be selected. In addition, the significant

environmental effect on the traits observed justifies multi-locational trials of varieties prior to their release. The significant GCA and SCA mean squares of the traits observed shows that both additive and non-additive gene action were involved in the expression of the traits. The GCA to SCA variance ratios ranged 0.54-0.79 for FSR, BIO, HI, MNR, and RDM, under no drought, indicating that additive gene action was predominant, while under drought environment, the ratios for BIO and MNR were 0.4 and 0.27 respectively, while FSR, HI and % RDM ranged 0.57-0.76,. This shows that non-additive gene action was predominant in their expression. Thus this study, for first time shows, predicting progeny performance based on GCA under drought environment, would largely be successful based on FSR, RDM and HI, but not with total biomass or number of storage roots. Mwanga et al. (2002) using half diallel reported GCA:SCA range of 0.51-0.87 for virus resistance on sweetpotato, meaning additive effects (GCA) were more important than non-additive effects (SCA). Collins (1977) also using a diallel analysis reported that sweetpotato fusarium wilt resistance had significant GCA/SCA of 87% and thus, additive gene effects were predominant.

The families that had DSI of ≤ 1 could be classified as drought tolerant and thus could be incorporated into breeding programmes for drought tolerance improvement. The other families with DSI above one were susceptible and thus could be culled and not used in next evaluation cycle for drought tolerance. The DSI based on the storage root yield indicated that parents P3 and P4 were susceptible to drought, while parent P5 was semi-tolerant and P6 was tolerant to drought stress. Therefore, parents P5 and P6 can be incorporated into breeding programmes for improving root yield and drought tolerance.

The best yielding three families with high storage root yield, relatively high total fresh biomass, HI, NSR and %RDM under drought were G7, G10 and G12, however, under no drought stress environments, families were G10, and G7 produced significantly similar yields relative to the highest storage root yielding families G5 and G8 except for G15. These progenies were crosses involving parents P6, P1 and P2 except for family G15 under no moisture stress environment. Parents P1, P2 and P6 had the highest root yield performance under drought, implying that one of the parents of the crosses or both passed on drought tolerance gene to the progenies. Under no drought stress, the best two crosses were G15, and G8 and involved crosses with parents P2, P3, and P5 of which, P3 and P5 were semi-tolerant to susceptible, and the yields of their progenies were not significantly different relative to the highest storage root yielding families under drought environment. This indicates that, donors of drought tolerance genes may not actually be drought tolerant themselves. Thus, the semi-drought tolerant to susceptible parents P3 and P5 can be

promoted for use in areas with reliable rainfall or can be incorporated in a breeding programme to improve yielding ability of low yielding drought tolerant genotypes.

6.4.2 Combining ability effects

Progenies G10, G12, and G15 from parents P5 and P6 had positive and significant GCA effects under drought and no drought stress on FSR. Among them, G10 and G15 also had high FSR in both environments, an indication that these two parents may be used in crosses for improving drought tolerance. The GCA effects for FSR for parents P2, and P6 under drought were positive and significant. However, under no drought stress, parent P2 had negative significant GCA effect, while parent P6 had positive and significant GCA effects. This is an indication that P6 can contribute towards high fresh storage root yield, under drought and no drought stress, indicating this parent may be carrier of genes for high yields and drought tolerance. However parent, P2 is probably a carrier for drought tolerance but not yielding ability. Parent P6 also, had positive significant GCA effects for total biomass, harvest index, number of marketable roots. Therefore, this parent can be used in wide ranging environments as a parent in crosses to improve sweetpotato productivity. Parent P4 had significant positive effects on harvest index under both drought and no drought stress hence, it can be used to improve the productivity of the other poor productive cultivars.

Although parents P2 and P6 had positive and significant GCA for FSR under drought, they did not produce progenies with positive and significant SCA effects both under drought and no drought stress except for %RDM. However, when crossed with other parents with negative GCA under the drought environment (P1, P3) produced progenies with positive and significant SCA effects for root yield in both drought and no drought stress environments. Thus, positive contribution of non-additive gene action to the expression of improved fresh storage root yield on the progenies may not depend on the parental GCA effects. Therefore, parents cannot be disqualified only based on negative GCA effects. Thus, crossing two drought tolerant parents may not result to drought tolerant progenies in sweetpotato. Similarly, GCA/SCA effects of sweetpotato could not be solely used to select the best recombining parents on improving storage root beta carotene (Chiona, 2010). However, Espasito et al. (2013) reported that additive gene action on yield was predominant in their study on combining abilities and heterotic groups in *Pisum sativum* L., and concluded that selection for best cross could be based on GCA and SCA effects. Therefore, these findings reveal the importance of GCA and SCA effects in selection trials.

Four of the 15 families (G3, G6, G9, and G11) had negative and significant SCA effects for fresh root yield under both drought and no drought stress. This portrays non-additive gene action towards low yields, therefore, these genotypes may be discarded in the advanced

trials. Five of the 15 families; G7, G8, G10, G12, and G15 had positive significant SCA effects for storage root yield under both drought and no drought stress environment. Among them, the highest yielding crosses with significant SCA effects under drought were G15, and G7 which suggested that, these families had progenies that possessed genes for drought tolerance. The highest yielding parental crosses G15, and G10 had negative significant %RDM SCA effects under drought but positive under no drought stress, an indication that, root dry matter probably, could be negatively correlated with yield and drought tolerance. Moreover, G7 and G8 which had relatively high storage root yields and showed drought tolerance, and had positive significant SCA effects on % RDM under both no drought and with drought stress, probably could be exploited for drought tolerance, high yield and high root dry matter.

Families with high SCA effects on yield under drought (G7, G10 and G12), also had positive significant SCA effects on harvest index (HI) under drought and no drought stress, and biomass (BIO) under no drought stress although their SCA effects on biomass (BIO) under drought fluctuated from negative to positive. The high HI confirmed the slow but persistent vine growth under moisture stress that produced assimilates which enabled some level of root enlargement. The fluctuating BIO SCA effects under drought stress probably suggest that the progenies with negative SCA effects had increased vine growth at the early growth stages followed by effective gradual assimilate translocation as moisture stress severity gradually increased. However, of importance is the persistent vine growth trait, which enables vine regrowth with availability of water that allows adequate multiplication of the planting materials for sweetpotato, after a dry spell. The high yielding families, G8 and G12 under drought stress had positive significant SCA effects on marketable number of roots under no drought stress, but under drought had negative SCA effects, this indicates drought mainly suppresses assimilate production which affect the size of the roots and therefore, genes that enhance assimilate production could be responsible for drought tolerance in sweetpotato especially under drought escape. Also, family G12 had low root yield under no drought stress but had high yield under drought, indicating that the family comprises of progenies that are carriers for drought tolerance and not yielding ability.

6.4.3 Performance of F1's in days to permanent wilting point (DPWP)

The genotypes could be divided into drought tolerant, semi-tolerant to neutral and susceptible based on DPWP. Two of the three highest-ranking families under drought (G15 and G10) also ranked high under no drought stress, indicating they were drought tolerant, high yielding and stable. The best two parental crosses in both drought and no drought stress environments were G15 (P3 x P5) and G5 (P4 x P5). Their parents P3 and P4 were susceptible to drought based on the DPWP, but combined well with drought susceptible

parent P5 to produce high yielding and drought tolerance progenies. This indicated that cross combinations of susceptible parents led to improved tolerance to drought, which suggests, for the first time, that the drought susceptible parents probably were carriers of the drought tolerance genes, which signifies the genes alleles for drought tolerance could have been homozygous recessive.

Parent P1 and P5 ranked 9th and 8th under no drought stress environment but ranked 12th and 19th under drought environment respectively, an indication that P1 was semi tolerant to drought and P5 was drought susceptible. However, these parents P1 and P5 cross combined well with P4 (drought susceptible) producing generally high root yielding progenies (G15 and G5) under both drought and no drought stress environment, even though, the two parents appeared to be drought susceptible. Therefore, these parents can be incorporated in breeding programmes for improving root yield and drought tolerance. Family G15 storage root yield ranked the highest under no drought and among the highest under drought stress, an indication that this progeny may be stable, high yielding and drought tolerant. However, the 2nd ranking highest yielding progeny (G8) under no drought stress ranked 7th under drought stress, while the 4th ranking (G10) under no drought stress ranked first under drought stress, an indication these genotypes (G8 and G10) were generally stable and can be recommended to be grown in areas with unpredictable rainfall. Also, this study shows that Parents P2 and P6 were semi-tolerant to tolerant to drought stress but the other parents (P1, P3, P4, and P5) were susceptible on the basis of DPWP. This is supported by the findings of Laurie et al. (2004), who reported that cultivar P6 (W119) was drought tolerant, P5 (Excel) ranged from neutral to drought tolerant, P2 (Resisto) ranged from neutral to susceptible while P3 (Bosbok) was susceptible to drought. However, in this study P2 (Resisto) appeared semi-tolerant.

6.4.4 Estimates of heterosis

Progenies outperform their parents due to transgressive segregation (Sleper and Poehlman, 2006; Rieseberg et al., 1999). The best three parental crosses for storage root yield under drought were G8-8 – P2xP3, G15-5 - P5xP3, G15-8 - P5xP3 and had high mid and best parent heterosis. These progenies involved the parent P3. However, the best three progenies for storage root yield under no drought stress were G4 (6, 9 and 10) – P4xP3, and had high mid and best parent heterosis. This again involved parent P3. Parent P3 in this study appeared susceptible to drought based on DPWP, but when crossed to susceptible or semi-tolerant parents produced progenies that had high storage root under both drought and no drought stress environments. This unique finding may imply that the gene responsible for drought tolerance in sweetpotato is homozygous recessive and the susceptible parents were

either carriers of the homozygous dominant or heterozygous dominant, but the mother parents (P4) that crossed with parent P3 and led to increased storage yield under drought (tolerant) was heterozygous parents. However, an allelism study could be conducted to confirm whether the genes responsible for drought tolerance in sweetpotato are homozygous recessive. Rieseberg et al. (1999) in their review indicated that studies conducted have shown that heterosis may be caused by mutation in hybrid populations, chromosome number variation, expression of rare recessive alleles, the action of complementary genes, over-dominance or epistasis, indicating a non-additive gene action is involved. In our study significant SCA effects showed there was non-additive gene effect, which could be the cause of the heterosis on the progenies observed.

The best three crosses under no drought stress for storage roots appeared also to do good under drought stress, showing that a combination of high yielding ability and drought tolerance was passed on to the progenies despite the parents being drought susceptible to semi-tolerant. The genotypes with low or negative mid or best parent heterosis on biomass under drought had high heterosis on storage root yield under drought and no drought stress environment. These are G15-1, G8-8, G4-9, G15-5, and G15-4, G10-7. This may indicate that they are early maturing and use drought escape as a mode of drought tolerance; hence, they could be evaluated for release as early maturing clones for drought prone areas. The same progenies had high root yield and high biomass, under no drought stress, which confirms their drought escape mechanism. Therefore, these genotypes exhibit developmental plasticity in that their growth was rapid in the initial stages of moisture stress and synthesized assimilates effectively translocating them to the roots gradually as the moisture stress severity levels gradually increased to unbearable levels. These genotypes may be screened in advanced trials and the best clones subsequently released as a variety. El-bandawy (2013) in his study with seven rice hybrids reported that the magnitude of heterosis varied among crosses and recommended that the hybrid with positive significant SCA effects and high heterosis could be advanced in the pre-release trials. Finally, genotypes that had high heterosis (biomass or roots) under no drought stress but low or negative heterosis under drought (G10-3, G10-8, G4-10) indicated they were unstable across environments and could be evaluated for areas with reliable rainfall regimes.

6.5 Conclusion

The GCA to SCA variance ratios indicated that additive gene action was relatively more predominant than non-additive gene action in controlling all the traits observed under drought and no drought stress except for total fresh biomass and marketable number of

roots under drought environment. Parents P3 and P4 combined well with P5 giving the highest root yielding progenies under both drought and no drought stress environment, thus can be incorporated in breeding programmes for improving root yield and drought tolerance. Progeny G15 whose parents were P3 and P5 and were susceptible to drought, had high root yield under drought and no drought stress environment indicating donors of drought tolerance genes may actually be drought susceptible themselves. Most progeny families with positive significant SCA effects on root yield had negative significant SCA effects on % RDM, however G7 and G8 which had high root yields, had positive SCA effects on % RDM hence could be exploited for drought tolerance, high yield and high root dry matter. The high DPWP indicated that persistent but slowed vine growth was one of the mechanisms of drought tolerance.

Positive and negative SCA effects for total biomass under drought implied effective photosynthates translocation to roots under increasing moisture stress was one of the drought tolerant mechanisms. Negative significant marketable storage roots for all the progenies under drought, indicated that drought mainly suppresses assimilate production thus hindering enlargement of the storage roots and therefore genes that enhance assimilate production could be responsible for drought tolerance in sweetpotato. Parent P3 that exhibited high heterosis, therefore contributed towards improved production under drought environment. Genotypes that had high heterosis (biomass or roots) under irrigation but low or negative heterosis under drought meant they were unstable across environments and could be evaluated for use in areas with reliable rainfall regimes. However, drought tolerant parents with high GCA effects did not always result in crosses with the highest SCA effects, which imply that selection of parents for drought tolerance programme needs to take into account both the GCA and SCA effects. Therefore, since sweetpotato clones are released as highly heterozygous F_1 progeny, then a breeding programme would factor in heterosis and SCA effects for significant genetic gain advances in breeding sweetpotato for drought tolerance.

Finally, this study for the first time uniquely combines yield performance, combining ability estimates of the crosses made, DPWP counted using rapid drought screening technique, and heterosis under drought and no drought stress to unmask the gene action of drought tolerance in sweetpotato, thus contributing a milestone to science.

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Appendix

Appendix 6.1 Characteristics of genotypes that were used for the crossing block upon which six parents were selected for this study

Genotype ID	Genotype name	Source	Status
G1	189151.38	Peru	CIP clone
G2	189150.1	Peru	CIP clone
G3	1990621	Peru	CIP clone
G4	422656	Peru	Breeders clone
G5	441725	Peru	Breeders clone
G6	194573.9	Peru	CIP clone
G7	194555.7	Peru	Breeders clone
G8	194515.15	Peru	CIP clone
G9	421066	Peru	CIP clone
G10	420014	Peru	CIP clone
G11	A56	South Africa	Breeders clone
G12	A2	South Africa	Breeders clone
G13	Beureguard	USA	Released clone
G14	Chingova	Mozambique	Improved clone
G15	Excel	Peru	USDA ARS germplasm release
G16	48 Gabagaba	Mozambique	Breeders clone
G17	Lodha	Kenya	Landrace
G18	Nyatonge	Kenya	Landrace
G19	Resisto	USA	Released variety
G20	Sinia	Kenya	landrace
G21	Tanzania	Uganda	Landrace
G22	Unawazambane06-01	Mozambique	Breeders cultivar
G23	W119	USA	USDA ARS germplasm release
G24	Xiadla-Xa-Kau	Mozambique	Breeders clone

Chapter 7: Overview of the Study

Introduction

This study focused on pre-breeding experiments to identify drought tolerant sweetpotato varieties with farmers' preferred traits that could increase sweetpotato production in Kenya. The first step was to carry out a survey in the major sweetpotato growing areas to identify farmers' sweetpotato production constraints and coping strategies in Kenya. The second step involved screening local and introduced sweetpotato genotypes to identify drought tolerant sources that could be used in breeding program to develop drought tolerant varieties suitable for Kenya. Further, a study of 24 genotypes selected as parents was carried to determine their genotypes x environment interaction effects. Moreover, a study on drought tolerance mechanism on sweetpotato was conducted in order to understand responses of the crop to moisture stress. Finally, a study to determine the combining ability and heterosis for drought tolerance of F1 recombinants was done. The findings of these studies were necessary in order to formulate an effective breeding programme for drought tolerant sweetpotato in Kenya. The summary of the major findings are highlighted below.

1. Determining the production constraints and farmers preferences on grown sweetpotato genotypes

- Majority of the 345 farmers interviewed were women while most farmers aged from 21-40 years.
- Orange fleshed varieties Vitaa, Kabonde and Bungoma were grown by the majority of farmers.
- Most farmers identified sweetpotato as both food and cash crop, however the farm sizes grown with sweetpotato were mostly 0.24 ha and below.
- Most farmers sourced sweetpotato seed mainly from previous crop and preferred using manure rather inorganic fertiliser.
- Farmers identified weevils as the major pest and viruses as the major disease.
- Drought caused hard soil pan, hindering land preparation and planting, harvesting and reduced storage roots yields especially due to terminal drought occurrence.
- Majority of the famers produced storage root yield of 5.5-7.4 t ha⁻¹, below the average production of 9 t ha⁻¹ in Kenya, and below the average production in Asia of 18 t ha⁻¹.
- Majority of farmers emphasised use of clean planting materials for increased storage root yield and reduced weevil and virus infestation

- Majority of farmers indicated use of drought tolerant varieties and irrigation were strategies used to cope with drought constraint

2. Evaluation of sweetpotato genotypes for tolerance to drought stress

- Moisture stress did not affect numbers of roots probably because there was sufficient soil moisture during the root initiation period, which is within the first few weeks after they are planted. Significant variation was observed among the genotypes and across environments for all the traits.
- Genotypes 194555.7, Unawazambane06-01, 441725, Tanzania, Chingova did well in both drought and irrigated environment and had DSI <1.
- Genotypes that took few days to permanent wilting point in the rapid box water stress screening also, had low yield across the environment, had DSI of >1, lower HI.

3. Genotype x environment interaction for storage root yield in sweetpotato under managed drought stress conditions in Kenya

- The environmental effects contributed the highest variation of 75.2%.
- Genotype ranking based on DSI, showed that genotype responses to moisture stress were not consistent over environments and thus both DSI and DPWP were vital in discriminating drought tolerance among genotypes.
- The GGE and AMMI biplot showed there was both broad and specific interaction between genotypes and environments,
- Genotype close to the regression line in the regression plot were stable while genotypes far away were not stable across environments
- The biplots showed that both sites (Kiboko or Thika) could be used as test sites for preliminary drought screening

4. Mechanisms of tolerance to drought stress in sweetpotato

The drought tolerance mechanisms were found to involve;

- Formation of pencil roots especially when the stress occurred in the first three months after planting but this does not benefit the grower.
- Decrease in the size of storage roots, and number of vine branches
- Reduced vine branches in drought tolerant cultivars resulting in reduced evapotranspiration.
- Longer pencil roots for genotypes under moisture stress than genotypes under no moisture stress.

- Increase in shoot and mature leaf pubescence in moisture drought tolerant genotypes.
- Reduced chlorophyll content (CC) in non-tolerant genotypes and in moisture stress regimes.
- Retention of some level of CC by drought tolerant genotypes.

5. Heterosis and combining ability for drought tolerance

- Significant GCA and SCA effects were observed for fresh storage roots (FSR), harvest Index (HI), number of storage roots (NSR) and percent root dry matter (%RDM)
- Ratio of GCA/SCA for traits (FSR, HI, %RDM) indicated additive gene action was predominant over non-additive in the inheritance of the traits.
- For total fresh biomass (BIO) and number of marketable storage roots (NMSR) under drought stress, GCA/SCA indicated non-additive gene action was predominant.
- Parents P3 and P4 combined well with P5 (susceptible) giving the highest root yielding progenies (G15 and G5) under both irrigation and drought environment.
- Most parental crosses with positive significant SCA effects on root yield had negative significant SCA effects on % RDM, however G7 and G8 which had high root yields, had positive SCA effects on % RDM.
- Parental crosses with high significant days to permanent wilting point (DPWP) SCA effects were G7, G8 and G15
- Negative, significant marketable storage roots SCA effects were observed for all the parental crosses under drought.
- Progenies found outperforming their parents were attributed to transgressive segregation which is an indication of drought tolerance of search genotypes.
- Parent P3 was common in these heterotic progenies and probably was the donor of the gene responsible for the improved production under drought environment.
- Parental crosses that had high heterosis (biomass or roots) under irrigation but low or negative heterosis under drought (G10-3, G10-8, G4-10) were unstable across environments.
- Drought tolerant parents with high GCA effects did not always result in crosses with the highest SCA effects.

Breeding implications and the way forward

In general, the findings of this study revealed that capacity building and technology transfers on sweetpotato need to target mostly women farmers aged from 21-40 years. There is also

a need to further promote beta carotene rich OFSP to benefit the young children and lactating mothers value addition (processing) and promotion of sweetpotato as a cash crop is important since it is a healthy food, thus boosting the income generation of the farmers. Further, the need to research on use of inorganic fertilisers on sweetpotato to boost production, as well as appropriate technology for seed multiplication and distribution method is required to ensure availability of clean and enough planting materials at onset of rains. Importantly, an intensified research programme is required towards generating resistant varieties to drought, weevil and virus, which are the major hindrance sweetpotato production.

Results of sweetpotato germplasm screening indicated high levels of genetic variability for various traits. The results also indicated that moisture stress only hindered the development to full size of the roots and not the numbers. Genotype 194555.7, Unawazambane06-01, 441725, Tanzania, Chingova did well in both drought and no drought stress environment and had DSI <1 and thus could be further investigated for confirmation of drought tolerance. These varieties may further be tested in many sites to validate their tolerance for use in drought areas. They could also be used as parents for breeding programs for improved drought tolerance.

The GGE and AMMI biplot analysis, in this study, showed there was a specific interaction between genotypes and environments, and therefore, genotype for drought tolerance need to be evaluated across environments to select for drought tolerance and thus breeding for specific adaptation for drought tolerance is required.

The study also highlighted a number of drought tolerant mechanisms upon which breeding for drought tolerance may be based. However, further physiological and biochemical studies may be appropriate to substantiate the mechanism at molecular level.

Significant GCA and SCA effects made that both additive gene effects and dominance gene effects were involved in the inheritance of resistance to drought, but additive effects were predominance in both environments. Progenies from families G5, G7, G10, G12 and G15 had good SCA in yield and total biomass, harvest index, in both drought and no drought stress environment an indication they could be having progenies that could be drought tolerant and thus could be further screened for drought tolerance. The GCA/SCA ratios which indicated the predominance of additive gene effects would enable accomplishing of genetic gain for drought tolerance by mass recurrent selection under adequate drought stress selection pressure. The relationship of the crosses and their parents in their yields

under drought and no drought stress environment revealed that drought tolerance in sweetpotato could actually be controlled by recessive genes. Since sweetpotato clones are released as highly heterozygous F_1 progeny, then a breeding programme would factor in heterosis and SCA effects for significant genetic gain advances in breeding sweetpotato for drought tolerance. In conclusion, the findings in this study; 1) lay a foundation for sweetpotato breeding programmes, especially on drought tolerance, 2) for the first time uniquely combines yield performance, combining ability estimates, days to permanent wilting point and heterosis under drought and no drought stress to unmask the gene action of drought tolerance in sweetpotato, a contribution to science.