YIELD EVALUATION, SELECTION AND DROUGHT TOLERANCE INDICES OF ORANGE-FLESHED SWEETPOTATO (*IPOMOEA BATATAS* LAM) UNDER WATER STRESS CONDITIONS

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(Horticulture)

JOMO KENYATTA UNIVERSITY OF AGRICULTURE AND TECHNOLOGY

2012

Yield evaluation, selection and drought tolerance indices of orange-fleshed sweetpotato (*ipomoea batatas* lam) under water stress conditions

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A thesis submitted in fulfillment for the Degree of Doctor of Philosophy in Horticulture in the Jomo Kenyatta University of Agriculture and Technology

2012

DECLARATION

This thesis is my original work and has not been presented for a degree in any other University

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DEDICATION

Dedicated to my late mother Lydia Adhiambo, who never lived to witness this wonderful achievement.

ACKNOWLEDGEMENT

I express profound gratitude and appreciation to the following persons, without whose contribution, this piece of work would not have been possible. I am deeply grateful to Dr. Bernard Nyende, my first supervisor for his constant encouragement, scientific support and kind guidance throughout this PhD research journey. His concern and sharing his expertise and time in conceptualizing this study, his patient, understanding, support and valuable suggestions provided throughout the entire process has served as inspiration for always striving for excellence. May God bless him. My thanks go to Dr. Peter Masinde whose supervision and scientific support has also been crucial in accomplishing this work. I am grateful to Professor Kamau Ngamau for expanding my perspectives in *in vitro* work and in tackling tissue culture issues. Gruneberg Wolfgang provided valuable comments and suggestions on statistical work and Regina Kapinga for her moral support.

Special thanks to 2006-2010 Harvest plus Challenge Program; "Orange- Fleshed sweetpotato for Alleviating Vitamin A deficiency in the Sub-Saharan Africa, South-West and South Asia" for funding this study. Dr. Robert Mwanga and Dr. Jan Low provided support and valuable advice during the conduct of the field trials.

I express my appreciation to Jomo Kenyatta University of Agriculture and Technology, Department of Horticulture staff for their endless support during the study. A very special thank you to all staff members of the Kenya Plant Quarantine Health Inspectorate Services at Plant quarantine Station, Muguga, for their technical

support with the greenhouse and laboratory experiments. My gratitude to the center directors for Kenya Agriculture Research Institute Kiboko and Marigat sub- stations for allowing me to use their field trial experiments. Susan Wasike for her continued support during the conduct and write-up of the thesis. Last but not least all International Potato Center staff based in Nairobi for their moral support during the period of study.

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ABBREVIATIONS AND ACRONYMS

ASAL	Arid and Semi-Arid Lands
AFLP	Amplified Fragment Length Polymorphism
CIP	International Potato Centre
DM	Dry Matter
FAO	Food and Agriculture Organization
GMP	Geometric mean productivity
GT	Genotype Trait
MS	Murashige and Skoog growth media
MP	Mean productivity
MDA	Malondialdehyde content
OFSP	Orange-Fleshed Sweetpotato
PCA	Principal Component Analysis
PEG	Polyethylene Glycol salt
RWC	Relative Water Content
RPP	Relative Plasma lemma Permeability
RBFW	Ratio of Free to Bound Water content
RDI	Recommended daily intake
STI	Stress tolerance index
SSI	Stress susceptibility index
SPVD	Sweetpotato virus disease
SSA	Sub-Saharan Africa
SSR	Simple Sequence Repeat markers

SOD	Superoxide dismutase activity
USDAARS	United States Department of Agricultural Research Service
USA	United States of America
UPGMA	Unweighted pair group method with arithmetic mean
VITA A	Vitamin A partnership for Africa
VAD	Vitamin A Deficiency
WRD	Water Saturation Deficits
WHC	Water holding capacity
Yp	yield potential of each genotype in a nonstress environment
Ys	yield of each genotype in a stress environment
µg-RE	micrograms retinol equivalent

ABSTRACT

Orange-Fleshed Sweetpotato (OFSP) varieties provides high levels pro-vitamin A and medium amounts of iron and zinc. Their drought susceptibility is perceived as one of the major drawbacks to production and adoption. Experiments were conducted in Kenya at different sites in the years between 2008 and 2010 in order to select drought tolerant, high yielding orange-fleshed sweetpotato genotypes that have acceptable levels of beta carotene. An in vitro screening was conducted in the tissue laboratory at Kenya Plant Health Inspectorate Services Quarantine station, Muguga, Kenya to assess plantlet regeneration of 59 OFSP genotypes. The second experiment was conducted at Kiboko experimental field between September 2007 and January 2008.The objective was to identify 10-20 promising drought tolerant OFSP genotypes for further evaluation, testing and selection. The trial was laid out as randomized complete block design. Susceptible genotype K566632 and drought tolerant genotype Marooko were used as checks. For selection criteria three traits were used: Root- flesh color, root dry matter content and average yield in t/ha. Final selection was based on the ranking of the genotypes based on summation index of these variables.

In the third experiment 18 OFSP genotypes selected from the rapid field screening were further evaluated for yields and stability at two sites: Kiboko and Marigat. A split-plot design was used with two water levels (non-irrigated and irrigated) as the main factor and the genotypes as the sub-factor. The experimental design was randomized complete block design laid out as split-plot. Stress tolerance index was

used to identify genotypes with high stress tolerance and high yield potential. In addition a pot experiment was conducted to identify and evaluate traits associated with water stress in sweetpotato genotypes during growth period. The pot experiment was set up in a completely randomized design with five genotypes, two water levels stressed and unstressed replicated three times. One drought tolerant check Marooko was used. Changes in soil water content were evaluated by weighing the pots; Relative water content of the leaves; leaf and stem growth characteristics; morpho-physiological responses; the relative parameters and available soil water. Results showed significant variations among the genotypes for water stress tolerance based on plant growth characters. Genotypes 189135.9, 192033.5, 194515.5, 194539.3, 401055, 441724, 440429, 441097, 441538,441768 were observed with outstanding ability to continue root and shoot growth under *in vitro* stress conditions. Out of the 59 genotypes screened in the field, 21 were found to be dark orange, 12 to be orange, 12 light orange and 14 were found to be either cream or white. The dry matter of fresh storage roots ranged from 15 to 35 % with majority of the dark orange to orange genotypes having less than 30%. Most of the dark orange to orange genotypes recorded high number of roots compared to the cream to white-fleshed genotypes. Overall genotype 440378 was the lowest yielding genotype with a yield of 7.43 t/ha. Genotypes 420027, 187017.1, 420024, 187016.2 and 420014 produced over 43 t/ha. Mean total number of roots were significantly lower in Kiboko (6.15) than Marigat (20.48) under non-irrigated treatment. High numbers of root production under the same treatment in both sites were observed for genotypes 189135.9, 194573.9, 440287 and 441725. In both site genotypes 194573.9, 420014, 440286 and 441725

showed high stress tolerance and yield potential compared with the check by registering higher stress index values that ranged between 0.37 and 0.96. Genotypes 421066 and 189148.2 had their leaf areas least affected by moisture stress. Genotypes 189148.2 and 194573.9 registered high biomass production. Least biomass production under stress treatment was observed for genotype 421066. Genotypes 194573.9 and 189148.2 had biomass partitioning that favored root system development. Genotypes 421066, 194573.9, 192033.3, 187017.1 and 189135.9 recorded the highest values of STI at both sites, were considered to be tolerant genotypes with high beta-carotene and high dry matter content.

Water stress reduced the number of leaves per plant and individual leaf area, the number of storage roots per plant, weight of each storage root and the harvest index. There was variation in tolerance to water stress among the genotypes; example genotypes 189148.2, 194573.9 and 421066 maintained high leaf area under stress conditions, high root: shoot ratios. The genotypes that had a high root: shoot ratio under water stress conditions in both Marigat and Kiboko had storage roots with high beta carotene and high dry matter content. These are desirable traits to meet vitamin A requirement.

CHAPTER ONE

1.0 GENERAL INTRODUCTION

1.1 Background information

Sweetpotato, *Ipomoea batatas* L. (Lam.) is important in the tropics(Collins and Walter, 1985) ranking seventh among food crops of the world and is a major source of food and nutrition in developing countries (CIP, 1997). The crop is grown in more than one hundred countries, with an annual production worldwide exceeding 106million tones (FAO, 2010). It is regarded as a food security crop because of its low input requirements, ease of production and ability to produce under adverse weather and soil conditions (Ndolo *et al*., 2001). Its role is changing from a reliable, low-input, low-output crop to an increasingly important market crop.

It combines tremendous agronomic and nutritive qualities with a maturity period of 3-8 months after planting which makes growing two crops in a year possible (Bradbury and Holloway, 1988). Most sweetpotato varieties grown in Africa are white, cream or yellow fleshed (Loebenstein and Thottappilly, 2009), and supply little or no Vitamin A. Hence due to the urgency of addressing the vitamin A deficiency (VAD), sweetpotato varietal development programs were focused since the late 1990's first on the adaptive testing of the introduced orange-fleshed varieties, then on breeding for orange-fleshed varieties more adapted to specific agro-ecologies. To date orange-fleshed varieties introduced from other parts of the world or bred locally have been readily accepted in pilot areas in East Africa, and

preliminary results have shown that they contain sufficient levels of ß-carotene to play an important role in eliminating VAD (Hagenimana *et al.,* 1999).More than 3 million children under the age of five suffer from vitamin A-related blindness in Sub-Saharan Africa (SSA). This deficiency is also one of the leading causes of early childhood death, and a major risk factor for pregnant women in Africa (Kapinga *et al*., 2005). One of the easiest ways to introduce more vitamin A into the diet is to consume orange-fleshed sweetpotato which is rich in beta-carotene that the body converts easily into vitamin A. They are easy to grow and the average consumer can easily access them. Adding 100g of the sweetpotato to the daily diet can prevent vitamin A deficiency in children (Nagujja and Yanggen 2005), dramatically reduce maternal mortality and lower the risk of mother-to-child transmission of HIV/AIDS.Deficiency of various micronutrients, including vitamin A, zinc, and iron is common in the developing world and affects billions of (Aguayo and Baker 2005). These can lead to, amongst other symptoms, a higher incidence of blindness, a weaker immune system, stunted growth and impaired cognitive development (Black 2003). The poor, particularly the rural poor, tend to subsist on a diet of staple crops such as rice, wheat and maize, which are low in these micronutrients, and most cannot afford or efficiently cultivate enough fruits, vegetables or meat products that are necessary to obtain healthy levels of these nutrients (McClafferty and Yassir, 2008). As such, increasing the micronutrient levels in staple crops can help prevent and reduce the micronutrient deficiencies.

In one trial in Mozambique, eating sweetpotatoes biofortified with beta-carotene reduced the incidence of vitamin A deficiency in children by 24% (Pray*et al*, 2007). The orange fleshed sweetpotato (OFSP) can provide the needed pro-vitamin A (β-carotene) and this ß-carotene in OFSP is more bio-available compared to other plant sources (Niederwieser, 2004). A recent study found that boiled orange-fleshed sweetpotato (OFSP) contained over 1,000 retinol activity equivalents (RAE) per 125g which, when fed to school aged children in South Africa provided their recommended daily allowance (Jaarsveld et al 2006). This approach may have advantages over other health interventions such as providing foods fortified after processing, or providing Vitamin A supplements. Although these approaches have proven successful when dealing with the urban poor, they tend to require access to effective markets and healthcare systems which often just do not exist in rural areas.

Biofortification is fairly cost effective after an initial large research investment – where seeds can be distributed. The implementation costs of growing biofortified foods are nil or negligible, as opposed to supplementation which is comparatively expensive and requires continued financing over time. Furthermore this may be jeopardized by fluctuating political interest (Low *et al*., 2001). Hence, OFSP is not only a life saver and a crop to achieve food security but it also improves health, reduces mortality rates, and saves foreign exchange spent on the purchase of vitamin A capsules (Mwanga *et al*., 2004).

Sweetpotato in Sub-Saharan Africa

Sweetpotato is one of the most widely grown root crops in Sub-Saharan Africa, covering around 2.9 million hectares with an estimated production of 14.2 million tonnes of fresh storageroots (FAOSTAT, 2010). It is predominantly grown in small plots by poor farmers; hence it is known as the poor man's food (Woolfe, 1992). Since sweetpotato is produced predominate by women the poor person's food would be more accurate. The crop is particularly important in countries surrounding the Great Lakes in Eastern and Central Africa; Malawi, Angola, Mozambique and Madagascar in Southern Africa, and Nigeria in West Africa, (Woolfe, 1992). Sweetpotato production is expanding faster than any other major crop in Sub-Saharan Africa.

Sweetpotato generates large amounts of food per unit area per unit time (Woolfe, 1992). It tolerates occasional dry spells and yields even on less fertile soils in contrast to other crops such as maize (Ewell, 1990). Compared to other crops, sweetpotato requires few inputs and relatively less labor. The rapid growth area under sweetpotato in SSA during the past decades is due to changes in cropping patterns, unstable economies and increasing commercialization of production (Loebenstein and Thottappilly, 2009).

Sweetpotato is a stable food crop in SSA. According to FAO statistics(2010). Uganda and Nigeria were the major sweetpotato producing countries in SSA with a production of more than 5.5 million tonnes. These were closely followed by

Tanzania 1.4 million tonnes, Rwanda 0.8 million tonnes, Burundi 0.9 million tonnes, Kenya 0.3 million tonnes and Madagascar 0.9 million tonnes. In the region, the crop is regarded as a food security crop since it bridges a hunger gap when cereals are still in the field (Masunba *et al*., 2004). The crop is widely grown in all SSA countries, where it serves the role of a classic food security crop and is often harvested as "piecemeal" over a period of several months. Often women control production and sale of sweetpotato current figures indicate that there is a trend of increasing sweetpotato production in SSA; however the production is low in countries with high drought risk like Mozambique, Zambia, Senegal, Mali, Niger, Sudan, Ethiopia, Angola and Madagascar. The crop is important in SSA, due to the crop's relatively high productivity, its short cropping season, and its flexibility in planting and harvesting schedules. Recently Harvest Plus has started to reach End Users in Uganda with OFSP varieties labeled as "biofortified in β-carotene". Furthermore, sweetpotato stem and leaves are often consumed by people in SSA. The stems and leaves can have spinach like taste and contain two to three times more iron than storage roots. Leaves are also used for animal feed**,** particularly for dairy cattle and goats, and fresh storage roots are an excellent pig feed.

Constraints to sweetpotato production

One of the major constraints for sweetpotato production in Sub-Saharan Africa is its drought susceptibility. Sweetpotato is reproduced vegetatively using the vines and hence drought tolerance is of crucial importance for producing planting material. Varieties that are susceptible to drought typically do not survive drought or

prolonged dry seasons, do not produce volunteer plants, and thus do not provide planting material for the next crop. Consequently, there arises a major bottleneck for drought-susceptible OFSP planting material. In a study monitoring the success of the introduction of OFSP in Uganda (CIP 2004), vine scarcity was mentioned as a principal disadvantage of new OFSP varieties. Without the availability of planting material, the sustainability of OFSP production is hampered and its importance for pro-vitamin A and mineral supply for the poor in the region is undermined.

Drought tolerance is more than just an advantageous agronomic characteristic that can increase production; it is a key necessary for the widespread diffusion of OFSP via the sustainable propagation of vine planting material. While it is a versatile crop for meeting food security needs at the household level, OFSP production is constrained particularly by lack of adequate planting material (Ewell, 1990). Yield gains of 30-60 % can be obtained through the use of healthy planting material (Clerk and Hoy, 2006; Gibson *et al*., 2004). In the tropics, farmers usually obtain cuttings from the previous plots of sweetpotato production just before harvesting. This presents three major problems: use of cuttings from old plants results in low yields; if planting period follows a long dry period, no planting material may be available; a crop that has been in the field for a long time has higher chances of the vines being infected with insect pest or virus diseases. Moreover vine multiplication is slow; it takes about four weeks for a single node to develop a good rooting system and well developed leaves in a growth media (Loebenstein and Thottappilly, 2009).

The other major constraint to sweetpotato production is pest and diseases. While there are many diseases which affect sweetpotato, viruses and sweetpotato weevil are the two major ones causing economic levels of damage. The weevil is the most important pest of sweetpotato in Africa and worldwide with production losses often reaching 60% to 100% (Stathers *et al*., 2003). Damage due to sweetpotato weevils is particularly common in drier production zones. The search for sources of resistance to sweetpotato weevils in crop's germplasm has not yielded reliable results and hence no convectional resistance breeding has been possible to date (Low *et al.,* 2009).

Sweetpotato virus disease (SPVD) caused by dual infection with the whitefly-borne sweet potato chlorotic stunt virus (SPCSV) and the aphid-borne sweetpotato feathery mottle virus (SPFMV). It is the most serious disease of sweetpotato in Africa (Gibson et al., 2004). The disease causes strap-shaped leaves, vein-clearing, puckering, chlorosis and stunting in susceptible sweetpotato varieties and yields are much reduced and in some cases 100 % loss. It occurs throughout Africa and is particularly prevalent in the Great Lakes region.

1.2 Problem statement

The susceptibility of orange-fleshed sweetpotato (OFSP) drought stress is perceived as one of the major drawbacks affecting this crop. The currently available varieties do not allow sustainable production in drought prone regions. Traditional OFSP varieties produce very low fresh storage root yields (3 t/ha) compared to the

introduced OFSP varieties that yield over 20t/ha. Development of improved, drought tolerant OFSP will increase sweetpotato fresh storage root yields especially in Arid and Semi-Arid Lands (ASAL), where seasonal drought is a significant problem.

1.3 Overall objectives

To contribute to food security situation in Kenya through identification of high yielding drought tolerant orange-fleshed genotypes with consumer preferred traits

1.4 Specific objectives

1. To screen and select genotypes of OFSP that are drought tolerant.
2. To evaluate the selected genotypes for high nutritional value and drought tolerance in drought prone environments.
3. To select high yielding OFSP genotypes in drought prone conditions
4. To identify morphological and physiological traits responsible for drought tolerance in orange-fleshed sweet potato.

1.5 Hypothesis

1. Orange-fleshed sweetpotato genotypes may respond differently in drought prone environments and the levels of tolerance may vary.
2. The mechanism of tolerance may involve adjustment that involves: variation in dry matter partitioning between storage roots, foliage and roots; adjustment of leaf area; variation in dry matter content in storage roots

1. 6 Justification and scope of the study

Orange-fleshed sweetpotato (OFSP) varieties are a potentially cheap source may be the source of pro-vitamin A and income generation in the food processing chain for the poor in SSA. They have high amounts of β-carotene or pro-vitamin A (up to 400 ppm of dry matter (DM) as well as medium amounts of iron (up to 40 ppm of DM) and zinc (up to 15 ppm of DM). A pre-school child needs 5 mg pro-vitamin A per day and 100 g fresh OFSP storage root provide between 4.8 mg and 12 mg pro-vitamin A. Insufficient drought tolerance of the OFSP varieties in SSA strongly limits the success of efforts to alleviating vitamin deficiency (VAD) in SSA. Increasing drought tolerance in OFSP will be a positive step for acceptance of OFSP in drought affected regions of SSA. Improving OFSP for drought tolerance could have an impact on the livelihood and health of VAD people in SSA.

For crops growing in regions with periodic drought like in SSA, drought tolerance is one of the most important agronomical traits. White-flesh sweetpotato varieties that have been grown and selected in SSA for more than 200 years are more drought tolerant than recently introduced OFSP which originate from temperate, more humid zones. Lower yields and increased susceptibility to pests on water stressed plants decrease the acceptability of this otherwise very valuable crop type. Furthermore, drought tolerance is of crucial importance for producing planting material, since sweetpotato is reproduced vegetatively using the vines.

The principal sources of vines for farmers are from their own previous crop. These vines are generally harvested from volunteer plants. That is, in the process of harvesting the previous crop, a small percentage of roots is inadvertently left in the soil and grows as volunteer plants at the beginning of the next rainy season. The vines of these volunteer plants are used for planting material. Varieties that are not drought tolerant typically do not survive droughts or prolonged dry seasons, do not produce volunteer plants, and thus do not provide planting material for the next crop. Consequently, there arises a major bottleneck for drought-susceptible OFSP planting material. In a study monitoring the success of the introduction of OFSP in Uganda (CIP 2004), vine scarcity was mentioned as a principal disadvantage of new OFSP varieties. Without the availability of planting material, the sustainability of OFSP production important for pro-vitamin A and mineral supply for the poor in the region is undermined. Given the lack of a commercial system of vine propagation and distribution, farmer's own sources of planting material are going to be particularly important and therefore drought susceptibility is of particular concern. Drought tolerance is more than just an advantageous agronomic characteristic that can increase production; it is a key necessity for the widespread diffusion of OFSP via the sustainable propagation of vine planting material.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Origin of sweet potato

Sweetpotato (*Ipomoea batas* (L.) Lam) is one of the major root crops grown in tropical and sub-tropical regions of the world. It is a dicotyledonous plant belonging to the family convolvulaceae (Firon *et al*., 2009). The family includes 50 genera and over 1000 species of which *Ipomoea batatas* is the only species of economic importance as food in the family. *Ipomoea* has been mentioned as a leaf vegetable in Ethiopia, other species are either ornamental plants such as morning glory (*I. pomoea purpurea* (L.) Lam.) or weeds such as hedge bindweed (*Convolvulus sepium* (L.) Lam.).

Current scientific evidence suggests that the sweetpotato is of American origin (Central or South America) where it was widely established by the time the first Europeans arrived. Sweetpotato may be one of the earliest domesticated plants (Yen, 1982).It was introduced into Polynesia before the 8th century AD, and named *kumara* (Yen, 1982). However it is not clear whether it reached Polynesia through human contact or by chance e.g. washing ashore (Woolfe, 1992; O'Brien, 1972).

The evidence for pre-historic spread of sweetpotato includes, the recovery of storage roots from archaeological sites in Hawaii, New Zealand, and Easter Island; the presence of pre-historic root storage facilities in temperate New Zealand; the fact that

sweetpotato germplasm is less diverse outside Americas and lexical parallels between Quechua (the Inca language) name (*apichu*) for sweetpotato and the Polynesian *kumara* (Yen, 1982). Two main groups of sweetpotato, the *aje* (an Arawakan word) group (starchy and slightly sweet) and the batata (a Spanish word) group (starchy and very sweet) were known and are evidence of the widespread distribution of sweetpotato through the migration routes in the New World tropics before the discovery of America (Austin, 1988). O'Brien (1972) showed linguistic and historic evidence indicating that sweetpotato had reached southern Peru and southern Mexico around 2000-2500 B.C.

According to linguistic evidence there are three lines of dispersal of sweetpotato. The *kumara* line is pre-historic and is based on lexical parallels between the Quechua name and the Polynesian word, kumara. This could explain the movement of sweetpotato by Peruvian or Polynesian voyagers from northern South America to eastern Polynesia around 400 AD. The *batata* line, which dates back to the first voyage of Columbus in 1492, resulted in the introduction of West Indian sweetpotatoes to western Mediterranean Europe. The Portuguese explorers had introduced sweetpotatoes from western Mediterranean Europe to Africa, India, South East Asia, Indonesia, the East Indies and South China by the 16th century, and Southern Japan by1698. The *camote* (derived from *camotli* in the Mayan language Nahuatl) line was directly introduced from Mexico by Spanish trading galleons between Acapulco, and Manila, the Philippines, and Guam, in the 16th century (Yen,

1982). Progress in subsequent sweetpotato development was probably due to chance seedlings and vegetative propagation of somatic mutants (Yen, 1982).

Sweetpotato was introduced into Africa by the Portuguese in the fifteenth and sixteenth centuries from the Atlantic coastal regions of mid-latitude America (O'Brien, 1972). The Portuguese port of Mozambique is considered an obvious source of the sweetpotato with the term batata introduced into East Africa. The introduction of the plant to West Africa, specifically Angola probably occurred with Paulo Disade Novals' Charter of colonization in 1571 which included provisions for peasant families from Portugal with all the seeds and plants which they could take from Angola and from the Island of Sao Torre (Boxer, 1969)

2.2 Botanical classification of sweetpotato

Sweetpotatoes are perennial dicots, but cultivated as an annual for vines and storage roots. They are photoperiod sensitive; 11.5 hours day length or less promotes flowering, while at 13.5 hours day light flowering ceases but storage root yield is not affected (Kays, 1985). Short days with low light intensity promote storage root development. Flowers are perfect and produce capsules with 1-4 seeds after pollination and seed set. Complex sporophytic self- and cross-incompatibility cause serious problems in breeding (Jones, 1977).

Sweetpotato is hexaploid with 2n = 6x = 90 chromosomes, and although some plants morphologically similar to *I. batatas* with 2n = 4x = 60 have been described and

named; they are considered synonyms of this species. Among the approximately 50 genera and more than 1000 species in the family Convolvulaceae, only *I. batatas* is of major economic importance as a food (Woolfe, 1992). However, *I. aquatica* is also used as a raw salad or a cooked green vegetable or used as animal fodder in South East Asia. Storage root initiation varies from 21-35 days after planting (Austin, 1988). Although grown as an annual, sweetpotato isa herbaceous perennial species with creeping or trailing stems which grow very rapidly and produce a shallow canopy. Sweetpotato cultivars differ from one another in branching pattern, internode length, overall stem length, leaf shape (broad and entire to deeply indented), size and length of petiole. The growth habit is predominantly prostrate with a vine system that expands rapidly horizontally on the ground. However, depending on the length of internodes and frequency of branching, cultivars may be described as erect, semi-erect, spreading and very spreading. They also differ in the depth of rooting, time of maturity, and color of the skin of the storage roots, color of the root flesh, storage root shape, resistance to diseases and pests, and in the taste and texture of the cooked roots (Woolfe, 1992)

2.3 Sweetpotato germplasm and phylogeny

Sweetpotato exhibits great phenotypic and genotypic diversity and this is reflected by the color of skin or flesh of the root, the size and shape of roots, leaves and branches (Bhagsari and Brown, 1986), the depth of rooting, and time to maturity, resistance to pests and diseases, and even the flavor and texture of cooked roots (Huaman, 1992; Woolfe, 1992). The high level of genetic diversity of sweetpotato is reflected in the

fact that over 8,000 accessions of sweetpotato are maintained at various gene banks worldwide.Kuo (1991) speculated that this might represent only a fraction of the existing diversity.A total of 1157 wild accessions of series *Batatas* and 5,526 accessions of *I.batatas* are maintained at the International Potato Center (CIP), Lima, Peru (Huaman and Zhang, 1997). The United States Department of Agricultural Research Service (USDAARS) collection at Griffin, Georgia, has 759 *I. batatas* and 440 wild accessions. *I. batatas* is not known in the wild state and its ancestor is not known with certainty.

Nishiyama (1963) considered 6x *I. trifida* (accession K123), a morphologically similar species to *I. batatas* with small, slightly swollen storage roots collected from Mexico, to be the potential wild ancestor of sweetpotato. However, Jones (1965) suggested that K123 could be an *I. batatas* derivative growing in the wild, and that traits considered by Nishiyima(1963) as typical of wild plants in determining his classification, such as twining habit, are common in sweetpotato. He also showed that the F1 (K123 x *I. batatas*) hybrids produced plenty of seed, and that chromosome pairing in metaphase I of the hybrids was similar to the crosses between sweetpotatoes.

Sexual polyploidization through the production of unreduced gametes might have facilitated the evolution of *I. batatas* to the hexaploid level (Huaman and Zhang, 1997). Allopolyploidy (Jones, 1965; Magoon *et. al*., 1970; Austin, 1988) and autopolyploidy (Shiotani, 1988) were both proposed as a means to obtain *I. batatas*.

In support of the alloploid hypothesis, unreduced pollen in diploid *I. trifida* (Orjeda *et al*., 1990) and in some tetraploid and hexaploid *I. batatas* and 2n egg production in 3x *I. trifida* that generated 6x genotypes in their progenies (Freyre,*et al*., 1991) have been reported. Austin (1988) considered *I. trifida* to be the most closely related species to sweetpotato and suggested an alloploid origin. According to Nishiyama (1971), 2x *I. leucantha* gave rise to 4x *I. littoralis* and the cross between the two species (2*x* x 4*x*) gave rise to 3x *I. trifida* from which 6x *I. trifida* was derived. Selection and domestication of 6x *I. trifida* wild plants gave rise to 6x *I. batatas*.

Magoon *et al*., (1970) indicated that the three genomes of sweetpotato are partly homologous and two of the genomes show closer homology than the third. On the basis of numerical analysis of key morphological characters Austin (1988), proposed *I. triloba* and *I. trifida* to be the donors of the sweetpotato genome, and suggested that *I. tiliacea* may also have been involved in the origin of sweetpotato. From cytogenetical evidence, Shiotani and Kawase (1989), and Shiotani (1988) ruled out a genomic differentiation with respect to the genomic homology proposed by Magoon *et al.*, (1970) and postulated the genome constitution of sweetpotato to be autohexaploid (B1B1B2B2B2B2, B1 is homologous to B2) with the B genome that exists in autotetraploids and diploids of the *I. trifida* complex.

However, the degree of homology could not be estimated accurately. Austin (1988) postulated that the center of origin of *I. batatas* was between the Yucatan Peninsula

of Mexico and the mouth of the Orinoco River in Venezuela, where *I. trifida* and *I. triloba* might have crossed to produce the wild ancestor of *I. batatas*.

Germplasm characterization work by Yen (1982) and Austin (1988) indicates that the primary center of diversity of sweetpotatoes is in north western South America (Colombia, Ecuador and Peru) and parts of Central America (e.g. Mexico, Guatemala, and Nicaragua) where a great diversity of sweetpotatoes, weeds and wild *Ipomoea* exist. Secondary centers of sweetpotato diversity outside of the Americans are in China, Southeast Asia, New Guinea and East Africa.(Yen(1982) and Austin (1988) using amplified fragment length polymorphism (AFLP) and simple sequence repeat (SSR) markers, observed greater molecular variability among sweetpotato from Central America compared to the South American samples, suggesting that Central America may be a more likely center of diversity compared to South East. Africa is known to have a wide range of sweetpotato landraces and therefore is considered to be a secondary center of diversity.

Gichuru*et al*., 2006 carried out a study to assess the diversity among sweetpotato landraces from Kenya, Uganda and Tanzania using morphological and simple sequence repeats (SSR) markers. Two hundred and sixty-six landraces collected from agro-ecologically-distinct locations were screened for morphological characters using the CIP Research Guide (Huaman, 1991). Morphological characters were recorded and phylogenetic analysis using unweighted pair group method with arithmetic mean(UPGMA) showed a close relatedness amongst the East African

sweetpotato landraces with the majority having a0.1-0.5 range of Nei's genetic distance from each other.

The landraces, however, formed two major sub-clusters, irrespective of geographical origin. Based on the morphological analysis, 57 landraces that were fairly distant were further analyzed using four SSR primers specific for sweetpotato. Each primer pair was able to generate between two and five polymorphic and clearly scorable fragments. Phylogenetic analysis using UPGMA revealed similar results for the morphological characters. However, in each analysis, landraces from Tanzania tended to cluster together, suggesting that they are morphologically and genetically distinct from the Kenyan and Ugandan accessions.

2.4 Root system

The root system of sweetpotato plants obtained by vegetative propagation starts with adventitious roots that develop into primary fibrous roots which branch into lateral roots. As the plant matures, thick pencil roots that become lignified are produced. Other roots without lignin, are fleshy and bulky, and are called storage roots. Growth of these roots occurs by continued activity of the vascular cambium and anomalous primary and secondary cambium in storage roots (Wilson and Lowe, 1973). Storage root formation is also inextricably linked to the canopy by promoting photo assimilate export and leaf photosynthesis (Keutgen *et al*., 2002). Plants grown from true seed form a typical root system with a central axle with lateral branches. Later on, the central axle functions as a storage root.

The sweetpotato root system consists of fibrous roots that absorb nutrients and water and anchor the plant and storage roots which are lateral roots that store photosynthetic products. The storage roots are the commercial part of the sweetpotato plant, and often times are mistakenly referred to as "tubers". Most cultivars develop storage roots at the nodes of the mother stem cuttings that are underground. However, the very spreading cultivars produce storage roots at some of the nodes that come in contact with the soil. These are rarely of marketable size and their development is discouraged by vine lifting.

The parts of the storage roots are the proximal end that joins to the stem, through a root stalk, and where many adventitious buds are found from which the sprouts are originated; a central part which is more expanded; and the distal end that is the opposite to the root stalk. The adventitious buds that are located in the central and distal parts usually sprout later than those located in the proximal end. A transverse section of the storage roots shows the protective periderm or skin, the cortex or the cortical parenchyma that, depending on the cultivar, varies from very thin to very thick, the cambium ring where the latex vessels are found, and the medulla or the central parenchyma (Huaman, 1992). The amount of the latex formed depends on the maturity of the storage root, the cultivar and the soil moisture during the growing period. The latex drops are produced when the storage roots are cut and they darken very quickly due to oxidation (Huaman, 1992).

2.5 Drought tolerance mechanisms of sweetpotato

Drought, defined as water availability below what is required for maximum crop yield is one of the main factors limiting crop productions (Ceccarelli *et al*., 2009). In areas where water availability is limited, the choice of crop is restricted to a few, and often to only one, thus making farmers in those areas vulnerable for lack of options. Most of the rural poor live in areas where crop productivity and crop diversification are limited by lack of water. Therefore it is not surprising that there is an on-going global research effort on social, agronomic, genetic, breeding, physiological and molecular aspects of drought resistance, or recentlymore often used, water productivity (Passioura, 2006). Drought has been always a challenge to plant breeders, despite many decades of research (Blum, 1993). The development through breeding of cultivars with higher and stable harvestable yield under drought conditions would be a major breakthrough (Ceccarelli and Grando, 1996). However, drought tolerance is a very elusive trait from a genetic point of view. This is because the occurrence, severity, timing and duration of drought vary from year to year, and although every year there are winners, it is difficult to find those that are consistently successful. To make matters worse, drought seldom occurs in isolation; it often interacts with other a biotic and biotic stress (Ceccarelli *et al*., 2009)

Drought resistance is most frequently a combination of drought escape, avoidance and tolerance (Blum, 1988)**.**Drought escape is defined as the ability of a plant to complete its life cycle before serious soil and plant water deficits develop. This mechanism involves rapid phenological development (early storage root formation,

early maturity), development plasticity (variation in duration of growth period depending on the extent of water-deficit) and remobilization of upper biomass assimilates to the storage roots.

Drought avoidance is the ability of plants to maintain relatively high plant tissue water potential despite a shortage of soil moisture. Mechanisms for improving water uptake (rooting depth, efficient root system), storage of water in plant cells (storage roots, hydraulic conductance) and reducing water loss (epidermal conductance and water use efficiency (stomatal and lenticular), reduced absorption of radiation (leaf rolling or folding) and reduced evaporation surface (leaf area) confer drought avoidance.

Drought tolerance is the ability to withstand water-deficit with low plant tissue water potential. The mechanisms of drought tolerance are maintenance of turgor by osmotic adjustment (solute accumulation in the cell by free amino-acids, polypeptides and soluble carbohydrates), increase in elasticity in the cell and decrease in cell size and desiccation tolerance by protoplasmic resistance.

Sweet potato is sensitive to water deficits, particularly during the establishment period, vine development and storage root initiation, (Indira and Kabeerathumma, 1998). It is considered to be moderately tolerant (Valenzuela *et al*., 2000). Different cultivars may respond differently to limited quantities of soil water. Selection for good cultivars that have good performance under drought conditions is considered to

be of a major importance. This enables adequate root harvest and the survival of planting material in critical drought years (Xie *et al*., 1998). CIP has demonstrated that sweetpotato cultivar differ in drought tolerance, which is correlated with the ability for deep rooting (Ekanayake, 1990).

Sweetpotato needs adequate water at planting and for several weeks thereafter, but can tolerate moderate drought in the 2nd and 3rd month of growth (mid-season drought during storage root formation), and fairly severe drought in the 4th or 5th month (terminal drought) (Martin, 1998). Mid-season drought, during storage root thickening may reduce the number of storage roots produced, whereas terminal drought causes smaller storage roots. It is assumed that drought escape, avoidance and tolerance participate with drought resistance in sweetpotato. The various drought coping mechanisms that includes drought escape, avoidance and tolerance or a range of combinations of these may have different impacts on plant performance and yield maintenance under moisture stress conditions. Therefore impact assessments of drought resistance traits on agronomic characteristics of the crop are required. While the genetic basis of drought resistance in sweetpotato is largely unknown, there are many reports describing stress resistant varietiesWang *et al*., 2003., Chavez *et al*.,2000.,Hou *et al*., 1999., Yang *et al*., 1999.,; Ding *et al*., 1997)**.**Sweetpotato roots can penetrate to about 2 m in the soil and can absorb water from deeper soil layers (Bouwkamp, 1985).

Differences in response of genotypes in irrigated and non-irrigated experiments appeared to be correlated ability for development of the deep root or extensive system in the early stage (Yen *et al*., 1964)**.** Relative water content and water use efficiency appear to be a further key trait (Kelm, 2000). Furthermore the relative contents of free amino acids, soluble sugars, and ATP and chlorophyll a/b ratio appear to correlate with drought tolerance indicating the participation of osmotic adjustment with drought tolerance in sweetpotato (Zhang *et al*., 2004; Zhang *et al*., 2003)**.**Under water stress, the relative plasma lemma permeability (RPP) and water saturation deficit (WRD) in sweetpotato leaves have been observed to increase, whereas the relative water content (RWC), ratio of free to bound water and water content in the vines (RBFW) and earthnut of the crop decreases. RWC was also positively and significantly correlated with drought tolerance, however the correlation between water content in the vine and the leaves to drought tolerance was not significant (Zhang *et al*., 2006).

Drought resistance has been highly and positively correlated with relative water content (RWC) and superoxide dismutase(SOD) activity, but highly and negatively correlated with malondialdehyde (MDA) content. Free proline was not correlated with drought tolerance. Cultivars with high tolerance show less decrease of RWC and increase of MDA and more increase of SOD activity (Zhang *et al*., 2005). A study conducted to investigate the relationship between paroxidation and membrane protection in sweetpotato leaves under water stress condition showed malondialdehyde relative value to be negatively and significantly correlated with

drought resistance, however superoxide dismutase, peroxidase, catalase values were correlated positively with drought tolerance (Zhang *et al*., 2003).

Preliminary microarray experiments on sweetpotato using DNA microarray has revealed 478 genes up-regulated and 487 genes down-regulated in response to water restriction. The up-regulated genes included metallothionins, lipid-transfer proteins, mannose-binding lectin, sporamins (trypsin inhibitor), and C-metabolism genes, the down-regulated ones sweetpotato-rich proteins, carbonic anhydrase, and chlorophyll a/b related proteins.

2.6 Vitamin A deficiency in Sub Saharan

An insufficiency of vitamin A in the diet results in vitamin A deficiency (VAD) in children, pregnant and lactating mothers and imuno-defecient persons suffering from various ailments Vitamin A deficiency is responsible for night blindness, increased susceptibility to infections and impaired growth and development. Xerophtalmia includes all manifestations of visual deficiency caused by vitamin A from the mild and reversible form of night blindness, conjonctival xerosis and Bitot spots to irreversible form of cornea ulceration where the eye can irreversibly be damaged or lost (Sommer, 1994). A larger proportion (20-24%) of child mortality from measles, diarrhoea and malaria can be attributed to vitamin A deficiency (WHO 2004). Children are at risk but so are pregnant and lactating women and imuno-deficient persons, such as those suffering from HIV and AIDS (Sommer, 1994). Vitamin A deficiency is a major public health issue in developing countries; with children and

pregnant/lactating women the most vulnerable (WHO, 2009). Sub-Saharan Africa is one of the most affected areas with 33 million pre-school children who are deficient, which accounts for a third of the world cases (West, 2002).

South Asia and Africa are the parts of the world most affected by vitamin A deficiency (WHO, 2004). In Sub-Saharan Africa the majority of sweetpotato that is consumed is white-fleshed and has low levels of provitamin A (β-Carotene) (Ameny and Wilson, 1997). There are efforts through the Vitamin A Partnership for Africa (VITAA) Initiative and also through a Bill and Melinda Gates Foundation Project led by the Harvest Plus Challenge Program (Reaching End Users) to promote the use of orange-fleshed varieties that have high β -carotene content (Kapinga *et al*., 2005). Harvest Plus is a global alliance of research institutions seeking to improve human nutrition in the developing countries by tackling micronutrient deficiencies in iron, zinc and vitamin A. Harvest Plus focuses on biofortification of staple food crops (cassava, sweetpotato, maize, rice, bean, millet) that are consumed by the poor.

Currently the biofortified sweetpotato varieties have shown to be capable of reducing vitamin A deficiency in studies on children in Sub-Saharan Africa (Jalal *et al.,* 1998; Van Jaarsveld *et al.,* 2005; Low *et al.,*. 2007). There are different strategies to tackle vitamin A deficiency. Traditional interventions consist of administration of vitamin A capsules. Although a single dose can be given every six months or every year, these medical interventions are costly (Nestel *et al.,* 2006). Food fortification is another approach used to reduce vitamin A deficiency that works by adding vitamin

A to food commodities (*e.g.* sugar). An alternative approach is biofortification, which consists of breeding staple crops to increase their content of vitamins and/or minerals. Compared to the two other strategies, biofortification is considered a more sustainable approach because it has the potential to provide vitamins or minerals throughout the year with a one-off intervention and in the longer term at lower cost (Kósambo *et al.,* 1998). For the same level of impact on public health, the cost of biofortification is estimated to be half that of vitamin A supplementation (Nestel *et al.,* 2006). Moreover, rural and low-income communities, which have been shown to be more at risk, can be reached by this approach and it also creates opportunities for income generation from production and marketing of these crops.

Two studies in South Africa (van Jaarsveld *et al.,* 2005) and Mozambique (Low *et al.,* 2007) have demonstrated that regular consumption of orange-fleshed sweetpotato (OFSP) significantly increased vitamin A status of children. The South African study measured the impact of the consumption of OFSP on primary-school children. The serum retinol of children (n=90) who consumed OFSP was significantly higher compared to the serum retinol of children consuming white-fleshed sweetpotato (WFSP) after 53 school-days. It proved that the consumption of OFSP significantly increased vitamin A status of children. Study undertaken by Low *et al.,* (2007) involved promoting OFSP consumption by households including young children (*ca.* n=40) for two agricultural cycles. At the end of the study period serum retinol of young children consuming OFSP was improved significantly. The OFSP was the least expensive source of vitamin A in local markets. The second study further

proved that OFSP, as part of an integrated agricultural and nutrition approach, could potentially play a significant role in tackling vitamin A deficiency in developing countries.

2.7 Selection criteria for identifying drought tolerant genotypes and high yielding genotypes in drought stress and non-stress condition

Drought is the main environmental constraint, which occurs in many parts of the world every year, often having devastating effects on crop productivity. Hence, improved tolerance to drought has been a goal in crop improvement programs since, the dawn of agriculture (Ludlow and Muchow, 1990). Drought tolerance is not a simple response, but is mostly conditioned by many component responses, which interact and may be different for crops in relation to types, intensity and duration of water deficit. Moreover, most agronomical characters are expressed differently in normal and stress conditions and are known to be affected by environmental factors. Therefore, selection based on the phenotype would be difficult for such traits (Hittalmani *et al*., 2003).

Drought is an important factor limiting crop production in arid and semi-arid conditions. Breeding for drought tolerance by selecting solely for root storage, tuber or grain yield is difficult because the heritability of yield under drought conditions is low, due to small genotypic variance or large genotype-environment interaction variances (Blum, 1988; Ludlow and Muchow, 1990). The genetic structure and phenotypic expression of a quantitative trait are highly influenced by environmental

factors, thus, one barrier for understanding the inheritance of a quantitative trait is genotype-environment interactions (Breese, 1969).

The relative yield performance of genotypes in drought stressed and favorable environments seems to be a common starting point in the identification of desirable genotypes for unpredictable rain-fed conditions. There is some agreement that a high yield potential is advantageous under mild stress, while genotypes with low yielding potential and high drought tolerance may be useful when stress is severe (Voltas *et al*., 1999; Panthuwan *et al*., 2002). Several researchers have chosen the mid-way and believe in selection under both favorable and stress conditions (Fischer and Maurer, 1978; Fernandez, 1992; Clarke *et al*., 1992; Rajaram and Van Ginkel, 2001).

Many methods have been employed to identify crop lines that are productive in dry environments (Reynolds *et al*., 2007).Some use mathematical models to compare the change in seed, storage or tuber yield between stressed and non-stressed environments (Rosielle and Hamblin, 1981). Loss of yield is the main concern of plant breeders and they hence, emphasize on yield performance under moisture-stress conditions. But variation in yield potential could arise from factors related to adaptation rather than to drought tolerance. Thus, drought indices providing a measure of drought based on yield loss under drought-conditions compared to normal conditions are being used in screening drought-tolerant genotypes (Mitra, 2001). Several reports on the association of the indices with drought tolerance of different crops have been documented (Fernandez, 1992).

Rosielle and Hamblin (1981) defined stress tolerance as the differences in yield under stress (Ys) and non-stress (Yp) environments and Mean Productivity (MP) as the average of Ys and Yp. Fischer and Maurer (1978) proposed a stress susceptibility index (SSI) of the cultivar. This is yield of a genotype under stress as a function of the yield without stress. Fernandez (1992) defined a new advanced index called Stress Tolerance Index (STI) which can be used to identify genotypes producing high yield under both stress and non-stress conditions. He declared that selection based on STI will result in genotypes with higher stress tolerance and yield potential. The other yield based estimates of drought tolerance is geometric mean (GMP), which is often used by breeders interested in relative performance, since drought stress can vary in severity in field environment over years (Ramirez and Kelly, 1998). Lin and Binns (1988) used the "superiority index" (Pi) (the mean square of the distance of the yield of a genotype from the maximum yield of all genotypes at a given location) as estimates of genotype adaptability over a range of environments. Bansal and Sinha (1991) used linear regression coefficient (*bi*) as a criteria for selection of drought tolerant genotypes. Karamanos and Papatheohari (1999) used a new index of relative adaptability to drought (bN).

Among the stress tolerance indicators, a larger value of tolerance index(TOL) and stress susceptible index(SSI) represent relatively more sensitivity to stress, thus a smaller value of TOL and SSI are favored. Selection based on these two indices favors genotypes with low yield under non-stress conditions and high yield under

stress conditions (Golabadi *et al*., 2006). In spring wheat cultivars, Guttieri *et al*., (2001) using SSI criterion suggested that SSI more than 1 indicated above-average susceptibility and SSI less than 1 indicated below-average susceptibility to drought stress. Ramirez and Kelly (1998) reported that selection based on combination of GMP and SSI may be more efficient for improving drought tolerance in common bean. Khalili *et al*., (2004) showed that based on geometric mean productivity (GMP) and STI indices, corn hybrids with high yield in both stress and non-stress environments can be selected. Fernandez (1992) proposed STI index which discriminates genotypes with high yield and stress tolerance potentials.

Limitations of using the SSI and TOL indices have already been described in wheat (Clark *et al*., 1992) and in common bean (Ramirez and Kelly, 1998). The SSI does not differentiate between potentially drought-tolerant genotypes and those that possessed low overall yield potential. Although low TOL has been used as a basis for selecting cultivars with tolerant to water stress, the likelihood of selecting low yielding cultivars with a small yield differential can be anticipated (Ramirez and Kelly, 1998).Stress Tolerance Index (STI) is calculated based on GMP and thus rank correlation between STI and GMP is equal to 1. The higher value of STI means higher tolerance and yield potential for genotype. The stress intensity value is also incorporated in the calculation of STI. Thus, STI is expected to be the most desirable index for drought tolerance. Same result was obtained by Fernandez (1992), Imamjomah (1999) and Farshadfar and Sutka (2003) for STI, Mp and GMP.

Under most yield trial condition, the correlation between Ys and Yp is between 0 and 0.5 and genetic variance ratio is <1 (Farshadfar and Sutka, 2003). Thus, genotypic selection for yield under a non-stress environment would increase the mean stress yield. MP is based on the arithmetic means and therefore, it has an upward bias due to a relatively larger difference between Yp and Ys, whereas, the geometric mean is less sensitive to large extreme values. Higher values of Stress Susceptibility Index (SSI) indicate a higher degree of susceptibility under stress conditions for genotype and vice versa (Bruckner and Frohberg, 1987; Solomon and Labuschagne, 2003).

Selection based on a combination of indices may provide a useful criterion for improving drought tolerance in most crops, but study of correlation coefficients are useful in finding out the degree of overall linear association solely between any two considered attributes. Thus, a better approach such as biplot analysis is needed to identify the superior genotypes for both stressed and non-stressed environments. Genotypes subjected to biplot analysis, are compared for assessing relationships between all the attributes at once.Biplot analysis has been used by many researchers for comparison of different genotypes for different criteria and in different plant species. Thomas *et al*., (1995) distinguished 25 accessions of meadow fescue collected from seven countries using biplot analysis. Kaya *et al*., (2002) were able to reveal that bread wheat genotypes with larger PCA1 and lower PCA2 scores gave high yields (stable genotypes) and genotypes with lower PCA1 and larger PCA2 scores had low yields (unstable genotypes). Yan and Rajcan (2002) showed that applying Genotype-Trait (GT) biplot to the multiple trait data illustrated that GT

biplots graphically displayed the interrelationships among seed yield, oil content, protein content, plant height and days to maturity and facilitated visual cultivar comparisons and selection in soybean.

2.8 Genotype X Environmental interactions

Genotype x environment interactions has been defined as the failure of genotypes to achieve the same relative performance in different environments (Baker, 1988). Identification of yield-contributing traits and knowledge of GE interactions and yield stability are important for breeding new cultivars with improved adaptation to the environmental constraints prevailing in the target environments.

A genotype grown in different environments will frequently show significant fluctuations in yield performance. Changes are influenced by environmental conditions. The GXE interaction reduces the genetic progress through minimizing the association between phenotypic and genotypic values. Hence GXE must either be exploited by selecting superior genotypes for each specific target environment or avoided by selecting widely adopted and stable genotypes across wide range of environments (Ceccarelli, 1989).

Currently, plant breeders have available many methods for the analyses of genotype yield adaptability and stability to help in the difficult task of identifying superior cultivars in the presence of significant GxE interaction (Eskridge, 1990). Genotype-by-environment interactions (GxE) are of great interest when evaluating the stability

of breeding clones under different environmental conditions. In spite of its ability to adapt to harsh growing conditions, sweetpotato is sensitive to environmental variation. Presence of a significant genotype x environment interaction in sweetpotato in both yield and quality traits has been reported (Ngeve, 1993; Naskar and Singh, 1992;Whyte, 1989). Highly stable and adaptable genotypes are important in sweetpotato productivity and evaluation across sites would form a basis for breeding varieties that are stable. This stability in performance is one of the most desirable properties of a genotype to be released as a cultivar for wide range of application. Large GxE interaction slows down selection progress and makes genotype recommendations difficult; therefore knowledge of genotype performance and yield adaptation in diverse agro-ecological zones would be highly beneficial for cultivar deployment.

2.9 In *vitro* screening for drought tolerance

Drought is one of the most common environmental stresses affecting plant growth and productivity (Boyer, 1982). Under field conditions, drought severity, timing and duration vary from year to year and a cultivar, which is successful in one year, might fail in another year hence the need to do in vitro screening. The unpredictable and variable forms in which drought stress manifest, complicates the selection of superior plant materials as well as breeding programs. Plant cell and tissue culture has been a useful tool to study stress tolerance mechanism under in vitro conditions (Baijji *et al*., 2000). In vitro culture techniques minimize environmental variations due to defined nutrient media, controlled conditions and homogeneity of stress application

(Sakthivelu *et al*., 2008). In addition, the simplicity of the technique enables studying large plant population and stress treatments in a limited space and short period of time.

Tissue culture offers opportunities to study cellular-level responses to osmotic stress and possibly identify cell lines that differ in osmotic adjustment capabilities. Cellular-level tolerance might also be most amenable to genetic manipulation because only a few genes for metabolic processes involved in osmo-regulation may be involved (Heikkila *et al*., 1984). Additional benefits would include development of methods to evaluate and screen potentially tolerant germplasm for drought tolerance, assuming that a similarity exists between cellular-level responses and whole-plant responses under field conditions. The ability to regenerate plants from tolerant cell lines and obtain enhanced tolerance at the plant level would be an additional advantage. Potential physiological studies of enzyme activity, osmo-regulatory compounds, nitrogen metabolism, and genetic markers with a tissue culture system could also advance the fundamental understanding of water stress.

Several studies support correlations between whole- plant and cell-culture responses for salt tolerance. Barlass and Skene (1981) found relative tolerance of grape (Vitis species) cultivars to salt to be the same in vitro and for whole plants. Likewise, Orton (1980) determined for cultivated barley (*Hordeum vulgare* L.) and a wild relative that salt tolerance at the cellular level is similar to that at the whole-plant level.

Nabors *et al*., 1980 selected salt tolerant tobacco cell lines in culture, and plants regenerated transmitted tolerance to subsequent generations.

Polyethylene glycol (PEG) is assumed to be a non-penetrating osmotic agent that lowers the water potential of the medium and has been used to simulate drought stress in plants (Bressan *et al*., 1981). This assumption has been questioned because Yaniv and Werker (1983) have demonstrated that PEG- induced water stress in solanaceae species resulted in PEG secretion from the leaves. Bressan *et al*., (1982, 1981) and Handa *et al*., (1984, 1983) reported using PEG to select tolerant tomato (*Lycopersicon esculentum* Mill) cell lines and indicated that PEG does not contribute to the osmotic adjustment of selected cells. The tolerant cells grew better than cells never exposed to PEG, but lost resistance in a medium lacking PEG (Bressan *et al*, 1981). These studies support the use of PEG to induce water stress at the cellular level.

Polythylene glycol (PEG) of high molecular weights have been long used to simulate drought stress in plants as non-penetrating osmotic agents lowering the water potential in away similar to soil drying (Larher *et al*., 1993). Selection for drought tolerance at early stage of seedlings is most frequently carried out by including chemical drought induced molecules like polyethylene glycol (PEG6000) in the medium. This can be used to modify the osmotic potential of nutrient solution culture and thus induce plant water deficit in a relatively controlled manner, appropriate to experimental protocols (Khanna and Garg, 1997). Simulation of drought stress under

in vitro conditions during the regeneration process constitutes a convenient way to study the effects of drought on morphogenic responses. In vitro selection for drought tolerant genotypes or breeding lines has been conducted for various crops like for wheat genotypes (Hsissou and Bouharmont, 1994); Tomatoes (Manoj and Uday, 2007); Rice (Shankhdhar *et al*., 2000); Soya bean cultivars (Sakthivelu *et al*., 2008) green grams mungbean (*Vigna radiate* L.) (Gulati and Jaiwal, 1993) and hence can also be used for sweetpotato.

CHAPTER THREE

3.0 GENERAL MATERIALS AND METHODS

3.1 Trial site and experimental design

The *in vitro* experiment was conducted in the tissue culture laboratory of Kenya Plant Health Inspectorate Service, Quarantine station, Muguga, Kenya, located at1° 11' 0" South, 36° 39' 0" East at an altitude of about 1950m above sea level. The rapid screening and selection of orange-fleshed genotypes was conducted between September 2007 to beginning of January 2008 on a Rhodic/ Orthic ferralsols at KARI Kiboko experimental field (Latitude 010 15' S; Longitude 360 44' E; Altitude 975 m above the sea level). Climate data were obtained from the Agro-meteorological station at KARI Kiboko experimental field. The multi-location evaluation of the selected orange-fleshed genotypes were conducted at Kenya Agricultural Research Center experimental fields at Kiboko (Latitude 010 15' S; Longitude 360 44' E; Altitude 975 m above sea level) and Marigat (Latitude 0° 28′ 0″ N, Longitude 35° 59′ 0″ E; Altitude 1067 m above sea level) during the year 2009.

3.2 Planting material and preparation of growth media

The plant materials used in this study were provided by International Potato Centre (CIP) in the year 2006 and were imported as in vitro plantlets from Lima, Peru. Seventy three genotypes with different beta carotene and mineral content levels were initially imported; sixteen genotypes never survived and only 57 were evaluated (Appendix 1 and 2). The materials were transferred into in vitro conditions and routinely propagated from the nodal cuttings. Each node consisted of 0.2-0.5 cm

stem segment with an axillary, with each circle lasting 2-4 weeks. The plantlets were raised on Murashige and Skoog (MS) basal solid medium, (Murashige and Skoog, 1962) containing 30 g/l sucrose and 28 g/l of phytogel maintained at pH 5.7. These were grown under long day conditions (16 hours of light at 3,000 lux and at temperatures ranging from 25° C to 28°C. These were later transferred to sterilized vermiculate soil in polythene bags in the greenhouse for a period of 2 months for acclimatization, multiplication and bulking. At harvest 24 cuttings each having a length of 30cm was obtained from each genotype for planting in the field.

3.3 Statistical analysis

Data were analyzed with ANOVA, and means separated by an LSD using $P < 0.001$. Water stress level and their interactions were employed using the SAS package (SAS version 8 of SAS Institute, Inc, 1999.

CHAPTER FOUR

In vitro evaluation of orange-fleshed sweetpotato for drought tolerance using polyethylene glycol

Abstract

In vitro techniques have been shown to be useful in identifying relatively salt tolerant genotypes at early stages of development. This is a useful tool for screening large number of breeding lines of genotypes within a short time. In this study, drought induced alterations in early shoot and root development of 59 sweetpotato genotypes. These genotypes were obtained from Lima, Peru and were evaluated against two Kenyan checks Marooko (drought tolerant) and K566632 (drought susceptible).These were assessed with polyethylene glycol (PEG 6000MW) at three different concentration levels 0, 10 and 15 g/l with three replications in completely randomized design. Data on shoot and root growth was recorded during tissue regeneration. Analysis of variance indicated genotypes, salt levels and salt level x genotype interaction, were highly significant ($p<0.01$) with respect to all the traits. At 15 g/l concentration of PEG, genotypes 189135.9, 194515.5, 440024, 441724 and 440001 had roots that were longer than those of Marooko. This level of stress severely affected the production of biomass in most of the genotypes. Genotypes 194515.5, 194539.3, 441724, 441538 (dark orange-fleshed) 189135.9, 401055, 441097 (orange-fleshed), 441768 (light-orange fleshed) 192033.5 (yellow-fleshed),440429 (light-cream) recorded high root and shoot growth at all salt levels indicating their ability to withstand severe water stress conditions. Genotypes

189151.38, 420027, 440132, 440104 (dark orange-fleshed) 440034, 421111 (Light-orange fleshed), 440166 and 441755 (yellow-fleshed) were susceptible.

4.0 INTRODUCTION

Selection for drought tolerance at early stage of seedlings is most frequently carried out by including chemical drought induced molecules like polyethylene glycol (PEG6000) in the medium. This can be used to modify the osmotic potential of nutrient solution culture and thus induce plant water deficit in a relatively controlled manner appropriate to experimental protocols (Khanna and Garg, 1994).

Simulation of drought stress under *in vitro* conditions during the regeneration process constitutes a convenient way to study the effects of drought on morphogenic responses. Information on application of in vitro methods in screening for drought tolerance in sweetpotato is still limited. The biotechnological approaches, including *in vitro* selection for stress tolerance will continue to have a significant place in the strategy of establishing plant systems with optimal stress reaction and productivity. The possibility of using in vitro screening for orange-fleshed sweetpotato genotypes for drought tolerance was investigated, with the aim of identifying at early stages of development those genotypes that are either drought tolerant or drought susceptible.

4.1 Materials and methods

4.1.1 Trial site and experimental design

As indicated in section 3.1.

4.1.2 Planting material and preparation of growth media

Planting material and preparation of growth media was done as explained in section 3.2. Murashige and Skoog (1962) basal media with concentration of polyethylene glycol salt (PEG6000) at 0, 10 and 15g/l was prepared, poured into Kilner jars and autoclaved at 121ºC and 15lb/sq inch for 15 minutes. Five cuttings per genotype with 2-3 nodes each were placed onto the media in Kilmer jars. All the planted jars were maintained under optimum culture conditions at 10 hours photoperiod per day with a photon light flux density of 70 μmol m^2/s and 28ºC temperature. The experiments were conducted in a completely randomized two-factor factorial design with three replications. The main factor was the genotypes and the sub-factor the salt levels. The experiment was laid out in factorial complete randomized design with three replications.

4.1.3 Data measurements

Harvesting was done at 65 days from the start of the study. The following data were recorded at harvest:

Root length (cm); this was determined by measuring the length of the longest root from each sample plant using a meter scale.

Root dry mass (g); fresh root samples from plants from each jar were weighed and heated to a constant weight in an oven for 48h at 65ºC and these were then re-weighed to determine the dry weight.

Leaf area (cm^2); the linear dimensions of length (L) and width (W) at the broadest part of the lamina of each 3rd leaf from the bottom of the plant were measured with a ruler. The leaf area was then calculated as A= LXW

Shoot length (cm); this was determined by measuring the plants in each treatment from the surface of the media in the jar to the tip of the tallest leaf

Shoot fresh and dry mass (g); fresh shoot samples separated from roots from plants from each jar were collected and weighed and then heated to a constant weight in an oven for 48h at 65ºC. These were re-weighed to determine the dry weight.

4.1.4 Statistical analysis

Data were analyzed with ANOVA, and means separated by an LSD using $P < 0.001$. Water stress level and their interactions were employed using the SAS package (SAS version 8 of SAS Institute, Inc, 1999.

4.2 Results

ANOVA results

Analysis of variance indicated genotypes, salt levels and salt level x genotype interaction, were highly significant ($p<0.001$) with respect to all the traits (Appendix 3).

Leaf Area

Significant decrease in leaf area for genotypes 420027, 440034, 440104, 194549.6 and 440643 was observed with increasing **s**alt concentration (Table 4.1). This decrease ranged from 0.17cm² to 0.57 cm² At the same higher concentration of 15 g/l genotypes 189135.9, 194515.5, 441097 and 441768 recorded higher leaf expansion that ranged from 5.7 to 6.6 cm² although not significantly different from that of the check (5.5 cm²). Higher mean area expansions relative to the check were noted for genotypes 189135.9 (6.5 cm²), 401055 (6.0 cm²), 441768 (7.5 cm²) and 441097 (7.4 cm

Table 4. 1 Effect of salt concentration on leaf area (cm²) of 59 sweetpotato genotypes during *in vitro* screening using different concentrations of polyethylene glycol

	Leaf area (cm²)					Leaf area (cm²)			
Genotype/salt conc.	**0 g/l**	**10 g/l**	**15 g/l**	**Mean**	**Genotype/salt conc.**	**0 g/l**	**10 g/l**	**15 g/l**	**Mean**
Marooko*	5.5a	6.5a	5.7a	5.9	440023	4.0a	4.3a	2.8a	3.7
187016.2	2.3a	1.7a	1.5a	1.8	440024	1.1a	8.7b	4.6c	4.8
187017.1	3.2a	2.7a	2.3a	2.7	440025	3.5a	5.0a	3.3a	3.9
189123.68	4.0a	0.6b	1.7b	2.1	440027	2.2a	5.5b	1.5a	3.1
189135.9	7.0a	7.3a	5.2b	6.5	440031	5.9a	5.7a	1.8b	4.5
189140	1.9a	1.6a	1.2a	1.6	440034	2.8a	0.9a	0.8a	1.5
189148.21	3.8a	2.5a	3.2a	3.2	440050	2.0a	4.2a	4.0a	3.4
189148.65	5.1a	1.7b	2.5b	3.1	440104	7.3a	3.9b	0.2c	3.8
189150.1	5.3a	4.3a	3.4a	4.4	440131	5.7a	10.2b	1.5c	5.8

Table 4.1 cont.

Genotype/salt conc.	Leaf Area (cm^2)			Mean	Genotype/salt conc	Leaf Area (cm^2)			Mean
189151.38	2.6a	5.7b	5.5b	4.6	440132	4.8a	6.2a	0.0b	3.7
192033.5	4.2a	6.3b	6.4b	5.6	440166	2.3a	1.5a	1.7a	1.8
194515.5	5.1a	9.5b	5.8c	6.8	440167	1.2a	2.1a	2.4a	1.9
194521.2	5.3a	2.1b	2.0b	3.1	440170	2.5a	2.8a	2.9a	2.8
194539.36	4.3a	6.0a	5.3a	5.2	440240	4.2c	0.4b	2.2a	2.2
194541.45	4.2a	3.0a	4.5a	3.9	440286	5.2a	0.0b	0.0b	1.7
194549.6	0.6a	0.6a	1.5a	0.9	440287	6.1a	5.8a	0.0b	4.0
194555.7	2.2a	3.8a	1.4a	2.5	440328	8.3a	3.3b	4.2b	5.3
194569.1	3.5a	2.5a	4.8a	3.6	440378	2.0a	2.3a	2.5a	2.3
194573.9	2.0a	0.8a	3.8b	2.2	440394	1.5a	1.2a	2.5a	1.7
400011	5.3a	4.3a	4.3a	4.7	440396	5.0a	8.3b	4.0a	5.8
401055	5.1a	7.2a	5.6a	6.0	440429	3.7a	3.5a	4.5a	3.9
420001	7.0a	1.2a	1.8b	3.3	440643	1.2a	5.6b	0.6a	2.4
420014	4.6a	6.1a	3.4b	4.7	441097	5.7a	10.0b	6.5a	7.4

Table 4.1 cont.

Genotype/salt conc	Leaf area (cm²)			Mean	Genotype/salt conc.	Leaf Area (cm²)			Mean
420027	1.1a	1.5a	0.6a	1.1	441538	5.7a	7.3b	5.8a	6.3
420064	2.2a	1.8a	6.6b	3.5	441724	3.5a	4.3a	2.0b	3.3
421066	2.5a	2.3a	1.5a	2.1	441725	4.1a	5.6a	6.3a	5.4
421111	3.8a	2.8a	1.2b	2.6	441755	0.3a	5.0b	3.4b	2.9
422656	8.0a	2.4b	4.4c	4.9	441768	7.0a	11.3b	3.8c	7.5
440001	2.2a	3.0a	2.2a	2.5	k566632**	11.2a	2.0b	1.7b	5.0
440017	1.5a	2.3a	3.5a	2.4	Salt level mean	3.82a	4.09a	3.06b	

Means followed by the same letter within the rows (showing differences among different salt levels) are not significantly different (P≤0.01); * tolerant check, ** susceptible check

Root length and root dry weight

Genotypes 189135.9, 421066, 440396, 440429, and 441097 formed the longest roots that ranged from 32 cm to 38 cm this was above that of the tolerant check length (26.0 cm) although not significantly different. At 15 g/l concentration of PEG, genotypes 189135.9, 194515.5, 440024, 441724 and 440001 exhibited long roots that ranged from 29.7cm to 40.2 cm (Table 4.2). Poor root growth at the same level was observed for genotypes 440031 (4.7 cm), 440286 (5.1), 440025, (3.5 cm), 440132 (1.9) and 420027 (2.6 cm). The performance of genotypes 440024 (27.5 cm), 194515.5 (31.8 cm), 441077 (30.7 cm) and 189135.9 (35.3 cm) registered high mean root lengths across the salt levels (Table 4.2). Genotypes 189135.9, 441538 and 441768 registered higher root weight that ranged from 5.23 to 6.0 g. These were significantly different from that of the check (1.3 cm) (Table 4.3).There was significant root weight reduction as stressed increased. Genotypes that exhibited higher root weight at 15 g/l concentration of PEG were 189135.9 (5 g), 194569 .1 (5.0 g), 440429(4.4 g) and 441768 (5.4 g). These were significantly higher than of the check (2.2 g). Higher mean root weight across the salt levels was recorded for genotypes 194515.5 (3.1 g), 441538 (4.8 g) and 441768 (3.9 g) (Table 4.3).

Table 4. 2 Effect of salt concentration on root length (cm) of 59sweetpotato genotypes during *in vitro* screening using different concentrations of polyethylene glycol

	Root length (cm)					Root length (cm)			
Genotype/salt con.	**0g/l**	**10g/l**	**15g/l**	**Mean**	**Genotype/salt conc.**	**0g/l**	**10g/l**	**15g/l**	**Mean**
Marooko*	26.0a	22.0a	21.3a	23.1	440023	21.0a	10.5a	13.2a	14.9
187016.2	17.7a	14.7a	13.3a	15.2	440024	28.8a	69.7b	40.2c	27.4
187017.1	27.0a	26.3a	27.0a	26.8	440025	17.8a	25.8b	3.5a	15.7
189123.68	18.0a	16.7a	15.3a	16.7	440027	30.3a	28.3a	16.7a	25.1
189135.9	33.0a	33.5a	35.3a	34.0	440031	5.3a	4.3a	3.8a	4.5
189140	29.1a	28.8a	25.8a	28.0	440034	29.8a	27.2a	28.1a	28.4
189148.21	17.3a	14.8a	17.5a	16.5	440050	13.3a	10.2a	9.8a	11.2
189148.65	10.3a	5.7a	8.0a	8.0	440104	22.0a	18.2a	22.0a	20.7
189150.1	15.3a	7.2a	5.3a	9.3	440131	13.6a	10.8a	9.8a	11.4
189151.38	11.0a	17.7a	13.3a	14.0	440132	17.9a	16.8a	1.9a	12.2
192033.5	12.7a	17.7a	15.7a	15.3	440166	18.7a	17.3a	12.0a	16.0
194515.5	31.3a	33.3a	30.7a	31.8	440167	30.7a	7.5b	6.5b	11.6
194521.2	26.3a	21.7a	12.2a	20.1	440170	20.7a	20.2a	24.0a	21.6
194539.36	23.8a	23.7a	23.7a	23.7	440240	21.3a	13.8a	12.6a	15.9

Table 4.2: Cont.

	Root length (cm)					Root length (cm)			
Genotype/salt conc.	**0g/l**	**10g/l**	**15g/l**	**Mean**	**Genotype/salt conc.**	**0g/l**	**10g/l**	**15g/l**	**Mean**
194541.45	10.5a	21.5a	24.9a	18.9	440286	11.9a	2.9a	1.4a	5.4
194549.6	17.3a	9.0a	24.3a	16.9	440287	27.3a	29.9a	3.5b	20.2
194555.7	7.3a	29.0b	16.1ab	17.5	440328	28.3a	26.0a	17.7a	24.0
194569.1	21.0a	4.0b	9.2b	11.4	440378	22.0a	48.3b	12.7a	21.0
194573.9	8.5a	4.7a	9.7a	7.6	440394	19.7a	10.3a	5.1a	11.2
400011	16.3a	25.0a	20.3a	20.6	440396	36.0a	14.0b	8.7b	19.6
401055	9.8a	6.3a	10.9a	9.0	440429	32.3a	25.7a	21.2a	23.1
420001	28.3a	23.7a	14.5a	22.2	440643	16.9a	9.3a	3.8a	10.0
420014	19.3a	16.3a	13.5a	16.3	441097	32.5a	34.2a	25.3a	30.7
420027	17.8a	3.6a	2.6a	8.0	441538	31.3a	21.5a	13.7a	22.2
420064	20.0a	23.0a	17.8a	20.2	441724	29.3a	25.0a	29.7a	28.0
421066	38.0a	16.7b	21.7b	22.1	441725	31.3a	25.5a	19.3a	25.4
421111	2.1a	27.3b	5.0a	11.4	441755	8.7a	9.7a	10.8a	9.8
422656	29.7a	25.2a	16.7a	23.8	441768	32.7a	25.8a	22.2a	26.9
440001	24.7a	15.0a	31.7a	23.8	K566632**	13.7a	8.0a	4.5a	8.7
440017	24.3a	33.7a	5.4b	21.1					

Means followed by the same letter within the rows (showing differences among different salt levels) are not significantly different (P≤0.01); * tolerant check, ** susceptible check

Table 4. 3 Effect of salt concentration on root dry weight (g) of 59 sweetpotato genotypes during *in vitro* screening using different concentrations of polyethylene glycol

Genotype/salt conc.	Root dry weigh (g) 0g/l	10g/l	15g/l	Mean	Genotype/salt conc.	Root dry weight (g) 0g/l	10g/l	15g/l	Mean
Marooko*	1.3a	1.6a	2.2a	1.7	440023	0.9a	0.4a	0.4a	0.6
187016.2	0.3a	0.3a	0.1a	0.2	440024	0.3a	0.9a	0.5a	0.5
187017.1	0.3a	1.0a	0.4a	0.6	440025	1.2a	0.2a	0.0b	0.5
189123.68	0.2a	0.4a	1.3ab	0.6	440027	0.7b	2.3a	0.0c	1.0
189135.9	6.0b	7.9a	5.0bc	6.3	440031	0.0a	0.0a	0.01a	0.0
189140	0.1a	0.0a	0.0a	0.0	440034	0.1a	0.0a	0.1a	0.0
189148.21	0.0a	0.0a	0.0a	0,0	440050	0.1a	0.0a	0.4a	0.2
189148.65	0.4a	0.0a	0.0a	0.2	440104	0.2a	0.0a	0.0a	0.1
189150.1	0.6a	0.2a	0.1a	0.3	440131	4.3a	0.1a	0.1a	1.5
189151.38	0.7a	2.0b	1.1ab	1.3	440132	0.0a	0.0a	0.0a	0.0
192033.5	0.7a	1.0a	0.9a	0.9	440166	0.3a	0.6a	0.0a	0.3
194515.5	4.8a	0.6b	3.8a	3.1	440167	0.1a	0.1a	0.0a	0.1
194521.2	1.3a	0.6a	0.4a	0.8	440170	2.0a	1.7a	1.9a	1.9
194539.36	1.5a	2.3a	3.2ab	2.3	440240	0.0a	0.2a	0.1a	0.1

Table 4.3: Cont.

Genotype/salt conc.	Root dry weight (g) 0	5	15	Mean	Genotype/salt conc.	Root dry weight (g) 0	5	15	Mean
194541.45	1.0a	0.8a	0.6a	0.8	440286	0.3a	0.0a	0.0a	0.1
194549.6	0.1a	0.2a	0.2a	0.5	440287	0.3a	0.4a	0.1a	0.3
194555.7	0.5a	0.1a	0.1a	0.2	440328	2.2a	1.4a	1.7a	1.8
194569.1	4.8b	0.0a	5.0bc	3.3	440378	1.9a	0.9b	0.8ab	1.2
194573.9	0.4a	0.6a	0.3a	0.4	440394	2.0bc	1.5b	0.1a	1.2
400011	0.5a	0.2a	0.6a	0.4	440396	2.1a	1.9a	1.2a	1.8
401055	0.5a	0.8a	0.4a	0.6	440429	2.3bc	1.7b	4.4a	2.8
420001	1.8b	0.8a	0.6a	1.1	440643	1.1a	0.2a	0.0a	0.5
420014	1.7a	1.7a	0.5b	1.3	441097	1.3bc	1.3b	3.5a	2.0
420027	0.1a	0.0a	0.0a	0.0	441538	5.2bc	6.1b	3.1a	4.8
420064	3.2b	0.8a	0.7a	1.6	441724	0.8b	2.7a	0.9c	1.5
421066	1.0a	0.3a	0.3a	0.5	441725	0.5a	0.0a	0.1a	0.2
421111	0.1a	0.1a	0.2a	0.1	441755	2.0b	0.8a	0.7a	1.1
422656	2.2a	1.2a	1.1ab	1.5	441768	5.9b	0.3a	5.4bc	3.9
440001	1.7b	0.3a	0.2a	0.7	K566632**	0.1a	0.0a	0.0a	0.0
440017	2.7b	1.4c	0.0a	1.4					

Means followed by the same letter within the rows (showing differences among different salt levels) are not significantly different (P≤0.01); * tolerant check, ** susceptible check

Shoot fresh and dry weight (g)

Under controlled treatment high shoot fresh weight above that of the tolerant check(1.6 g) were recorded for genotypes 189135.9 (6.5 g), 440170 (4.9 g), 440328 (5.3 g), 441538 (5.5g). A sharp and significant decrease in shoot fresh weight was recorded for genotypes 194541.45 (0.8 g), 420027 (0.2 g), K566632 (0.2 g), and 440167 (0.2 g) at high 15g/l PEG concentration. At the same level of stress genotypes 194515.5 (2.7 g), 194573.9 (2.5 g), 401055 (2.7 g), 440429 (3.3 g), 441097 (4.3 g), 441538 (2.2 g) and 441768 (3.1 g) recorded high fresh root weight (Table 4.4). In the control treatment genotypes 189135.9, (2.8 g) 440328 (2.1 g), 440170 (2.4 g), 440378 (2.1 g) and 441538 (2.5 g) produced significantly high shoot dry matter content than the check (0.7 g), whereas genotypes 440429 (1.7 g), 194539.36 (2.6 g), 441538 (4.4 g), 401055 (1.2 g), 194515.5 (1.2 g) and 189135.9 (1.2 g) recorded higher shoot dry weight at 15g/l of PEG concentration. The same genotypes recorded higher mean shoot dry weight across the salt levels that were significantly higher than that of the check (0.70 g). Lowest mean shoot dry weight were recorded for genotypes 420027 (0.1 g), 440024 (0.1 g), 440050 (0.2 g), 440167 (0.1 g), 440240 (0.1 g) and 440286 (0.1 g) (Table 4.5).

Shoot length

Increased stress at 15 g/l induced longer shoot length for genotypes 187016.2 (14 cm), 187017.1 (14.9 cm), 194539.36 (16.7 cm), 420064 (18.2 cm), 440378 (13.8 cm), and 441097 (13.7 cm) which was way above that of the tolerant check (8.50 cm). The same genotypes registered high mean shoot values across the salt level.

Significant reduction in growth was observed for genotypes 189148.65 (3.9 cm), 194541.45 (4.3 cm), 440286 (2.7 cm) (Table 4.6).

Table 4. 4 Effect of salt concentration on shoot fresh weight (g) of 59 sweetpotato genotypes during *in vitro* screening using different concentrations of polyethylene glycol

	Shoot fresh weight (g)					Shoot fresh weight (g)			
Genotype/salt conc.	**0g/l**	**10g/l**	**15g/l**	**Mean**	**Genotype/salt conc.**	**0g/l**	**10g/l**	**15g/l**	**Mean**
Marooko*	1.6a	1.6a	2.2b	1.8	440023	2.0b	0.9a	1.0a	1.3
187016.2	1.1a	1.0a	0.3b	0.8	440024	0.1b	1.4a	0.5bc	0.7
187017.1	2.3a	1.9a	0.8b	0.7	440025	1.1a	0.9a	0.5ab	0.8
189123.68	1.2b	0.7a	1.4c	1.1	440027	1.4c	4.3b	0.1a	1.9
189135.9	6.45c	5.6b	2.8a	5.0	440031	0.6a	0.4a	0.2a	0.4
189140	0.6c	0.1b	1.9a	0.9	440034	3.1c	2.0b	1.5a	2.2
189148.21	0.7a	1.0a	1.0a	0.9	440050	0.2a	0.3a	0.8b	0.4
189148.65	0.6a	0.5a	0.2a	0.4	440104	1.0b	0.1a	0.2a	0.4
189150.1	1.9a	2.0a	2.1a	2.0	440131	3.5c	0.1b	0.8a	1.5
189151.38	1.6c	4.5b	2.3a	2.8	440132	0.8a	0.7a	0.1b	0.5
192033.5	1.5c	4.8b	2.2a	2.8	440166	1.2a	1.1a	0.0b	0.9
194515.5	4.8a	4.3a	2.7b	4.0	440167	0.3a	0.3a	0.1a	0.2
194521.2	3.0c	0.9b	1.6a	1.8	440170	4.9a	2.8b	1.7c	3.1
194539.36	4.1a	4.5a	5.7b	4.8	440240	0.3c	0.2b	0.3a	0.3
194541.45	1.6c	0.7b	0.1a	0.8	440286	1.0b	0.1a	0.0a	0.4
194549.6	0.7a	0.7a	1.4b	1.0	440287	1.0b	1.7a	1.9a	1.5

Table 4.4: Cont.

Genotype/salt conc.	Shoot fresh weight (g) 0g/l	10g/l	15g/l	Mean	Genotype/salt conc.	Shoot fresh weight (g) 0g/l	10g/l	15g/l	Mean
194555.7	1.3b	0.6a	0.2a	0.7	440328	5.3b	1.7a	2.1a	3.0
194569.1	1.6b	0.2a	1.7c	1.7	440378	5.2c	2.9b	1.4a	3.2
194573.9	1.1a	1.1a	2.5b	1.5	440394	3.9c	2.5b	0.3a	2.2
400011	2.0b	1.3a	1.9c	1.7	440396	3.8a	3.5a	1.0b	2.8
401055	1.2c	2.0b	2.7a	1.9	440429	3.8b	3.1a	3.9c	3.6
420001	4.3c	1.0b	1.7a	2.4	440643	2.3c	0.9b	0.1a	1.1
420014	1.4c	0.9b	0.2a	0.8	441097	1.9c	3.1b	4.3a	3.1
420027	0.3a	0.2a	0.0a	0.2	441538	5.5c	4.8b	2.2a	4.2
420064	1.6a	1.2a	1.0ab	1.2	441724	1.8b	6.2a	1.5bc	3.2
421066	2.2b	1.0a	0.7a	1.3	441725	1.3a	1.5a	1.8b	1.5
421111	0.7a	0.8a	1.0a	0.9	441755	0.2b	1.4a	0.6bc	0.8
422656	4.4b	1.6a	1.7a	2.5	441768	6.1a	5.7a	3.1b	5.0
440001	2.5c	1.3b	0.8a	1.6	K566632**	0.2a	0.3a	0.0a	0.2
440017	4.4c	2.3b	0.3a	2.3					

Means followed by the same letter within the rows (showing differences among different salt levels) are not significantly different (P≤ 0.01); * tolerant check, ** susceptible check

Table 4. 5 Effect of salt concentration on shoot dry weight (g) of 59 sweetpotato genotypes during *in vitro* screening using different concentrations of polyethylene glycol

	Shoot dry weight (g)					Shoot dry weight (g)			
Genotype/salt conc.	**0g/l**	**10g/l**	**15g/l**	**Mean**	**Genotype/salt conc.**	**0g/l**	**10g/l**	**15g/l**	**Mean**
Marooko*	0.7a	0.7a	1.0a	0.8	440023	1.0b	0.4a	0.5a	0.3
187016.2	0.3a	0.4a	0.1a	0.3	440024	0.1a	0.5b	0.2ab	0.4
187017.1	1.1bc	1.0b	0.3a	0.8	440025	0.5a	0.5a	0.2a	0.4
189123.68	1.2b	0.7a	1.4bc	1.1	440027	1.4a	4.3c	0.1b	1.9
189135.9	2.8bc	2.4b	1.2a	2.1	440031	0.3a	0.1a	0.1a	0.2
189140	0.3ab	0.1a	0.7ab	0.4	440034	1.1a	0.9a	0.6a	0.9
189148.21	0.3a	0.4a	0.4a	0.4	440050	0.1a	0.0a	0.4a	0.2
189148.65	0.2a	0.2a	0.1a	0.2	440104	0.7b	0.0a	0.1a	0.3
189150.1	0.9a	0.9a	0.9a	0.9	440131	1.4b	0.0a	0.4a	0.2

Table 4.5 cont.

Genotype/salt conc.	Shoot dry weight (g) 0g/l	10g/l	15g/l	Mean	Genotype/salt conc.	Shoot dry weight (g) 0g/l	10g/l	15g/l	Mean
189151.38	0.7b	1.8a	1.0bc	1.1	440132	0.4a	0.3a	0.0a	0.2
192033.5	0.9b	2.0a	0.7bc	1.2	440166	0.4a	0.5a	0.2a	0.4
194515.5	2.0bc	1.9b	1.2a	1.7	440167	0.1a	0.1a	0.0a	0.1
194521.2	1.3b	0.4a	0.7a	0.8	440170	2.4b	1.3a	1.0a	1.6
194539.36	1.8bc	2.1b	2.6a	2.2	440240	0.2a	0.0a	0.2a	0.1
194541.45	0.7a	0.3a	0.0a	0.3	440286	0.4a	0.0a	0.0a	0.1
194549.6	0.4a	0.3a	0.7a	0.5	440287	0.4ab	0.7a	0.0b	0.4
194555.7	0.4a	0.3a	0.1a	0.3	440328	2.1b	0.7a	0.9a	1.2
194569.1	0.7b	0.1a	0.8bc	0.5	440378	2.1a	1.2c	0.5b	1.3
194573.9	0.5a	0.4a	0.4a	0.4	440394	1.7a	1.1c	0.1b	0.9
400011	0.8a	0.7a	0.7a	0.7	440396	1.7bc	1.7b	0.5a	1.3

Table 4.5 cont.

	Shoot dry weight (g)					Shoot dry weight (g)			
Genotype/salt conc.	**0g/l**	**10g/l**	**15g/l**	**Mean**	**Genotype/salt conc.**	**. 0g/l**	**10g/l**	**15g/l**	**Mean**
401055	0.5bc	0.6b	1.2a	0.8	440429	1.6a	1.4a	1.7a	1.6
420001	1.0b	0.4a	0.4a	0.6	440643	0.5ab	0.9a	0.1b	0.5
420014	0.6a	0.3a	0.1a	0.3	441097	0.7b	1.5a	1.6a	1.2
420027	0.1a	0.1a	0.1a	0.1	441538	2.5bc	2.2b	4.4a	3.0
420064	0.7a	0.3a	0.5a	0.5	441724	0.8b	2.6a	0.6c	1.3
421066	0.8a	0.5a	0.3a	0.4	441725	0.6a	0.8a	0.8a	0.7
421111	0.3a	0.4a	0.4a	1.0	441755	0.2a	0.2a	0.2a	0.2
422656	1.6b	0.7a	0.7a	0.6	441768	2.5b	1.3a	1.3a	1.7
440001	0.9a	0.5a	0.3ab	1.0	K566632**	0.1a	0.0a	0.0a	0.1
440017	1.8a	1.1c	0.1b	0.6					

Means followed by the same letter within the rows (showing differences among different salt levels) are not significantly different (P≤0.001); * tolerant check, ** susceptible check

Table 4. 6 Effect of salt concentration on shoot length (cm) of 59 sweetpotato genotypes during *in vitro* screening using different concentrations of polyethylene glycol

	Shoot length (cm)					Shoot length (cm)			
Genotypes/salt conc.	**0g/l**	**10g/l**	**15g/l**	**Mean**	**Genotype/salt conc.**	**0g/l**	**10g/l**	**15g/l**	**Mean**
Marooko*	7.2a	5.2a	8.5a	7.0	440023	5.7a	2.0b	2.7ab	3.4
187016.2	10.3a	12.2a	14.0ab	12.2	440024	2.8b	7.1a	6.8a	5.6
187017.1	10.3b	13.8a	14.9a	13	440025	2.0b	8.2a	2.8bc	4.3
189123.68	8.0a	4.3b	6.7ab	6.3	440027	7.0a	10.3a	8.0a	8.4
189135.9	15.3a	12.8a	13.2a	13.8	440031	7.3ab	4.2a	7.7b	6.4
189140	5.5a	5.3a	4.8a	5.2	440034	0.2b	5.5a	4.6a	3.4
189148.21	5.5ab	5.0a	8.6b	6.4	440050	4.1bc	5.6b	9.0a	6.2
189148.65	6.9b	3.0a	1.8a	3.9	440104	14.7c	1.5b	7.6a	7.9
189150.1	4.8a	4.3a	5.0a	4.7	440131	7.9c	2.3b	11.6a	7.3

Table 4.6: Cont.

	Shoot length (cm)					Shoot length (cm)			
Genotype/salt conc.	**0g/l**	**10g/l**	**15g/l**	**Mean**	**Genotype/salt conc.**	**0g/l**	**10g/l**	**15g/l**	**Mean**
189151.38	7.0a	11.0b	9.7ab	9.2	440132	5.6bc	5.8b	1.3a	4.2
192033.5	10.3a	14.7b	12.2ab	12.4	440166	9.0b	15.2a	13.2a	12.4
194515.5	12.6a	10.0a	11.0a	11.2	440167	5.7b	1.8a	6.3bc	4.6
194521.2	14.0b	8.4a	8.3a	10.2	440170	7.7b	12.3a	12.0a	10.7
194539.36	9.3bc	10.0b	16.7a	12.0	440240	6.8b	1.7a	5.4bc	4.6
194541.45	6.7a	4.5a	1.3ab	4.2	440286	5.8b	1.0a	1.2a	2.7
194549.6	1.8bc	2.8b	7.7a	4.1	440287	5.5a	5.2a	3.5a	4.7
194555.7	6.7a	4.8a	6.5a	6.0	440328	17.0b	9.2a	11.0a	12.4
194569.1	8.0b	1.5a	7.3bc	5.6	440378	10.3a	12.0a	13.8ab	12.1
194573.9	7.0a	7.7a	9.7a	8.1	440394	7.0bc	6.5b	2.0a	5.2
400011	5.7a	4.8a	5.6a	5.4	440396	8.0a	7.3a	4.7a	6.7

Table 4.6: Cont.

Genotype/salt conc.	Shoot length (cm) 0g/l	10g/l	15g/l	Mean	Genotype/salt conc.	Shoot length (cm) 0g/l	10g/l	15g/l	Mean
401055	8.0a	8.4a	10.2a	8.8	440429	15.3a	9.3b	12.3ab	12.3
420001	16.3b	8.2a	8.3a	10.9	440643	6.9bc	8.2b	1.5a	5.4
420014	6.7a	5.9a	5.8a	6.1	441097	12.7a	15.7a	13.7a	14.0
420027	6.7b	1.9a	2.8a	3.8	441538	14.7a	9.5b	11.8ab	12.0
420064	10.3bc	11.5b	18.2a	13.3	441724	9.0a	10.7a	8.0a	9.2
421066	11.0b	6.0a	6.3a	7.8	441725	9.1a	4.7b	7.3ab	7.0
421111	8.9bc	10.1b	4.8a	7.9	441755	1.3a	1.5a	1.5a	1.3
422656	16.3b	11.2a	9.7a	12.4	441768	16.2a	16.0a	12.7ab	15.0
440001	9.3a	5.3b	8.3ab	7.7	K566632**	4.5a	3.5a	1.9a	3.3
440017	9.0bc	10.3b	1.3a	6.9					

Means followed by the same letter within the rows (showing differences among different salt levels) are not significantly different (P≤0.001); * tolerant check, ** susceptible check

Treatment effects

Fisher's F-test indicated that all effects i.e. salt levels, genotypes and salt level x genotypes interaction, are highly significant ($p<0.01$) with respect to all the responses (Appendix 3). All major processes contributing to crop yield including, leaf expansion, shoot and root growth were inhibited as stress increased. These growth-supporting processes showed no further net growth (i.e. increase in biomass) at 15 g/l of PEG (Fig 4.1(a-b).

a) b)

Figure 4. 1 Effect of different salt levels on shoot fresh weigh, root fresh weight and shoot dry weight (a) and shoot and root length (b) for the screened 59 sweetpotato genotypes during invitro screening using different concentrations of polyethylene glycol

4.3 Discussion

Leaf area is among the most sensitive of the processes that are affected by water deficit. High concentration of PEG severely reduced leaf area in the susceptible genotypes like 440034, 440104, 420027, 189140 and 421111 unlike in tolerant genotypes 189135.9, 194515.5, 440131, 441097 and 441768 that showed high leaf area. Reduction in leaf area in a canopy results in drastic reduction in transpiration surface (Barta*et al*, 2002) and subsequently resulting to low biomass production. This reduction may be due to inhibition of cell division as a result of water stress (Hsiao, 1973)

Early detection of such genotypes with high leaf area indicating tolerance under moisture stress condition can save resources in the breeding process.

High PEG concentration significantly reduced total dry matter production in susceptible genotypes 194541.45, 420014, 420027, 440167 and 440394; their means were not significantly different from that of the susceptible variety K566632. Genotypes 189135.9, 194515.5, 194539.36, 440027, 440429, 441538 and 401055 were observed to be relatively tolerant with high dry matter production at high PEG concentration of 15g/l. similar observation has been made in crops like Alfalfa (Barta *et al*., 2002). Stress affects rate of photosynthesis thus reducing the supply of assimilate to various parts of the plant (Handa *et al.,* 1982).

Stem acts as main reservoir of stored starch during stress situation of plants survival as well as optimum yield levels. Stem parameters such as length plays an important role in dry matter partitioning of plants for sustaining water stress situation (Kulkarni and Deshpande 2006). This might explain why genotypes like 187017.1 and 194539.36 exhibited high stem length elongation at high salt concentration.

Two major dimensions describe the root: root depth and root-length density. Early and rapid elongation of roots is important indication of drought tolerance; this facilitates extraction of soil moisture from deep in the soil profile under limited water conditions. The rapid elongation of roots also indicates the strength and ability of genotype moisture absorption. These parameters are genetically governed and can be introgressed (Kulkarni and Deshpande, 2006). Ability of continued elongation of the root under situation of water stress was remarkable character of some of the genotypes screened. Genotypes 189135.9, 194515.5, 441097, 187017.1, 440034,441768 and 441538 observed with high root length and weight have the ability to survive under high moisture stress conditions.

The present study revealed different response of genotypes to various levels of PEG concentrations. Higher concentration of PEG at 15 g/l reduced significantly growth parameters in susceptible genotypes like 420027, 440034, 440104, 440643, 189148.65, 194541.45, 420014 and 440131. Such negative effects have been observed for susceptible genotypes in wheat (Javed, 2002**),** Soya bean *(*Sakthivelu *et al*., 2008). At the same level of stress genotypes 189135.9, 194515.5, 194539.3

401055, 440429, 441097, 441538 and 441768 were observed with outstanding ability to continue root and shoot growth indicating their ability to tolerate stress

4.4 Conclusion

The results showed significant variations among the genotypes for salt tolerance based on plant growth characters. Higher concentration of the salt at 15 g/l severely affected the production of biomass for most of the genotypes. Genotypes 189135.9, 192033.5, 194515.5, 194539.3, 401055, 441724, 440429, 441097, 441538,441768 were observed with outstanding ability to continue root and shoot growth under *in vitro* stress conditions at all salt levels indicating their ability to withstand severe water stress situation. The highly susceptible genotypes observed were 189151.38, 420027, 440034, 440166, 440132, 441755, 421111 and 440104. Greater leaf area expansion under high moisture stress condition was observed for genotypes 189135.9, 194515.5, 441097 and 441768. Poor leaf expansion area was recorded for genotypes 194549.6, 420027 and 440034. From this screening trial 10 genotypes were identified as drought tolerant, this included genotypes: 194515.5, 194539.36, 441724, and 441538 (dark orange); 189135.9, 401055 (orange); 441768 (light orange); 192033.5 (yellow) 440027 and 440429 (light cream). They all showed higher leaf expansion, higher stem length elongation, high root and shoot growth and high dry matter production at high salt concentration level.

CHAPTER FIVE

Rapid field screening and selection of orange-fleshed sweetpotato genotypes with drought tolerance potential and high β-carotene content

Abstract

Fifty nine sweetpotato genotypes were rapidly screened in the field to identify promising drought tolerance OFSP genotypes for yield evaluation. Initiation and multiplication of planting material for the 59 genotypes was from nodal cuttings which were initially grown in Murashige and Skoog (MS) growth media in the lab. These were later transferred to sterilized vermiculate soil in polythene bags in the greenhouse for acclimatization before being transferred to the field. The field experiment was conducted from the month of September 2007 to beginning of January 2008.The trial was laid out as randomized complete block design with three replications. The plot size was 2.4m². (2.4 m x 1 m) with 8 plants /plot. Planting distance was 0.30 m. Two checks were used, a drought susceptible genotype K566632 and drought tolerant genotype Marooko. Vine tip cuttings 30 cm long were used as planting material and were planted on ridges. The crop was irrigated every 3 to 4 day intervals using an overhead sprinkler system until four weeks after planting when approximate full ground cover was established and thereafter irrigation was stopped and plants left to grow under natural conditions for a period of 5 months after which harvesting was done. For selection criteria three traits were used: Root-flesh color, root dry matter content and average yield in t/ha. Final selection was based on the ranking of the genotypes based on the summation index of their

attributes. General linear model procedure (GLM) was used for the simple statistical analysis and correlation coefficient calculation done using the SAS package (SAS, version 8 of SAS Institute, Inc, 1999). Out of the 59 genotypes screened 21 were found to be dark orange- fleshed, 12 to be orange-fleshed, 12 light orange-fleshed and 14 were found to be either cream or white fleshed. The dry matter ranged from 15 to 35 % with majority of the dark orange to orange genotypes having less than 30% DM. The foliage yield for most of the genotypes ranged from 4 to15 t/ha. Most of the dark orange to orange genotypes recorded high number of storage roots compared to the cream to white-fleshed genotypes. Total fresh storage root yield ranged from 7.43 to 45.83t/ha. Overall, genotype 440378 had the lowest yield with a storage root yield of 7.43 t/ha, while genotypes 420027, 187017.1, 420024, 187016.2 and 420014 produced over 43 t/ha. A total of 18 genotypes with least summation index for these attributes were considered to be superior and were advanced for further screening. Based on these ranking genotypes 187017.1, 422656, 420014, 440287 and 189135.9 were noted to be of outstanding performance than the rest. The same genotypes had dark orange to orange-fleshed color, an indication of high beta-carotene, dry matter content of 25% and high fresh storage root yield ranging between 28 and 43 t/ha.

5.0 INTRODUCTION

One of the major constrained for sweetpotato production in Sub-Saharan Africa is its drought susceptibility. Drought tolerance is more than just an advantageous agronomic characteristic that can increase production; it is a key necessary for the

widespread diffusion of OFSP via the sustainable propagation of vine planting material.

Rapid field screening for 59 sweetpotato genotypes was done to identify 10-20 promising drought tolerant OFSP genotypes that had valuable traits and could be advance for further evaluation, testing and selection.

5.1 Materials and Methods

5.1.1 Plant material and propagation

As explained in section 3.2

5.1.2 Experimental site

As indicated in section 3.

5.1.3 Experimental layout, treatments and crop husbandry

The trial was laid out as a randomized complete block design (RCBD). The plot size was 2.4 m² rows (2.4 m x 1 m) with 8 plants /plot. Planting distance was 0.30 m (8 m x 0.30 = 2.4 m²).This gave a plot area of 2.4 m². Two checks were used, a drought susceptible genotype K566632 and a drought tolerant genotype Marooko. Vine tip cuttings of 30cm length were used as planting material and were planted on ridges. Gap filling was done two weeks after planting. Weeding was done until sufficient ground foliage cover to smoother the weeds was achieved. Earthing–up was also

done during weeding to seal any soil cracks through which roots could be exposed. The crop was irrigated 3 to 4 day intervals using a 12 m x 12 m grid overhead sprinkler system with a 3 main sprinkler lines until four weeks after planting. At approximate full ground cover irrigation was stopped and plants left to grow under natural conditions for a period of 5 months before harvesting.

5.1.4 Data recorded

Number of plants established per plot. This was determined 3 weeks after planting.

Vine vigor: was recorded in scores from 1-9 Where:

1 = nearly no vines,

2= weak vines, thin stems, very long internode distances,

3 = weak to medium strong vines, medium thick stems, and long internode distances,

4 = medium strong vines, medium thick stems, and medium internode distances,

5 = medium strong vines, thick vines, and long internode distances,

6 = medium strong vines, thick stems, and medium internode distances,

7 = strong vines, thick stems, short internode distances, and medium long vines,

8 = strong vines, thick stems, short internode distances, and medium to long vines,

9 = very strong vine strength, thick stems, short internode distances, and very long vines.

Weight of fresh vines in kg per plot: Vines from the net plots were harvested and weighed in kg

Root observation: The following parameters were taken: number of plants harvested per plot; number of plants with storage roots; number of commercial and non-commercial roots per plot. The last two parameters were further weighed in kg and later converted to yields in tons per hectare.

Weevil damage of the roots: This was recorded on plot basis as percentages based on a scale from 1 to 5 (Wolfgang et al 2009), where:

1 =Very severe (>60% roots affected).

2.= Severe (30-60% of roots< 20%),

3 = Moderate (10-30% damaged),

4 = Light (few roots affected),

5 = None

Root dry matter content. A six- storage roots sample per plot was used in the determination of root dry matter content. This was done within 24 hours of harvesting. The middle portion of the fresh roots was cut into thin slices and samples weighing 250g placed in open trays and dried in an oven at 70°C for 72 hours or until a constant dry weight was achieved. This weight was then recorded and from it % dry matter content determined.

Root flesh color. The root flesh color was visually determined and genotypes grouped into three main categories: very deep orange-fleshed, orange-fleshed; pale orange-fleshed; yellow; cream to white-fleshed.

5.1.5 Selection criteria of genotypes for further screening

A first selection criterion was based on root-flesh color, dry matter content, and average yield (Table 5.1).These genotypes were further ranked based on various attributes. Each genotype was ranked for each attribute and the sum of the ranks across the attributes used as the summation index. Those genotypes with the least summation index were considered to be superior genotypes. For final selection those genotypes with the least summation indices and were orange-fleshed, high yielding and had high dry matter content above 25% were selected as potential genotypes for further evaluation.

Table 5. 1 Selection criteria for the promising genotypes for advanced screening and evaluation

Variable/trait	Acceptable level	Comments
Root-flesh color	Orange-deep orange	Deep orange being an indicative of high beta carotene content Ejumula and Resist to act as a basis for selection
Dry matter content	> 25% acceptable by most consumers	Resisto and Ejumula range between 25- 27%
Average Yield	> 15 t/ha	
Total sum of ranking for various attributes ŧ	Top 20 to be selected	

ŧ Ranked summation index

5.2. Statistical analysis

General linear model procedure (GLM) was used for the simple statistical analysis and correlation coefficient calculation done using the SAS package (SAS, version 8 of SAS Institute, Inc, 1999. For selection criteria three traits or variable were used: Root-flesh color, root dry matter content and average yield in t/ha.

5.3 Results

5.3.1 General observation on climate and soil conditions

No rainfall was recorded during the month of September 2008. Less than 10 mm was recorded for the period the trial was conducted. The rainfall received between

September and December 2008 was only 3.3 mm. The soil pH for the testing site was 7.31 this classified the soils as alkaline. Most of nutrients in the soil were in adequate amount except total nitrogen and organic carbon that were low while p levels were high (Appendix 3).

5.3.2 Agronomic performance

The analysis of variance showed very high level of significance for all traits recorded except for non-marketable roots. Out of the 59 genotypes screened 21 had dark orange flesh, 12 orange, 12 light orange and 14 were found to be either cream or white. Summary of mean values for various traits taken are presented in Table 5.2. The dry matter for storage roots ranged from 15 to 35 % with majority of the dark orange to orange genotypes falling below 30 %. The fresh foliage yield for most of the genotypes ranged from 4-15 t/ha although generally recording high root yield. Most of the dark orange to orange genotypes recorded high number of roots compared to the cream to white-fleshed genotypes.

Total root yield ranged from 7.43 to 45.83 t/ha. Overall, genotype 440378 was the lowest yielding with a yield of 7.43 t/ha. Genotypes 420027, 187017.1, 420024, 187016.2 and 420014 produced over 43 t/ha. The percentage of the roots infected with sweetpotato weevil (*cylas spp*.) was greater in genotypes 440104 (35.3%), 440643 (53%) and 421006 (33%) compared with local check Marooko (14 %). Genotypes 422656, 440394, 420027, 189135.9, 440031 and 187016.2 produced higher number of total roots that ranged between 30 t/ha and 36.7 t/ha and this was

significantly different from that of the check Marooko (12 t/ha). Low foliage yield that was significantly different from that of the check Marooko (26.4 t/ha)) were recorded for genotypes 440001 (3.5t/ha), 194541.45 (3.4 t/ha), 440104 (2.8 t/ha) and 440643 (3.3 t/ha). High dry matter content greater than 30 % were noted for genotypes 440240, 440023, 192033.5, 400011 and 441755; these genotypes had cream to yellow fleshed storage roots. Based on the selection criteria that was developed a total of 18 genotypes were selected for further screening and selection (Tables 5.3 and 5.4 and Plate 5.0 (a-r).

Table 5. 2 Mean values of observed attributes of 59 sweetpotato genotypes evaluated at Kiboko- Move to appendix

Genotype		Predominant color	Foliage vigor	Number of plants harvested	Number of plants with storage roots	Foliage fresh yield t/ha	Number of commercial roots	Total number of roots	Average number of roots/plant	Yield of commercial roots t/ha	Total root yield t/ha	% weevil damage	Dry matter content (%)
1	441768	Light orange	2.7	7.7	7.7	18.07	10.00	18.67	2.47	18.77	26.73	13.00	30
2	441755	yellow	2.3	6.0	5.3	11.10	8.33	11.33	2.23	17.37	20.43	27.67	30
3	441725	Dark orange	2.3	5.7	5.3	12.07	11.67	16.00	3.07	15.30	17.83	19.00	25
4	441724	Dark orange	3.0	7.0	6.7	10.40	12.67	18.67	2.90	14.60	18.10	11.00	25
5	441538	Dark orange	2.7	6.0	6.0	15.73	12.67	20.33	3.33	18.07	22.50	11.33	25
6	441097	Orange	2.7	5.3	5.3	19.43	8.00	10.33	1.97	24.30	25.97	27.33	20
7	440643	Light orange	2.0	3.3	3.0	4.17	2.67	6.00	2.13	9.03	11.13	53.00	25
8	440429	Light cream	2.3	7.3	7.3	8.30	17.33	28.00	3.87	31.27	38.90	8.00	20
9	440396	Light orange	2.33	6.0	6.0	7.63	7.00	14.33	2.40	16.70	22.97	14.33	20
10	440394	Light orange	2.0	6.0	6.0	8.33	13.67	33.33	4.17	25.00	34.73	6.67	20
11	440378	Light orange	2.7	6.0	3.3	14.57	3.67	11.00	3.43	3.93	7.43	25.33	25
12	440328	Light orange	2.0	6.3	6.0	8.33	11.00	17.00	2.67	22.93	28.53	12.00	25
13	440287	Dark orange	2.7	7.7	7.7	13.20	11.00	20.67	2.70	22.93	28.93	13.33	25
14	440286	Dark orange	2.3	7.0	7.0	13.17	10.00	22.67	3.30	18.77	25.70	10.00	25
15	440240	Orange	2.3	7.3	7.3	8.30	8.33	17.33	2.33	16.30	18.93	14.00	30
16	440170	Light cream	2.3	7.7	7.7	9.73	11.33	19.00	2.53	28.47	33.77	17.00	25
17	440167	Light cream	3.0	8.0	5.3	28.07	6.33	12.33	3.67	10.40	16.00	26.67	35
18	440166	Yellow	2.7	8.0	8.0	14.43	17.33	27.67	3.47	32.67	40.30	9.00	35
19	440132	Dark orange	2.3	6.7	6.7	6.97	17.00	25.33	3.80	22.93	24.90	15.67	20

Table 5.2 Cont.

Genotype		Predominant color	Foliage vigor	Number of plants harvested	Number of plants with storage roots	Foliage fresh yield t/ha	Number of commercial roots	Total number of roots	Average number of roots/plant	Yield of commercial roots t/ha	Total root yield t/ha	% weevil damage	Dry matter content (%)
20	440131	Light cream	3.7	7.3	6.7	28.50	8.67	13.67	2.20	18.77	20.17	16.00	30
21	440104	Dark orange	2.0	3.7	2.3	2.77	3.33	8.00	3.50	4.60	6.00	35.33	25
22	440050	Dark orange	2.0	7.7	7.7	8.60	16.00	28.67	3.60	36.80	44.43	9.67	20
23	440034	Light orange	2.7	7.7	7.7	15.97	14.33	21.33	2.73	28.50	31.43	13.33	30
24	440031	Dark orange	2.3	8.0	8.0	12.50	14.33	30.00	3.73	27.77	36.07	9.33	20
25	440027	Light cream	2.3	8.0	8.0	7.63	13.00	21.33	2.70	22.27	26.90	9.67	25
26	440025	Light cream	2.0	7.0	7.0	7.63	11.33	24.33	3.57	22.00	32.00	9.67	30
27	440024	Light cream	2.3	7.3	7.3	9.03	16.33	28.00	3.80	38.20	45.67	11.00	20
28	440023	Light cream	2.0	4.3	4.3	5.83	6.33	8.00	1.83	21.53	22.63	30.67	30
29	440017	Dark orange	2.3	7.7	7.7	6.23	13.33	27.00	3.50	25.00	32.60	9.00	15
30	440001	Dark orange	2.0	8.0	7.0	3.50	9.33	21.00	3.27	11.10	17.33	14.67	25
31	422656	orange	3.3	8.0	8.0	9.87	22.33	36.67	4.60	24.33	30.63	5.33	25
32	421111	Light orange	2.7	6.0	5.0	10.40	3.67	7.33	1.50	6.27	7.97	36.67	30
33	421066	orange	2.7	6.3	5.3	12.50	10.67	15.00	2.63	18..07	21.13	33.00	20
34	420064	Light orange	2.7	7.3	7.0	13.20	10.33	18.33	2.53	21.13	25.20	18.33	25
35	420027	Dark orange	3.0	8.0	8.0	13.20	17.33	30.67	3.83	34.03	43.07	7.33	20
36	420014	orange	3.0	8.0	8.0	21.57	15.00	28.67	3.83	33.33	40.70	12.33	25
37	420001	Light orange	2.7	7.7	7.7	12.67	9.00	20.33	2.67	16.67	25.67	9.67	25
38	401055	Orange	2.3	4.3	4.3	6.97	7.00	15.00	3.37	18.07	22.23	12.67	25
39	400011	Light cream	2.7	7.3	7.3	18.33	11.33	22.00	3.00	20.13	27.47	11.67	30
40	194573.9	Dark orange	2.7	5.7	5.7	9.03	8.33	12.67	2.13	21.57	24.67	18.33	25

Table 5.2 Cont.

Genotype		Predominant color	Foliage vigor	Number of plants harvested	Number of plants with storage roots	Foliage fresh yield t/ha	Number of commercial roots	Total number of roots	Average number of roots/plant	Yield of commercial roots t/ha	Total root yield t/ha	% weevil damage	Dry matter content (%)
41	194569.1	Dark orange	2.3	5.3	5.3	5.27	11.67	21.67	4.17	22.90	28.47	13.00	25
42	194555.7	Light orange	2.0	3.7	3.7	11.10	8.00	14.33	3.83	19.43	23.47	20.67	30
43	194549.6	Dark orange	3.0	7.0	6.7	12.50	11.33	17.33	2.67	17.37	20.17	16.00	25
44	194541.45	orange	2.0	5.0	5.0	3.37	6.67	12.00	2.30	8.33	10.03	33.67	25
45	194539.36	Dark orange	2.0	4.3	4.3	3.23	11.00	23.33	5.77	16.70	21.30	16.33	20
46	194521.2	orange	2.0	4.7	4.7	10.40	10.67	26.67	4.00	17.37	22.90	7.67	25
47	194515.15	Dark orange	2.3	3.7	3.7	9.00	9.00	19.00	5.20	18.77	25.30	10.67	25
48	192033.5	Yellow	3.0	6.0	6.0	13.90	5.00	15.67	2.50	10.43	18.77	21.33	30
49	189151.38	Dark orange	1.3	4.3	4.3	6.93	8.33	17.67	2.77	9.73	14.60	5.33	20
50	189150.1	orange	2.0	3.0	2.7	13.90	9.00	20.00	7.27	18.07	28.20	19.67	20
51	189148.65	Light cream	1.3	5.7	5.0	8.47	8.67	19.67	4.07	8.20	11.67	10.33	35
52	189148.21	Orange	2.3	4.0	5.0	8.47	6.67	19.67	2.23	8.20	15.97	7.33	25
53	189140.32	Dark orange	2.3	5.0	5.0	7.53	7.00	21.33	3.90	10.40	18.73	13.33	30
54	189135.9	Orange	2.3	6.3	6.3	4.90	18.67	35.33	5.47	27.10	34.03	9.33	25
55	189123.68	Dark orange	2.3	4.3	4.0	5.07	12.33	20.00	5.03	11.10	16.70	16.67	25
56	187017.1	Orange	3.0	8.0	8.0	26.40	16.00	28.67	3.60	36.20	43.77	7.33	25
57	187016.2	Light orange	3.0	7.0	7.0	25.97	9.33	31.33	4.47	34.03	45.83	10.33	15
58	K566632	Dark orange	2.0	7.7	7.7	13.87	8.67	24.67	3.23	19.43	23.73	9.00	25
59	Marooko	Light cream	3.3	7.3	7.3	26.43	7.33	12.00	1.67	16.00	19.37	14.33	35
MEAN			**2.44**	**6.35**	**6.14**	**11.51**	**10.62**	**20.04**	**3.31**	**19.89**	**25.25**	**15.75**	
LSD(0.05)			**0.94**	**2.12**	**2.44**	**10.06**	**7.43**	**13.44**	**2.38**	**11.93**	**13.19**	**16.77**	

Table 5. 3 Ranking of observed attributes based on summation index for sweetpotato genotypes screened at Kiboko

Genotype		Foliage vigor	Number of plants harvested	Number of plants with storage roots	Foliage fresh yield t/ha	Number of commercial roots	Total number of roots	Average number of roots/plant	Yield of commercial roots t/ha	Total root yield t/ha	% weevil damage	Summation index	Rank
1	194549.6	4	25	26	22	21	39	40	37	41	39	294	28
2	189123.68	12	49	53	53	18	29	5	47	50	42	358	44
3	441725	12	41	37	25	19	42	33	45	48	46	348	41
4	440104	44	55	59	59	58	56	24	58	59	57	529	58
5	440287	12	10	8	17	11	26	38	17	17	31	187	15
6	441724	4	25	26	28	16	35	35	46	47	22	284	27
7	440017	12	10	8	50	14	13	24	13	13	8	165	11
8	194569.1	12	44	37	52	19	21	8	20	19	29	261	25
9	440050	44	10	8	36	8	7	21	2	3	14	153	10
10	194573.9	12	41	36	33	41	48	54	23	30	44	362	45
11	441538	58	34	31	11	16	27	29	33	36	24	299	30
12	194515.15		12	55	54	35	35	33	4	29	27	21	35
13	440286	12	25	21	20	31	19	30	29	25	18	230	19
14	420027	12	1	1	17	3	5	14	4	5	4	66	2
15	189140.32	12	46	43	38	48	22	12	50	46	31	348	41
16	189151.38	58	49	49	49	41	38	36	52	53	1	426	54
17	440031	12	1	1	22	11	6	19	11	9	12	104	6
18	440001	44	1	21	56	33	25	31	47	49	37	344	39
19	194539.36	44	49	49	58	25	17	2	40	38	41	363	46

Table 5.3 Cont.

	Genotype	Foliage vigor	Number of plants harvested	Number of plants with storage roots	Foliage fresh yield t/ha	Number of commercial roots	Total number of roots	Average number of roots/plant	Yield of commercial roots t/ha	Total root yield t/ha	% weevil damage	Summation index	Rank
20	440132	12	30	26	47	6	15	17	17	29	37	236	23
21	K566632	44	10	8	16	38	16	32	27	31	8	230	19
22	422656	2	1	1	31	1	1	6	15	16	1	75	3
23	440240	12	18	16	41	41	39	49	43	44	34	337	36
24	421066	12	31	37	22	28	44	43	33	39	55	344	39
25	189148.21	12	41	43	38	38	31	10	55	52	19	339	37
26	194541.45	44	46	43	22	51	51	50	54	56	56	473	57
27	401055	12	49	49	47	48	44	28	33	37	28	375	49
28	189135.9	12	31	26	54	2	2	3	12	11	12	165	11
29	187017.1	4	1	1	4	8	7	21	3	4	4	57	1
30	441097	12	44	37	7	45	55	56	16	24	52	348	41
31	189150.1	44	59	58	14	35	29	1	33	20	47	340	38
32	194521.2	44	48	48	28	28	14	11	37	34	7	299	30
33	420014	4	1	1	6	10	7	14	6	6	27	82	4
34	440643	44	58	57	55	59	59	54	53	55	59	553	59
35	420001	12	10	8	21	35	27	40	40	26	14	233	21
36	421111	12	34	43	28	56	58	59	57	57	58	462	55
37	440396	12	34	31	43	48	46	48	40	33	35	370	47
38	440394	44	34	31	39	13	2	8	13	10	3	197	16
39	420064	12	18	21	17	30	37	44	25	28	44	276	26

Table 5.3 Cont.

	Genotype	Foliage vigor	Number of plants harvested	Number of plants with storage roots	Foliage fresh yield t/ha	Number of commercial roots	Total number of roots	Average number of roots/plant	Yield of commercial roots t/ha	Total root yield t/ha	% weevil damage	Summation index	Rank
40	440378	12	34	56	12	56	54	27	59	58	49	417	53
41	441768	12	10	8	9	31	35	47	29	23	29	233	21
42	440328	44	31	21	40	25	41	40	17	18	26	313	33
43	187016.2	4	25	21	5	33	2	7	5	1	19	122	7
44	440034-	12	10	8	10	11	22	37	9	15	31	165	11
45	194555.7	44	55	54	26	45	46	14	27	32	48	391	52
46	192033.5	4	34	31	14	55	43	46	49	45	49	370	47
47	441755	12	34	27	26	41	53	51	37	40	53	384	51
48	440166	12	1	1	13	3	12	26	7	7	8	90	5
49	440027	4	1	1	43	15	22	38	21	22	14	181	14
50	440023	44	49	49	51	53	56	57	24	35	54	472	56
51	400011	12	18	16	8	21	20	34	26	21	37	213	17
52	440429	12	18	16	41	3	10	13	8	8	8	137	8
53	Marooko	3	18	16	3	47	51	58	44	43	35	318	34
54	440025	44	25	21	43	21	17	21	22	14	14	242	24
55	440131	1	18	26	1	38	48	53	29	41	39	294	28
56	440024	12	18	16	33	7	10	17	1	2	22	138	9
57	189148.65	12	41	43	37	38	31	51	55	54	19	381	50
58	440167	4	1	37	7	45	55	56	16	24	52	348	44
59	440170	12	10	8	32	21	33	44	10	12	43	225	18

Table 5. 4 Selected 18 genotypes and 2 checks (*) at KARI Kiboko advanced for further evaluation in phase 2

Genotype		Predominant color	Foliage vigor	Number of plants harvested	Number of plants with storage roots	Foliage fresh yield t/ha	Number of commercial roots	Total number of roots	Average number of roots/plant	Yield of commercial roots t/ha	Total root yield t/ha	% Weevil damage	DM%
1	194549.6	Dark orange	3.0	7.0	6.7	12.50	11.33	17.33	2.67	17.37	20.17	16.00	25
2	422656	orange	3.3	8.0	8.0	9.87	22.33	36.67	4.60	24.33	30.63	5.33	25
3	440287	Dark orange	2.7	7.7	7.7	13.20	11.00	20.67	2.70	22.93	28.93	13.33	25
4	440240	Orange	2.3	7.3	7.3	8.30	8.33	17.33	2.33	16.30	18.93	14.00	30
5	441097	Dark orange	3.0	7.0	6.7	10.40	12.67	18.67	2.90	14.60	18.10	11.00	25
6	192033.5	Dark orange	2.3	5.3	5.3	5.27	11.67	21.67	4.17	22.90	28.47	13.00	25
7	194573.9	Dark orange	2.7	5.7	5.7	9.03	8.33	12.67	2.13	21.57	24.67	18.33	25
8	441538	Dark orange	2.7	6.0	6.0	15.73	12.67	20.33	3.33	18.07	22.50	11.33	25
9	194515.15	Dark orange	2.3	3.7	3.7	9.00	9.00	19.00	5.20	18.77	25.30	10.67	25
10	440286	Dark orange	2.3	7.0	7.0	13.17	10.00	22.67	3.30	18.77	25.70	10.00	25
11	189135.9	Orange	2.3	6.3	6.3	4.90	18.67	35.33	5.47	27.10	34.03	9.33	25
12	187017.1	Orange	3.0	8.0	8.0	26.40	16.00	28.67	3.60	36.20	43.77	7.33	25
13	421006	Orange	2.0	4.7	4.7	10.40	10.67	26.67	4.00	17.37	22.90	7.67	25
14	K566632*	Dark orange	2.0	7.7	7.7	13.87	8.67	24.67	3.23	19.43	23.73	9.00	25
15	420014	Orange	3.0	8.0	8.0	21.57	15.00	28.67	3.83	33.33	40.70	12.33	25
16	189148.18	Orange	2.3	4.0	5.0	8.47	6.67	19.67	2.23	8.20	15.97	7.33	25
17	401055	Orange	2.3	4.3	4.3	6.97	7.00	15.00	3.37	18.07	22.23	12.67	25
18	441725	Dark orange	2.3	5.7	5.3	12.07	11.67	16.00	3.07	15.30	17.83	19.00	25
19	440001	Dark orange	2.0	8.0	7.0	3.50	9.33	21.00	3.27	11.10	17.33	14.67	25
20	Marooko*	Light cream	3.3	7.3	7.3	26.43	7.33	12.00	1.67	16.00	19.37	14.33	35

a) Genotype 440287 b) Genotype 422656 c) Genotype 441725

Color- Dark orange Color- orange Color Dark orange

Dry matter content**25%** Dry matter content**25%** Dry matter content**25%**

d) Genotype 420014 e) Genotype192033.5 f) Genotype 440240

Color- orange Color- yellow Color - orange

Dry matter content**25%** Dry matter content**30%** Dry matter content**30%**

g) Genotype 421006 h) Genotype 440001 i) Genotype 187017.1

Color- Orange Color- Dark orange Color- orange

Dry matter content **20%** Dry matter content- **25%** Dry matter content- **25 %**

Plate 5. 1 (a – i) Genotypes selected from rapid field screening for further evaluation and selection

j) Genotype 189135.9

Color- Orange

Dry matter content-**25%**

k) Genotype 401055

Color- Orange

Dry matter content- **25 %**

l) Genotype 440286

Color- Dark orange

Dry matter content-**25%**

m) Genotype194515.15

Color-Dark orange

Dry matter content-**25%**

n) Genotype 441538

Color- Dark orange

Dry matter content-**25%**

o) Genotype 194573.9

Color- Dark orange

Dry matter content-**25%**

p) Genotype 189148.21

Color- Orange

Dry matter content- **25%**

q) Genotype 194549.6

Color- Dark orange

Dry matter content-**25%**

r) Marooko

Color- Light cream

Dry matter content- **35%**

Plate 5. 2 (j – r) Genotypes selected from rapid field screening for further evaluation and selection

5.4 Discussion

The selection criterion was able to classify the genotypes into three major groups based on the flesh-color: Dark orange (21), Orange (12), Light orange (12), yellow (3) and light cream (11). The deeper the orange color of the flesh the more vitamin A.

The storage root is the commercial part of the sweetpotato plant and root yield is said to be a variable quantitative character (Jones, 1977). Wide range of variability was observed for root yield with most of the genotypes screened (72%) having root yield exceeding 20t/ha. Commercial root yield performances of the evaluated genotypes were generally better than the local checks. Genotypes that were deep orange-fleshed that yielded high were recorded for 420027 (34.03 t/ha), 440050 (36.80 t/ha) and 440031 (27.77 t/ha).Storage root weight per plant is a measure of total root sink capacity. The screening trial indicated that, the variation in root yield in different genotypes may be either due to the difference in the number of storage roots per plant or size of individual roots or difference in bulking rate as reported by Lowe and Wilson (1975). In this screening trial, it was observed that β-carotene content was associated with storage root flesh color as reported by Zhang and Xie (1998) and Lin *et al* (1989).

For most of the genotypes the dry matter content varied from 15 – 25 %. It was found that the intensity of the orange-flesh color was negatively related with dry matter content which is in confirmation with the observation of Hernandez *et al* (1967); Simonne *et al* (1993). The average dry matter content in sweetpotato is

approximately 30% and also found to vary widely with the genotypes (Bradbury and Holloway, 1988). 47% of the genotypes screened had a dry matter content of 25%; 24% had dry matter content below 20% and 9% of the genotypes screened had dry matter content greater than 30%that was above that of Resisto and Ejumula.

5.5 Conclusion

Some of the genotypes screened were noted to be very susceptible to moisture stress and registered very low foliage and root yield. Such genotypes included 440001, 194541.45, 440104 and 440643 and 440378.Genotypes that performed well and were noted to withstand severe moisture stress included 194549.6,189123.68,441725, 422656 and 440287 the same genotypes were also observed to have very low weevil infestation that was less than 15%. High dry matter content greater than 30% was noted in genotypes 440240, 440023, 192033.5, 400011 and 441755. Genotypes that were noted to be having cream to yellow fleshed storage roots had high dry matter content greater than 30%, this was in contrast with the deep orange-fleshed that were generally of low dry matter content of below 25%. Deep orange-fleshed genotypes that recorded high commercial root yield included 420027, 440050 and 440031.

CHAPTER SIX

Multi-location field evaluation and selection of the prescreened orange-fleshed (OFSP) sweetpotato genotypes for drought tolerance

Abstract

In this study 18 OFSP genotypes selected from rapid field screening and 2 Kenyan checks genotypes Marooko (drought tolerant) and K566632 (drought susceptible) were screened for drought tolerance at Kiboko and at Marigat during the years 2008-2009. Randomized complete block design laid out as split plot was used with two water levels i.e. rainfed and irrigated; water level was the main factor and the genotypes the sub-factor. Data was recorded on agronomic performance during the growth period. Five drought tolerance indices comprising: stress tolerance index (STI), stress tolerance (TOL), stress susceptibility index (SSI), mean productivity (MP), and geometric mean productivity (GMP) were used. The indices were adjusted based on root yield under drought (Ys) and normal (Yp) conditions. Stress tolerance index was used to identify genotypes with high stress tolerance and high yield potential. Irrigation significantly increased biomass, total root and fresh foliage yield, total number of roots as well as harvest index. The genotypes that had high foliage production under non- irrigated treatment in both sites were 189148.2, 441097,194515.2 and 194573.9. The biomass ranged from 9.73 to 10.70t/ha at Kiboko and 31.37 to 31.67t/ha at Marigat. Mean total number of roots were significantly lower in Kiboko (6.2) than Marigat (20.5) under non-irrigated treatment. High numbers of root production under the same treatment in both sites were observed for genotypes 189135.9, 194573.9, 440287 and 441725. The significant and positive correlations of Yp and (MP, GMP and STI) and Ys and (MP,

GMP and STI) under both non-irrigated and irrigated treatment as well as significant negative correlation of SSI and TOL under stressed treatment revealed that selection could be conducted for high MP, GMP and STI under both environments and low SSI and TOL under non-irrigated treatment. The calculated correlation coefficients revealed that STI, MP, and GMP are the superior criteria for selection of high yielding genotypes both under stress and irrigated treatment. Genotypes 421066, 194573.9, 192033.3, 187017.1 and 189135.9 with the highest values of STI in both sites were considered to be tolerant genotypes, whereas genotypes 422656, 440240, 440001, Marooko and 401055 with the lowest STI were considered to be sensitive to moisture deficit conditions. High dry matter content were noted for genotypes 192033.5, 440240 and 194549.6, whereas higher levels of beta-carotene were noted for genotypes K566632, 189148.2, 441725 and 440240

6.0 INTRODUCTION

Drought stress is the most important factor limiting access to high yield by restricting growth in most stages of crop growth in arid and semi-arid areas. Breeding for drought tolerance by selecting solely for root storage, tuber or grain yield is difficult due to low heritability of drought tolerance and lack of efficient selection strategies (Blum, 1998; Ludlow and Muchow, 1990).. In order to identify drought tolerant genotypes under non-stressed and stressed environment, some selection indices that includes geometric mean productivity (GMP), mean productivity (MP), Tolerance (TOL), stress tolerance index (STI) and stress susceptible index (SSI) have been used in different conditions. (Sio-Semardeh et al., (2006). Golabadi et al.,(2006) evaluated F3 and F4 generations of durum wheat.

These were obtained from the intercross of two durum wheat genotypes at different moisture regimes. They calculated drought tolerance indices based on yield in both stressed and non-stressed conditions and concluded that there is meaningful correlation between yield in non-stressed environment and indices MP, GMP and STI and also between yield in stressed environment and indices MP, GMP and STI, so these indices can be appropriate predictors of Yp and Ys as compared with SSI and TOL indices. Components analysis of indices MP, GMP, SSI and STI and biplot drawing in this experiment showed that genotypes with one addition component and two smaller components are suitable for moisture stressed and non-stressed conditions. Fernandez (1992) in his review used bi-plot method to identify effective indices on evaluation and selection of Vetch genotypes that are tolerant to moisture stress and concluded that there is positive and meaningful correlation between and MP and STI indices and also between Ys and STI and MP indices. Therefore, the same indices can be used as appropriate indices to identify stress tolerant genotypes.

Kaya et al., (2002) in their study concluded that genotypes with large PC1 and small PC2 have higher yield in both stressed and non-stressed conditions (stable) and genotypes with large principal component 1 (PC1) and small principal component 2 (PC2) have lower yield (unstable). Mollasadeghi (2010) in their study on wheat genotypes concluded that indices MP, GMP and STI are very appropriate to identify high yielding genotypes in both stressed and non-stressed conditions. Thus, drought indices providing a measure of drought based on yield loss under drought-conditions compared to normal conditions are being used in screening drought-tolerant genotypes (Mitra, 2001). A field evaluation study was conducted in two sites over a

season to evaluate and select for drought tolerant orange-fleshed sweetpotato genotypes that were high in dry matter content and β-carotene levels.

6.1 Materials and Methods

6.1.1 Plant material and propagation

Test material consisted of 18 genotypes that were earlier selected from the rapid screening trial conducted at KARI Kiboko. Healthy Planting materials for the trial establishment were sourced from the bulking plot at KARI Kiboko. The 18 genotypes were tested against 2 local checks: Marooko (drought tolerant) and K566632 (drought susceptible).

6.1.2 Experimental site

As indicated in section 3.1

6.1.3 Experimental layout, treatment and crop husbandry

At each location, 3 blocks were planted with irrigation and 3 without irrigation. In each block, the 18 genotypes plus the 2 checks were included. Selected non-rooted sweetpotato apical stem cuttings approximately 30cm long having 3 nodes were planted below the soil surface. Randomized complete block design laid out as split plot was used with two water levels i.e. non-irrigated and irrigated; water level as the main plot and the genotypes the sub-plot. The treatments were laid out in a randomized complete block design with 3 replicates. Individual plots consisted of five 1.2m long ridges, 1m apart with 4 plants per ridge. Planting distance was 0.3m and the plot area of 4.8 m². The planting vines were 30cm long. Normal agronomic

practices were carried out including regular manual weeding and earthing-up when it was deemed necessary. Overhead irrigation was done for all the plots for 4 weeks until all the plants had established and thereafter stress treatment imposed throughout the growth period for the non-irrigated treatment but continued with irrigation for the irrigated treatment.

6.1.4 Data recorded and statistical analysis

The number of plants established per plot was determined 3 weeks after planting. During harvesting the two outer rows in each plot were left out and only the three inner rows with a net plot size of 2.4 m² was used for data collection. The fresh weight of the vines in kg per plot was recorded and later converted to tonnes per hectare. Samples of leaves and vines were oven dried at 70 ºC for 72 hours or until a constant weight and expressed as percentage of vine dry matter. This weight was then recorded and from it % vine dry matter determined. This value was used in computing the vine dry matter yield. The number of plants with storage roots, number of commercial and non-commercial roots and their weight was determined. The β-carotene value was determined during harvesting as per the royal horticultural society (RHS) color chart developed (Burgos *et al.,* (2009).

Weevil damage of the roots was determined using a scale of 1to 5 as shown in Table 6.1.

Table 6. 1 Weevil damage rating of sweetpotato roots

Score	Description
1	very severe (>60% roots affected)
2	severe few roots affected
3	Moderate (10-30% roots affected
4	light (30-60% roots affected)
5	none

6.1.5 Evaluation of OFSP genotypes for susceptibility and tolerance

Stress tolerance indices were used to identify genotypes with high tolerance to drought. The biplot display of principal component analysis (Gabriel, 1971) was used to identify stress-tolerant and high yielding genotypes and to study the interrelationship between the stress-tolerant attributes. For every genotype, the six drought tolerance indices were calculated based on their root yield in normal irrigation and water deficit conditions. The drought tolerance indices were calculated as follows:

- Stress Susceptibility Index (Fischer and Maurer, 1978): This is yield of a genotype under stress as a function of the yield without stress

$$SSI = \left[1 - \left(\frac{Y_s}{Y_p}\right)\right] / SI$$ ---------- equation 1

Where: $SI = 1\left(\overline{Y_s}/\overline{Y_p}\right)$

- Mean Productivity (Rosielle and Hamblin, 1981): This is the average of yield under irrigation and stress

$$MP = \frac{Y_p + Y_s}{2}$$ ---------- equation 2

- Tolerance (Rosielle and Hamblin, 1981):

$$TOL = Y_p - Y_s$$ ---------- equation 3

- Stress Tolerance Index (Fernandez, 1992):

$$STI = \frac{(Y_p . Y_s)}{\left(\overline{Y_p}\right)^2}$$ ---------- equation 4

- Geometric Mean Productivity (Fernandez, 1992):

$$GMP = \sqrt{Y_p . Y_s}$$ ---------- equation 5

Where:

Yp = Yield of a genotype in normal irrigation condition

Ys = Yield of a genotype in water deficit condition

$\overline{YP}$ = Mean yield in normal irrigation condition

$\overline{YS}$ = Mean yield in water deficit condition

The multivariate display as a bi-plot was used to investigate the relationships between more than two variables. The bi-plot graph provides a useful tool for data analysis and allows the visual appraisal of the structure of a large two way data matrix. To display the genotype by trait two way data in bi-plot, a principal component analysis is required. An analysis of principal components often reveals relationships that were not previously suspected and thereby allows interpretations that would not ordinarily result (Johanson and Wichern, 1996). The bi-plot display of principal component analysis was used to identify stress tolerant and high-yielding genotypes and to study the interrelationship among the drought tolerance indices.

6.1.6 Statistical Analysis

The effects of the treatments and their interactions were evaluated at $p<0.05$. The effects of the treatments and their interactions were evaluated and means separated using least significant differences ($LSD_{0.05}$). Data for each site was analyzed separately. The PC-SAS procedures, general linear model, PRINCOMP, GPLOT (SAS 1988) and procedure for principal component analysis of qualitative data(PRINQUAL) (SAS 1988) were used in developing the SAS codes to display the bi-plots.

6.2 Results

6.2.1 Soil analysis results

The results of soil test for both sites are presented in Appendices 5 and 6. Both fields had similar soil fertility conditions. The soil pH at the two sites ranged between 7.75

and 8.10 and this classified the soils as medium alkaline. Very low values for total nitrogen, organic carbon was also observed for both sides. Phosphorus levels were generally high in Kiboko than in Marigat. There were adequate levels of most nutrients required throughout the growth period.

6.2.2 Weather condition during the experimental period

High rainfall was recorded during the month of November 2008 for both sites (Table 6.2). The rest of the months received mean average rainfall of less than 10mm which allowed expression of drought tolerance of the genotypes evaluated. High temperatures were also recorded during the trial period at Kiboko.

Table 6. 2 Rainfall (mm) (Kiboko and Marigat) and Temperature (ºC) for Kiboko during the evaluation of sweetpotato genotypes

Month	Rainfall (mm)		Mean temperature(ºC) Kiboko	
	Kiboko	Marigat	Maximum	Minimum
September 2008	0	24	30	15.50
October 2008	10	7	32	15.32
November 2008	80	80	29.5	17.00
December 2008	8	0	30.1	18.50
January 2009	30	4	30.5	19.00
February 2009	17	0	33.4	18.60
Total	**145**	**115** **Mean**	**30.91**	**17.32**

6.2.3 Agronomic performance of the genotypes

The analysis of variance (ANOVA) results indicated that there were highly significant differences among the genotypes for all the characters except for foliage yield, weevil damage and biomass. No significant differences for GXE interaction were observed for foliage yield and harvest index (Appendix 7).

6.2.3.1 Plants harvested and Foliage vigor

The mean number of plants harvested show the non-irrigated treatment were lower at Kiboko (4.83) compared to Marigat (7.52) (Table 6.3). At Kiboko higher mean numbers of plants harvested under irrigated treatment were observed for genotypes 192033.5, 441725 and K566632 although not different from the tolerant check Marooko. Under non-irrigated treatment in the same site genotypes 194515.2, 4200014 and 441725 had high mean number of plants harvested that ranged from 6.0

to 10.0 (Table 6.4) High mean numbers of plants harvested in Marigat under non-irrigated treatment were observed for genotypes 189148.2, 194515.2, 420014 and 441725 and this ranged from 8.33 to 9.00 (Table 6.4).

The main effects for genotype and treatment levels on vine vigor were both very highly ($p>0.001$) significant (Table 6.3 and appendix 7). However no significant interactios were noted for site and clone, site genotype and treatment. In Kiboko under non-irrigated treatment genotypes 421066,441725 and 189135.9 recorded medium strong vines, medium thick vines and long internode distances. They were all rated in the scale ranging from 4.33 to 5.33.This rating was not very far from that of the check that had a rating of 6.0. In Marigat genotypes that showed high vigor under moisture stress condition were observed for genotypes 189135.9 (3.67), 189148.2 (4.00), 421066 (4.00) and 189135.9 (3.67). This was an indication of their ability to withstand moisture stress and to have a high rating of vine survival under the same treatment (Table 6.4).

Table 6. 3 Foliage vigor and number of plant harvested for sweetpotato genotypes as affected by management treatments at Kiboko and Marigat, Kenya

Site	Treatment	Foliage Vigor	No of plants harvested
Kiboko	Irrigated	5.18	9.05
	Not irrigated	3.47	4.83
	LSD(0.05)	**0.06**	**1.29**
Marigat	Irrigated	5.68	8.14
	Not irrigated	2,90	7.52
	LSD(0.05)	**0.68**	**0.75**

Table 6. 4 Mean for foliage vigor and number of plant harvested for 20 sweetpotato genotypes evaluated at Kiboko and Marigat, Kenya

Genotype	Kiboko				Marigat			
	Foliage vigor		Number of plants harvested		Foliage vigor		Number of plants harvested	
	Water level		Water level		Water level		Water level	
	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)
187017.1	6.33	3.67	10.67	5.33	6.00	2.67	10.00	7.33
189135,9	4.67	4.33	7.67	5.00	5.33	3.67	9.33	7.67
189148.2	5.00	3.33	10.00	3.00	5.33	4.00	9.67	9.00
192033.5	4.33	3.67	11.00	4.33	5.33	2.67	6.00	7.67
194515.2	5.33	4.00	9.67	8.00	6.00	1.67	7.67	9.00
194549.6	5.67	4.00	9.00	5.00	6.00	3.33	7.33	6.00
194573.9	4.67	4.00	10.00	5.00	5.67	3.33	5.00	9.00
401055	5.00	2.33	5.00	3.33	5.00	1.67	9.33	7.67

Table 6.4 cont.

	Kiboko				Marigat			
	Foliage vigor		Number of plants harvested		Foliage vigor		Number of palnts harvested	
	Water level		Water level		Water level		Water level	
Genotype	Irrigated	Non-irrigated	Irrigated	Non-irrigated	Irrigated	Non-irrigated	Irrigated	Non-irrigated
420014	5.00	3.00	10.00	6.33	6.00	3.00	9.00	10.00
421066	5.33	5.33	10.33	8.33	5.00	4.00	8.00	8.67
422656	5.00	4.67	4.67	5.67	6.33	3.67	9.67	8.00
440001	5.33	2.67	6.00	2.33	5.67	3.67	8.33	6.33
440240	6.33	1.33	10.00	1.33	5.33	2.00	7.67	5.67
440286	4.67	2.33	8.67	2.00	5.33	2.67	9.00	7.00
440287	5.00	2.67	9.67	4.67	6.33	2.67	9.00	6.67
441097	4.33	2.67	8.67	3.67	7.00	3.67	9.00	7.6
441538	5.67	2.33	8.33	4.00	5.00	1.67	6.67	5.00

Table 6.4 cont.

	Kiboko				Marigat			
	Foliage vigor		Number of plants harvested		Foliage vigor		Number of plants harvested	
	Water level		Water level		Water level		Water level	
Genotype	Irrigated	Non-irrigated	Irrigated	Non-irrigated	Irrigated	Non-irrigated	Irrigated	Non-irrigated
441725	5.33	5.00	11.33	7.67	6.33	2.67	7.00	8.33
K566632	5.33	2.00	11.00	3.00	5.33	2.33	8.33	6.00
Marooko	5.33	6.00	9.33	8.67	5.67	3.00	7.00	7.67
LSD	**1.72**		**2.75**		**1.70**		**0.75**	

6.2.3.2 Foliage yield

There were very highly significant ($p>0.001$) differences for sites and interaction between site and treatment for foliage yield (Table 6.5 and Appendix 7). However no interactions were observed for genotype and treatment and site, genotype and treatment. Biomass was 2 to 3 times higher under irrigation in the two sites. Large responses of biomass to irrigation at KIboko, Large response of biomass to irrigation at Kiboko compared to Marigat may be due to soil differences (Table 6.5). Best performing genotypes across the sites were 189135.9, 421006 and 441725 (Table 6.6). These had mean values that were higher than the drought tolerant check Marooko. Genotype 441725, 192033.5, 422656 and 187017.1 had high fresh foliage dry matter yields under rain fed than irrigated condition. The biomass under non-irrigated condition was 300% and 210 % lower at Kiboko and Marigat respectively compared to that under irrigation.

Table 6. 5 Fresh and dry matter yield (t/ha) for sweetpotato foliage at Kiboko and Marigat, Kenya

Site	Treatment	Fresh Foliage yield t/ha	Foliage dry matter yield t/ha
Kiboko	Irrigated	14.21	6.01
	Non-irrigated	5.02	2.00
$LSD_{(0.05)}$		**2.56**	**0.37**
Marigat	Irrigated	53.30	8.84
	Non-irrigated	17.13	4.17
$LSD_{(0.05)}$		**3.20**	**0.75**

Table 6. 6 Means for foliage fresh and dry matter yield (t/ha) of sweetpotato genotypes evaluated at Kiboko and Marigat, Kenya

	Kiboko				Marigat			
	Fresh foliage yield t/ha		Foliage dry matter yield t/ha		Fresh foliage yield t/ha		Foliage dry matter yield t/ha	
	Water level		Water level		Water level		Water level	
Genotype	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)
187017.1	13.33	6.13	4.30	2.77	68.90	15.57	11.03	3.47
189135,9	3.77	3.75	1.33	0.80	35.87	24.60	3.60	4.33
189148.2	6.57	2.10	3.73	1.00	28.90	31.37	4.13	8.83
192033.5	33.50	8.77	12.30	2.50	56.00	20.43	9.67	4.60
194515.2	25.13	10.70	10.87	4.93	51.40	7.93	6.60	1.73
194549.6	18.87	5.33	7.03	2.20	57.67	35.20	7.67	5.60
194573.9	2.63	9.73	1.27	1.97	50.80	10.83	10.20	2.37
401055	4.60	2.50	2.00	1.20	37.63	24.30	5.10	6.50
420014	13.07	4.20	5.37	2.00	72.50	14.43	8.30	3.10
421066	11.83	7.10	5.30	2.93	57.37	13.20	12.67	5.70
422656	24.87	7.37	14.57	4.30	58.77	23.73	8.73	5.07

Table 6.6 cont.

	Kiboko				Marigat			
	Fresh foliage yield t/ha		Foliage dry matter yield t/ha		Fresh foliage yield t/ha		Foliage dry matter yield t/ha	
	Water level		Water level		Water level		Water level	
Genotype	**Irrigated (W1)**	**Non-irrigated (W0)**	**Irrigated (W1)**	**Non-irrigated (W0)**	**Irrigated (W1)**	**Non-irrigated (W0)**	**Irrigated (W1)**	**Non-irrigated (W0)**
440001	3.33	0.83	1.50	0.50	66.97	14.03	9.30	2.70
440240	7.37	0.67	3.00	0.37	40.13	11.80	6.23	2.97
440286	6.13	0.97	2.67	0.30	50.13	6.83	11.53	1.63
440287	7.93	4.47	3.67	1.60	45.13	10.13	7.67	2.00
441097	16.83	1.70	6.77	1.07	72.90	31.67	10.40	8.77
441538	19.03	2.80	8.27	1.10	53.33	2.93	11.80	0.90
441725	16.50	7.20	8.33	1.87	33.60	24.03	7.77	6.07
K566632	11.00	0.83	4.87	0.57	43.33	6.40	6.43	1.27
Marooko	31.80	10.57	13.03	5.93	91.23	25.43	18.50	5.87
LSD(0.05)	**4.25**		**1.87**		**7.25**		**2.40**	

6.2.3.3 Number of commercial roots and number of plants with roots

The number of commercial roots formed was highly affected by the treatments imposed (Appendix 7 and Table 6.7). Number of commercial roots increased under irrigation compared to non-irrigated conditions; the number of storage roots was 4.6 times (460 %) higher under irrigation at Kiboko compared to 160 % higher at Marigat. The number of plants with storage roots was highly affected by treatment and interaction between treatment and site (Appendix 7 table 6.8). High number of plants with roots was three times higher in Kiboko than in Marigat under irrigation treatment.

The proportion of number of commercial storage roots varied among the irrigated and non-irrigated treatments in each site. At Kiboko the proportion under irrigation and non-irrigated conditions was 43% and 55% respectively compared with 39% and 31% at Marigat under the same conditions (Table 6.8).

Table 6. 7 Number of commercial and non-commercial roots for sweetpotato genotypes evaluated at Kiboko and Marigat, Kenya

Site	Management	Number of commercial roots	Number of plants with storage roots
Kiboko	Irrigated	19.02	8.30
	Non-irrigated	4.17	2.94
$LSD_{(0.05)}$		**3.57**	**2.45**
Marigat	Irrigated	11.87	5.90
	Non-irrigated	7.56	4.78
$LSD_{(0.05)}$		**2.28**	**0.98**

Table 6. 8 The number of plants with storage roots and number of commercial roots from genotypes evaluated at Kiboko and Marigat, Kenya

	Kiboko				Marigat			
	Number of plants with storage roots per net plot		Number of commercial roots		Number of plants with storage roots		Number of commercial roots	
	Water level		Water level		Water level		Water level	
Genotype	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)
187017.1	10.00	2.50	31.67	3.00	6.33	4.00	23.00	6.00
189135,9	7.67	4.00	16.00	6.67	6.00	6.33	15.33	11.67
189148.2	11.00	3.00	31.33	4.00	7.00	6.33	14.33	12.00
192033.5	8.33	3.33	23.67	4.50	4.33	6.00	4.00	5.00
194515.2	10.00	4.33	14.67	5.00	5.00	3.33	8.33	5.00
194549.6	7.00	1.33	8.33	3.00	5.50	4.00	1.00	2.00
194573.9	8.67	5.67	26.00	8.00	4.50	6.33	3.50	13.67
401055	4.33	1.00	4.00	4.00	9.00	6.00	12.50	5.00
420014	10.67	3.33	27.00	3.33	5.67	5.33	19.00	8.67
421066	9.00	4.33	31.67	5.33	5.00	6.00	8.00	5.67
422656	5.00	3.00	7.00	2.00	7.33	4.00	17.67	6.00

Table 6.8 cont.

	Kiboko				Marigat			
	Number of plants with storage roots per net plot		Number of commercial roots		Number of plants with storage roots per net plot		Number of commercial roots	
	Water level		Water level		Water level		Water level	
Genotype	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)
440001	7.00	2.00	10.00	1.50	7.33	5.00	11.00	8.00
440240	8.33	1.00	9.67	1.00	4.00	3.33	6.00	6.00
440286	8.67	1.50	16.67	3.00	6.00	4.50	21.67	6.50
440287	9.00	2.67	29.00	3.67	8.33	4.00	18.33	5.00
441097	8.33	3.00	23.00	5.50	5.50	5.67	8.00	5.00
441538	6.00	2.00	17.00	2.00	5.33	1.50	2.67	5.72
441725	8.67	5.00	24.00	6.67	6.50	5.33	20.50	12.00
K566632	10.00	3.00	22.33	3.00	6.33	6.00	11.67	2.00
Marooko	7.33	2.00	7.33	1.67	3.67	2.00	2.67	2.50
LSD(0.05)	**0.95**		**5.01**		**0.79**		**3.30**	

6.2.3.4 Number of storage roots

Total number of roots varied across the 2 sites (Table 6.9).The number of roots formed in Kiboko under non-irrigated treatment were generally low (6.9). Genotypes 189135.9 (13.00), 192033.5 (10.50), 440287 (12.00) and 441725 (11.67) produced more roots than the tolerant check (1.67) under the same treatment. In Marigat high production of roots under non-irrigated treatment were recorded for genotypes 189135.9 (32.67), 189148.2 (43.33), 194573.9 (44.00), 401055 (55.00), 420014 (42.67) and 441725 (24.33). High number of total roots production under irrigated treatment across the two sites were observed for genotypes 187017.1, 189135.9, 189148.2 and 441725. Very low production of roots under non-irrigated treatment was observed for genotypes 440240 in Kiboko and 441538 in Marigat.

6.2.3.5 Average number of storage roots per plant

Average number of roots per plant was significantly affected by the treatments imposed in both sites (Table 6.9). Genotypes at Kiboko under non-irrigated treatment had the least mean number of roots per plant (1.33) compared to that of Marigat under the same treatment. Under non-irrigated treatment genotypes 440001 (1.75), 420014 (1.24), 401055 (1.38), 194573.9 (2.27), 189133.9 (2.68) and 189148.2 (1.04) produced higher number of roots per plant in Kiboko and genotypes 187017.1 (3.33), 189135.9 (5.01), 189148.2 (6.76), 194573.9 (6.21), 401055 (9.17) and 420014 (7.94) in Marigat.

Table 6. 9 Total number of roots and average number of roots per plant of sweetpotato genotypes evaluated at Kiboko and Marigat, Kenya

	Kiboko				Marigat			
	Total number of storage roots Water level		Average number of roots per plant Water level		Total number of storage roots Water level		Average number of roots per plant Water level	
Genotype	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)
187017.1	76.67	3.50	7.5	0.59	50.33	12.33	9.29	3.33
189135,9	35.33	13.00	4.63	2.68	30.33	32.67	4.76	5.01
189148.2	81.67	4.50	8.06	1.04	54.67	43.33	7.14	6.76
192033.5	88.00	10.50	8.37	3.00	21.33	14.00	3.46	2.33
194515.2	26.00	7.33	2.71	0.93	25.00	9.00	5.00	2.45
194549.6	12.67	3.50	1.44	0.63	7.00	12.00	1.29	4.17
194573.9	53.67	11.00	5.40	2.27	24.00	44.00	5.13	6.21
401055	9.33	5.50	1.75	1.38	29.50	55.00	3.29	9.17
420014	45.33	6.00	4.79	1.24	33.00	42.67	4.84	7.94
421066	50.33	8.00	5.11	1.01	25.00	21.67	4.82	3.65
422656	18.67	4.00	4.00	0.70	32.00	14.00	4.42	3.50
440001	37.00	4.50	6.17	1.75	27.67	27.33	3.63	5.43

Table 6.9 cont.

	Kiboko				Marigat			
	Total number of storage roots		Average number of roots per plant		Total number of storage roots		Average number of roots per plant	
	Water level		Water level		Water level		Water level	
Genotype	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)
440240	21.33	1.00	2.12	1.00	20.67	11.00	4.86	2.28
440286	38.67	3.50	4.69	1.75	30.00	10.50	5.51	2.25
440287	83.33	12.00	9.41	2.69	38.33	22.50	4.93	4.50
441097	34.00	6.50	3.94	1.43	16.00	13.67	3.31	2.45
441538	29.33	2.50	3.53	0.55	10.33	2.50	1.89	1.50
441725	56.00	11.67	4.82	1.44	54.50	24.33	8.88	4.47
K566632	64.33	4.00	5.81	0.94	22.67	17.00	3.64	2.83
Marooko	13.67	3.00	1.49	0.34	3.67	3.00	0.93	1.50
LSD(0.05)	**12.7**		**1.20**		**8.18**		**1.09**	

6.2.3.5 Non-commercial root yield

Very low mean non-commercial root yield was recorded in non-irrigated treatment at the two sites (Table 6.10). High yields were obtained under irrigation at the two sites in some genotypes. These were 401055, 189135.9, 421066 at Kiboko and 89135.9,422656, 189148.2, 194549.6 and 401055 for Marigat. This indicates their suitability as genotypes that can be harvested piece-meal

6.2.3.6 Commercial root yield

Commercial root yield refers marketable storage roots for human consumption. Very low storage root yields were observed in non-irrigated treatment at the two sites (Table 6.10), High yielding genotypes under the same treatment in both sites were 189135.9, 194573, 9, 421006 and 441725. Their yields varied between 3.90 and 7.20 t/ha which were above that of the tolerant check Marooko at Marigat, (2.37t/ha) and at Kiboko (1.0t/ha). The high yielding genotypes under non-irrigation at Kiboko included 441725 (5,83 t/ha), 421066 (3.90 t/ha), 194573.9 (9.43 t/ha), 194515.2 (7.10 t/ha), 189135.9 (7.20 t/ha), 440287 (8.9 t/ha) and 441725 (9.60 t/ha) (Table 6.10).

Table 6. 10 Non-commercial and commercial root yield of sweetpotato genotypes evaluated at Kiboko and Marigat, Kenya

	Kiboko				Marigat			
	Non-commercial root yield t/ha		Commercial root yield t/ha		Non-commercial root yield t/ha		Commercial root yield t/ha	
	Water level		Water level		Water level		Water level	
Genotype	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)
187017.1	11.53	0.40	39.73	2.95	3.00	0.30	23.73	6.12
189135,9	6.67	1.97	15.13	4.77	2.47	0.33	15.00	7.20
189148.2	12.07	0.60	26.67	2.10	4.63	0.57	16.93	5.42
192033.5	11.40	1.70	26.70	2.50	2.50	0.10	5.55	1.70
194515.2	3.20	0.83	20.13	5.00	1.27	0.37	9.30	7.10
194549.6	1.40	0.40	25.57	2.50	0.65	0.75	0.40	1.85
194573.9	11.13	1.10	31.53	4.17	0.50	0.60	6.88	9.43
401055	1.00	1.05	4.03	2.50	1.60	1.10	7.10	2.50
420014	6.70	0.67	32.80	2.37	8.50	0.63	19.30	7.07
421066	5.83	2.23	47.27	3.90	2.80	0.60	17.62	5.55
422656	2.93	0.40	9.57	1.70	1.57	0.75	14.20	5.00

Table 6.10 Non-commercial and commercial root yield of sweetpotato genotypes evaluated at Kiboko and Marigat, Kenya (Cont.)

	Kiboko				Marigat			
	Non-commercial root yield t/ha		Commercial root yield t/ha		Non-commercial root yield t/ha		Commercial root yield t/ha	
	Water level		Water level		Water level		Water level	
Genotype	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)
440001	4.03	1.05	4.43	1.90	3.27	0.33	15.17	4.30
440240	2.80	0.80	16.83	1.70	2.43	0.30	15.15	2.90
440286	4.80	0.40	25.90	2.10	2.97	0.10	33.60	7.90
440287	9.87	1.00	23.17	1.97	1.63	0.60	19.33	8.95
441097	5.17	0.40	36.67	2.70	1.15	0.20	11.25	2.08
441538	1.83	0.60	23.47	1.70	0.30	0.20	0.97	0.84
441725	9.30	1.93	8.47	5.83	5.40	0.47	26.90	9.60
K566632	10.40	1.30	26.53	2.30	2.13	0.20	13.77	1.07
Marooko	2.53	0.40	14.03	1.00	0.80	0.10	2.08	3.53
LSD(0.05)	**1.87**		**6.90**		**0.83**		**4.27**	

6.3 Weevil damage

Most root damage by weevil was observed in genotypes evaluated in Marigat (1.91, indicating 60% of the roots were affected) than in Kiboko (2.24, indicating 30-60% roots were affected) under non-irrigated treatment (Table 6.11). Moderate root weevil damage in Marigat under non-irrigated treatment was observed in genotypes 441725, 194573.9, 421006 and 189135.9. Very minimal weevil storage root damage was observed in storage roots grown under irrigation in both sites.

Table 6. 11 Effects of irrigation and site on sweetpotato damage by weevil (*cylas formicarius*)

	Kiboko		**Marigat**	
	Water level		**Water level**	
Genotype	**Irrigated (W1)**	**Non-irrigated (W0)**	**Irrigated (W1)**	**Non-irrigated (W0)**
187017.1	5.00	1.50	4.67	2.67
189135,9	4.67	3.00	5.00	3.00
189148.2	5.00	1.00	4.67	3.00
192033.5	4.67	2.50	4.33	2.00
194515.2	4.67	3.00	4.67	1.67
194549.6	5.00	1.50	4.50	1.50
194573.9	4.67	3.00	4.00	3.00
401055	4.00	2.00	5.00	3.00

Table 6.11 cont.

	Kiboko		Marigat	
	Water level		Water level	
Genotype	**Irrigated (W1)**	**Non-irrigated (W0)**	**Irrigated (W1**	**Non-irrigated (W0)**
421066	4.67	3.00	4.33	3.00
422656	5.00	1.00	4.67	1.50
440001	4.33	1.50	5.00	2.33
440240	4.67	1.00	4.33	1.33
440286	5.00	1.50	4.33	3.00
440287	4.33	2.67	4.67	2.50
441097	5.00	1.50	5.00	1.33
441538	4.67	1.50	3.67	1.00
441725	4.67	3.00	4.50	2.33
K566632	5.00	1.50	4.67	2.00
Marooko	4.33	1.00	4.33	2.50
LSD(0.05)	**1.53**		**1.36**	

6.4 Harvest index and biomass production

Harvest index is a ratio of total fresh storage root yield to the total above and below ground fresh biomass at harvest; this ration can be expressed as a percentage. Very low harvest indices that ranged from 17.46 to 23.56 were recorded for stress treatment at both sites (Table 6.12 and Figure 6.1). Genotypes 189135.9, 189148.2, 194573.9 and 420014 had higher harvest indices that were significantly different from that of the drought tolerant check Marooko. Least harvest indices under stress treatment in Kiboko were observed for genotypes 192033.5, 194549.6 and 401055 these we not different from that of the drought susceptible check K566632. Mean biomass yield across the environments are presented in Table 6.12 and Figure 6.2. Biomass production significantly increased under irrigation environment across the two sites. Very low mean biomass production of 7.94 t/ha was observed for genotypes grown under non-irrigated treatment in Kiboko than in Marigat (20.6 t/ha). High biomass productions under the same treatment across the sites were observed for genotypes 194515.2, 194573.9 and
441725 (Table 6.12 and Figure 6.2).

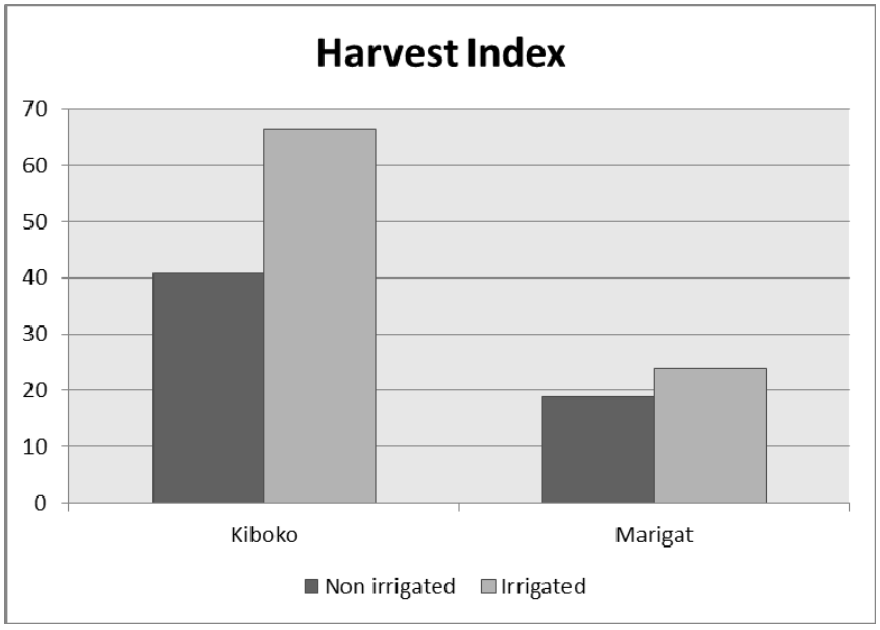


Figure 6. 1 Harvest index for roots of sweetpotato genotypes evaluated at Kiboko and Marigat, Kenya under non-irrigated and irrigated treatment

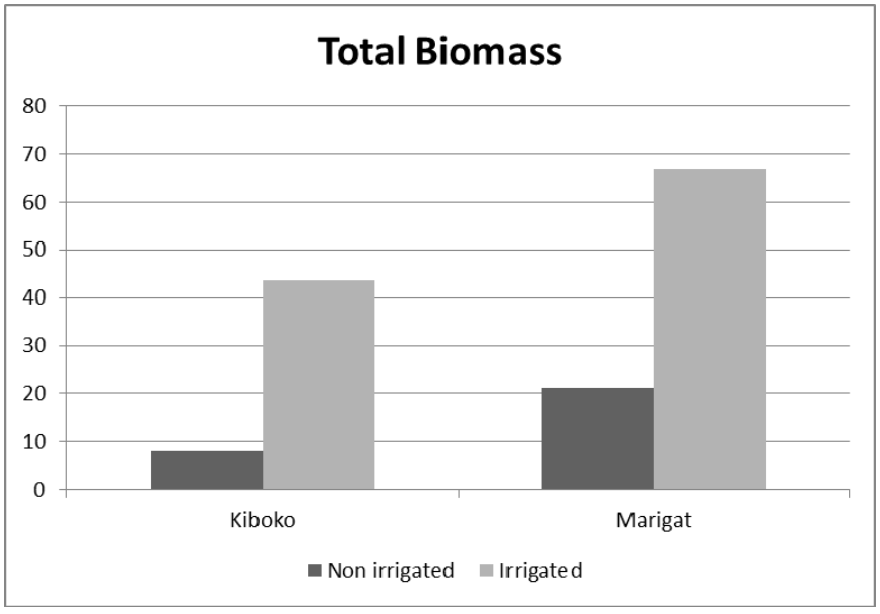


Figure 6. 2 Total biomass production of sweetpotato genotypes evaluated at Kiboko and Marigat, Kenya under non-irrigated and irrigated treatment

Table 6. 12 Mean for Harvest Index and total biomass of sweetpotato genotype evaluated at Kiboko and Marigat, Kenya

Genotype	Kiboko				Marigat			
	Harvest index Water level		Total biomass t/ha Water level		Harvest index Water level		Total biomass t/ha Water level	
	Irrigated (W1)	Non-irrigated(W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)	Irrigated (W1)	Non-irrigated (W0)
187017.1	75.23	23.53	64.60	8.40	33.63	28.77	95.63	21.90
189135,9	85.80	52.97	25.57	12.93	34.27	32.33	53.30	32.17
189148.2	85.10	38.10	45.27	3.37	50.50	19.90	50.43	37.37
192033.5	46.23	29.03	71.50	11.73	8.90	5.60	62.37	21.17
194515.2	45.03	37.40	48.47	16.57	20.47	16.27	62.00	10.67
194549.6	59.00	33.47	45.83	7.50	1.07	1.97	58.27	23.50
194573.9	94.07	38.40	45.30	15.00	19.37	50.90	55.67	20.87
401055	51.50	31.87	9.60	4,13	11.97	5.40	43.53	25.73
420014	76.17	44.87	52.50	7.23	30.37	38.73	97.47	22.13

Table 6.12 cont

	Kiboko				Marigat			
	Harvest index		Total biomass t/ha		Harvest index		Total biomass t/ha	
	Water level		Water level		Water level		Water level	
Genotype	**(W1)**	**(W0)**	**(W1)**	**(W0)**	**(W1)**	**(W0)**	**(W1)**	**(W0)**
421066	73.37	48.20	64.87	13.23	27.10	37.90	77.77	19.37
422656	37.67	20.10	37.37	8.87	27.00	8.67	24.50	26.00
440001	72.73	60.07	11.80	2.87	26.37	25.53	85.40	18.67
440240	73.77	52.17	26.97	1.63	24.87	6.90	57.70	13.10
440286	87.17	44.07	47.67	2.03	36.93	34.77	86.77	12.23
440287	79.77	41.77	40.97	7.37	34.67	10.53	66.07	11.37
441097	69.30	45.10	58.63	3.70	22.83	6.37	69.27	33.93
441538	57.83	31.47	44.33	3.87	2.40	4.53	54.57	3.10
441725	40.53	52.53	33.93	15.00	12.97	16.20	55.17	30.87
K566632	76.83	65.13	48.47	2.90	24.97	10.40	45.28	8.20
Marooko	36.60	24.13	48.33	11.83	7.00	13.37	93.63	27.90
LSD(0.05)	**9.59**		**7.79**		**10.55**		**14.74**	

6.5 Root-flesh color, Beta carotene levels (mg/100g, FW) and Vitamin A (µgRE/100, FW)

Root-flesh colors of the genotypes evaluated are presented in Table 6.13. The color ranged from cream to deep-orange. The variation in color also reflected different levels for beta carotene and vitamin A. Roots with deep orange flesh color had ß-carotene and vitamin A ranging from 10.5 to 14.37mg/100g and 875 to 1197.5µgRE/100g on fresh weight basis (FW), while orange color fresh storage roots had 6.12mg/100g and 5105µgRE/100g respectively on a fresh weight basis (Table 6.13).. Roots with intermediate orange primary flesh color had ß-carotene and vitamin A ranging from 4.92 to 7.23 mg/100 g and 410 to 602.55µgRE/100g FW, respectively. Most of the genotypes with orange or deep and intermediate orange fleshed roots showed had secondary color (pale yellow orange, pale orange and intermediate orange). Roots with pale orange as the primary flesh color had ß-carotene and vitamin A ranging from 0.69 to 4.47 mg/100g and from 57.5 to 260µgRE/100g, respectively on fresh mass basis. Pale orange fleshed storage roots had high ß-carotene concentration when the secondary colors were orange and intermediate orange, and those represent a substantial proportion (some small spots or veins) of the flesh storage root.

Table 6. 13 Root-flesh colors, beta carotene milligram per 100 grams on fresh weight basis (FW) (mg/100g, FW) and Vitamin A microgram retinol equivalent per 100 grams (µgRE/100g, FW) levels for the genotypesevaluated in Marigat and Kiboko trial

Genotype		Primary color	Secondary color	Beta-carotene mg/100g,FW	Vitamin A(µgRE/100g, FW	Dry matter content %
1	192033.5	Pale- yellow	Intermediate	0.69	57.5	30.17
2	K566632	Deep	Intermediate	13.39	1032.5	25
3	194573.9	Intermediate	Intermediate	4.92	410	25
4	421066	Intermediate	Intermediate	4.92	410	26.0
5	187017.1	Intermediate	Intermediate	4.92	410	25
6	189148.2	Intermediate	Intermediate	7.23	602.5	25
7	441097	Intermediate	Intermediate	3.76	313.3	26.1
8	441725	Deep	Intermediate	11.03	919.2	25
9	440240	Intermediate	Intermediate	7.23	602.5	30
10	194549.6	Pale orange	Intermediate	4.47	260	29.7
11	401055	Orange	Intermediate	6.12	510	*25*
12	440287	Pale orange	Pale orange	1.65	137.5	*25*
13	420014	Pale yellow	Intermediate	1.5	125	*25*
14	440286	Deep	Intermediate	10.5	875	*25*
15	194515.2	Pale yellow	Intermediate	1.38	115	*25*
16	189135.9	Orange	Intermediate	6.12	510	*25*
17	422656	Pale orange	Pale orange	1.65	137.5	*25*
18	440001	Deep	Intermediate	14.37	1197.5	*25*
19	441538	Deep	Intermediate	12.39	1032.5	*25*
20	Marooko	Cream	-	0.03	2.5	37.1

6.6 Correlation matrix and estimation of drought tolerance indices

Correlation coefficients between yield under water deficit condition (Ys) and yield of a genotype in normal irrigation condition(Yp) and other quantitative indices of drought tolerance were calculated for both sites (Table 6.14 and Figure 6.3 for Marigat and Table 6.15 and Figure 6.4 for Kiboko) to determine the most desirable drought tolerance criteria. High significant correlations were found between root yield under stress environment and the drought indices mean productivity (Mp), geometric mean productivity (GMP), stress tolerance index(STI) and tolerance index (TOL). Similar correlations were reported in common bean (Ramirez and Kelly, 1998) durum wheat (Mohamadi *et al.,* 2010) and bread wheat (Bilge and Mehmet, 2010). Under irrigated condition significant correlation were found for root yield with Mp, GMP TOL, and STI. The results showed high significant correlations among some drought tolerant parameters for root yield. A correlation of nearly one was found between STI and GMP, and these were positively correlated with Mp and not with SSI. SSI was found to be correlated with TOL only at both sites.

Using Fernandez's (1992) parameter, STI, genotypes 421066, 194573.9, 192033.5, 187017.1 and 189135.9 with the highest values in both sites were considered to be tolerant genotypes, whereas genotypes 422656, 440240, 440001, Marooko and 401055 with the lowest STI were intolerant (Tables 6.16 and 6.17). In case of the parameter TOL, the lowest difference between yields in both conditions was observed for genotypes 401055, 440001, 422656, 441725 and 189135.9 but the highest difference belonged to genotypes 187017.1, 421066, 440286, 441097 and

194573.9. These results indicate genotypes with high STI usually have high difference in yield in two different conditions.

In general, similar ranks for the genotypes were observed by GMP and MP parameters as well as STI, suggesting that these three parameters are equal for selecting genotypes. According to Fischer and Maurer's (1978) using parameterSSI, genotypes 441725, 401055, 189135.9, 194515.2 and 440001 for Kiboko and 187017.1, 189135.9, 440287, 194549.6 and 440286 for Marigat were in the lowest and were considered as genotypes with low drought susceptibility and high yield stability in the both conditions. Genotypes 440001 and 422656 for Marigat and genotypes 440286 and 189148.2 for Kiboko with SSI values higher than one were identified as high drought susceptible with poor yield stability' (Table 6.17). In case of comparison between the parameters for selection of the genotypes, TOL and SSI gave same results.

Table 6. 14 Pearson Corrélation Coefficients (N = 20) for various drought tolerant indices for genotypes evaluated at Marigat

	Yp	Ys	SI	Mp	GMP	TOL	SSI	STI
Yp	1.000	0.671	0.434	0.098	0.875	0.965	0.435	0.862
		0.0012	0.056	<0.0001	<0.0001	<0.0001	0.055	<0.0001
Ys	0.671	1.000	-0.202	0.793	0.875	0.965	0.435	0.862
	0.001		0.393	<0.0001	<0.0001	<0.0001	0.055	<0.0001
SI	0.434	-0.202	1.000	0.308	0.875	0.965	0.435	0.862
	0.056	0.393		0.187	<0.0001	<0.0001	0.055	<0.0001
Mp	0.983	0.793	0.307	1.000	0.945	0.903	0.310	0.923
	<0.0001	<0.0001	0.187		<0.0001	<0.0001	0.184	<0.0001
GMP	0.875	0.935	0.818	0.945	1.000	0.722	0.085	0.968
	<0.0001	<0.0001	0.732	<0.0001		0.0003	0.723	<0.0001
TOL	0.965	0.454	0.593	0.903	0.722	1.000	0.594	0.722
	<0.0001	0.044	0.006	<0.0001	0.0003		0.006	0.0003
SSI	0.435	-0.199	1.000	0.310	0.085	0.594	1.000	0.080
	<0.0001	0.400	<0.0001	0.184	0.723	0.006		0.738
STI	0.862	0.889	0.0773	0.923	0.967	0.722	0.075	1.000
	<0.0001	<0.0001	0.746	<0.0001	<0.0001	0.0003	0.738	

Y_P: Total root yield under normal irrigation condition; GMP: Geometric mean productivity;

Y_S: Total root yield under water deficit condition; STI: Stress tolerance index

SI Susceptible index;

MP: Mean productivity;; TOL: Tolerance;

SSI: Stress susceptibility index

Table 6. 15 Pearson Corrélation Coefficients (N = 20 Prob > |r| Under H0: Rho=0) for various drought tolerant indices for genotypes screened at Kiboko

	Yp	Ys	SI	Mp	GMP	TOL	SSI	STI
Yp	1.00	0.071	0.660	0.991	0.760	0.991	0.655	0.718
		0.767	0.002	<.0001	0.0001	<.0001	0.002	0.0004
Ys	0.071	1.000	-0.569	0.203	0.676	-0.065	-0.574	0.660
			0.009	0.391	0.001	0.785	0.008	0.002
SI	0.660	-0.569	1.000	0.572	0.165	0.737	1.000	0.139
	0.002	0.009		0.009	0.488	0.0002	<.0001	0.558
Mp	0.991	0.203	0.572	1.000	0.836	0.964	0.566	0.792
	<.0001	0.391	0.009	1.000	<.0001	<.0001	0.009	<.0001
GMP	0.760	0.676	0.165	0.836	1.000	0.668	0.158	0.975
	0.0001	0.001	0.488	<.0001		0.001	0.507	<.0001
TOL	0.991	-0.065	0.737	0.964	0.668	1.000	0.733	0.628
	<.0001	0.785	0.0002	<.0001	0.001		0.0002	0.582
SSI	0.655	-0.574	1.000	0.566	0.158	0.733	1.000	0.131
	0.002	0.008	<.0001	0.009	0.507	0.0002		0.582
STI	0.718	0.660	0.139	0.792	0.975	0.628	0.131	1.000
	0.0004	0.002	0.558	<.0001	<.0001	0.003	0.582	

Y_P: Total root yield under normal irrigation condition; Y_S: Total root yield under water deficit condition; SI Susceptible index; MP: Mean productivity; GMP: Geometric mean productivity; STI: Stress tolerance index; TOL: Tolerance; SSI: Stress susceptibility index

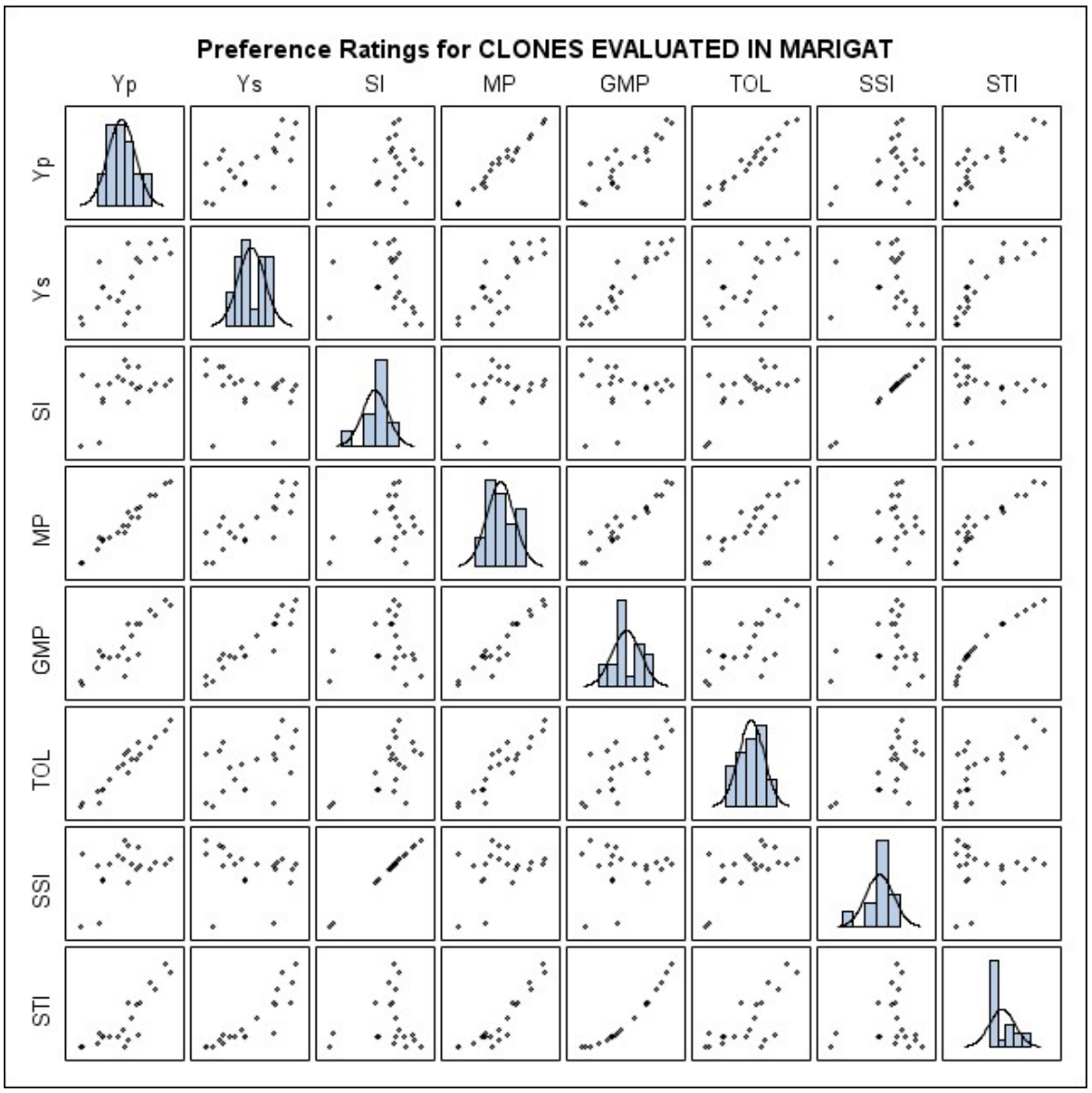


Figure 6. 3 Scatter diagramsfor various drought tolerant indices for genotypes evaluated at Marigat

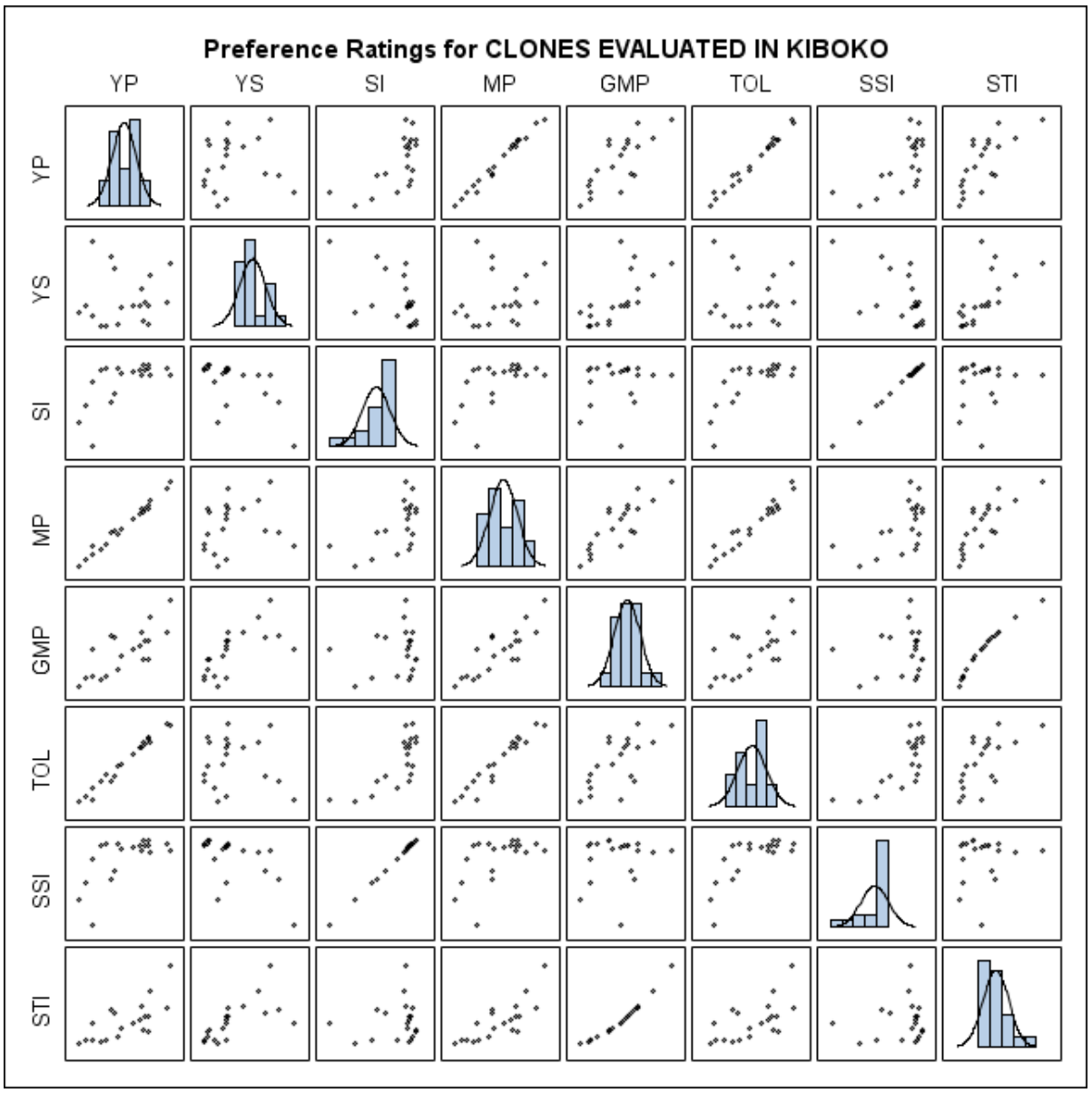


Figure 6. 4 Scatter diagrams for for various drought tolerant indices for genotypes screened at Kiboko

Table 6. 16 Estimation of drought tolerance indices based on total root yield of sweetpotato genotypes under normal irrigation and water deficit conditions in Kiboko (SI= 0.84)

Genotype	*Yp*	*Ys*	*Mp*	*GMP*	*TOL*	*SSI*	*STI*
421066	53.1	6.1	29.69	18.00	47.0	1.006	0.375
194573.9	42.6	5.3	23.95	15.03	37.3	0.995	0.261
192033.5	38.1	4.2	21.15	12.65	33.9	1.011	0.185
187017.1	51.3	3.1	27.20	12.61	48.2	1.068	0.184
189135.9	21.8	6.7	14.25	12.09	15.1	0.787	0.169
194515.2	23.3	5.8	14.55	11.62	17.5	0.853	0.156
420014	39.4	3.1	21.25	11.05	36.3	1.047	0.141
441097	41.8	2.9	22.35	11.01	38.9	1.058	0.140
K566632	36.9	2.9	19.90	10.34	34.0	1.047	0.124
440287	33.1	2.9	18.00	9.80	30.2	1.037	0.111
441725	12.2	7.8	10.00	9.76	4.4	0.410	0.110
194549.6	26.9	2.7	14.80	8.52	24.2	1.022	0.084
189148.2	38.8	1.7	20.25	8.12	37.1	1.087	0.076
440286	41.4	1.5	21.45	7.88	39.9	1.095	0.072
441538	25.3	1.5	13.40	6.16	23.8	1.069	0.044
422656	12.5	2.1	7.30	5.13	10.4	0.945	0.030
440240	19.6	1.3	10.45	5.05	18.3	1.061	0.029
440001	8.5	2.9	5.70	4.97	5.6	0.749	0.029
Marooko	16.5	1.3	8.90	4.64	15.2	1.047	0.025
401055	5.0	2.3	3.65	3.39	2.7	0.614	0.013
Mean	29.41	3.41	16.41	9..39	26.00	0.95	0.12
LSD(0.05)	**5.64**	**1.35**	**6.51**	**3.73**	**10.32**	**0.38**	**0.05**

Y_P: Total root yield under normal irrigation condition; Y_S: Total root yield under water deficit condition; MP: Mean productivity; GMP: Geometric mean productivity; STI: Stress tolerance index; TOL: Tolerance; SSI: Stress susceptibility index

Table 6. 17 Estimation of drought tolerance indices based on total root yield of sweetpotato genotypes under normal irrigation and water deficit conditions in Marigat (SI= 0.84)

Genotype	Yp	Ys	Mp	GMP	TOL	SSI	STI
421066	30.7	8.00	19.35	15.67	22.70	0.999	0.959
194573.9	32.3	6.80	19.55	14.82	22.50	1.067	0.858
192033.3	25.0	7.70	16.35	13.87	17.30	0.935	0.752
187017.1	26.8	6.30	16.55	12.99	20.50	0.034	0.660
189135.9	17.4	7.60	12.50	11.50	9.80	0.761	0.517
194515.2	21.6	6.00	13.80	11.38	15.60	0.976	0.506
420014	20.4	6.29	13.30	11.25	14.20	0.941	0.494
441097	18.4	4.60	11.50	9.20	13.80	1.014	0.331
K566632	15.7	3.22	9.46	7.11	12.48	1.074	0.197
440287	7.1	6.00	6.55	6.52	1.10	0.209	0.166
441725	20.9	1.70	11.30	5.96	19.20	1.241	0.139
194549.6	8.7	3.60	6.15	5.59	5.10	0.792	0.122
189148.2	13.6	2.30	7.95	5.59	11.30	1.123	0.122
440286	8.4	3.60	6.00	5.50	4.80	0.772	0.118
441538	10.6	2.70	6.65	5.35	7.90	1.007	0.112
422656	17.6	1.30	9.45	4.79	16.30	1.252	0.089
440240	6.4	1.70	4.05	3.30	4.70	0.992	0.043
440001	15.9	0.20	8.05	1.79	15.70	1.334	0.012
Marooko	0.9	0.80	0.85	0.84	0.10	0.150	0.003
401055	1.2	0.18	0.69	0.45	1.02	1.149	0.001
Mean	15.98	4.03	7.67	7.67	11.96	0.94	0.31
LSD(0.05)	**3.56**	**1.04**	**2.16**	**1.84**	**2.96**	**0.12**	**0.10**

Y_P: Total root yield under normal irrigation condition; Y_S: Total root yield under water deficit condition; MP: Mean productivity; GMP: Geometric mean productivity; STI: Stress tolerance index; TOL: Tolerance; SSI: Stress susceptibility index

6.7 Biplot Analysis

Present results obtained from biplot output for Marigat (Table 6.18, Fig 6.5) and Kiboko (Table 6.19, Fig 6.6) confirmed correlation analysis between studied criteria. Principal Component Analysis (PCA) done to analyze the correlation matrix for the indices revealed that the first PCA explained 66.05% of the variation of Kiboko and 73.08% for Marigat of the variation with Yp, Ys, MP, GMP and STI. Thus, the first parameter was the yield potential and drought tolerance. The second PCA explained 30.59% (Kiboko) and 23.14% (Marigat) of the total variability of the indices. Therefore, the second component can be named as stress-tolerant dimension and it separates the stress-tolerant genotypes from non-stress tolerant ones. Thus, selection of genotypes that have high PCA1 and low PCA2 are suitable for both stress and non-stress environments.

Principal component axes divided the genotypes into four groups. Group 1-genotypes with high storage root yield and high drought tolerance, included genotypes 420014,440286, 189148.2, 440287 and 44097 at Kiboko and genotypes 440286, 420014, 421006 and 189135.9 and 441725 at Marigat. These genotypes also had the highest Yp, Ys, GMP, MP and STI values. Group 2 which include genotypes with low storage root yield were stable and less sensitive to drought. This group consisted of genotypes 401055, 194573.9 and 194549.6 at Marigat and genotypes 441538, 440240, 422656, 440001 and 194549.6 at Kiboko. Group 3 that included genotypes with low to moderate storage root yield and low relative sensitivity or tolerance to drought. Genotypes in this group included 422656, 440240, 441097, 194515.2, 192033.5 and 441538. Group 4 included genotypes with high storage root

yield but very sensitive to drought. Genotypes identified under this group included 421066 and 194573.9 atKiboko and 440001 and 440287 at Marigat.

Table 6. 18 Principal component loadings for drought tolerance indices on the 20 sweet potato genotypes evaluated at Marigat.

Component	Cumulative	Yp	Ys	Mp	TOL	SSI	STI
1	73.08	0.471	0.370	0.476	0.435	0.169	0.444
2	96.22	0.107	-0.032	-0.032	0.304	0.763	-0.254
3	99.04	-0.259	0.509	-0.090	-0.491	0.624	0.191
4	100.00	0.158	0.463	0.241	0.026	0.00	-0.838
5	100.00	0.335	0.307	-0.084	0.295	0.000	0.000
6	100.00	-0.750	0.220	0.000	0.624	0.000	0.000

Table 6. 19 Principal component loadings for drought tolerance indices on the 20 sweet potato genotypes evaluated at Kiboko.

Component	*Cumulative %*	*Yp*	*Ys*	*Mp*	*TOL*	*SSI*	*STI*
1	66.05	0.499	0.057	0.497	0.491	0.333	0.385
2	96.64	-0.027	0.723	0.070	-0.125	-0.511	0.440
3	99.10	-0.029	0.177	-0.259	-0.031	0.709	0.467
4	100.00	0.069	0.638	0.153	-0.018	0.354	-0.066
5	100.00	-0.814	0.002	0.407	0.414	0.000	0.000
6	100.00	0.000	0.187	-0.070	0.688	0.000	0.000

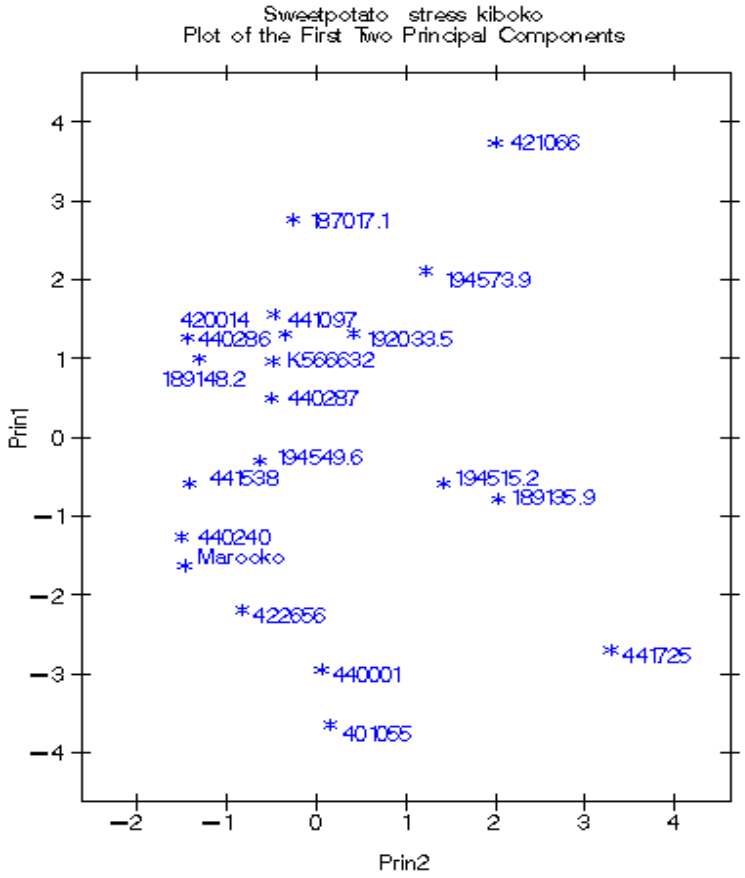


Figure 6. 5 Biplot based on first two principal component axes (PC1 and 2) of 20 sweetpotato genotypes evaluated in Kiboko

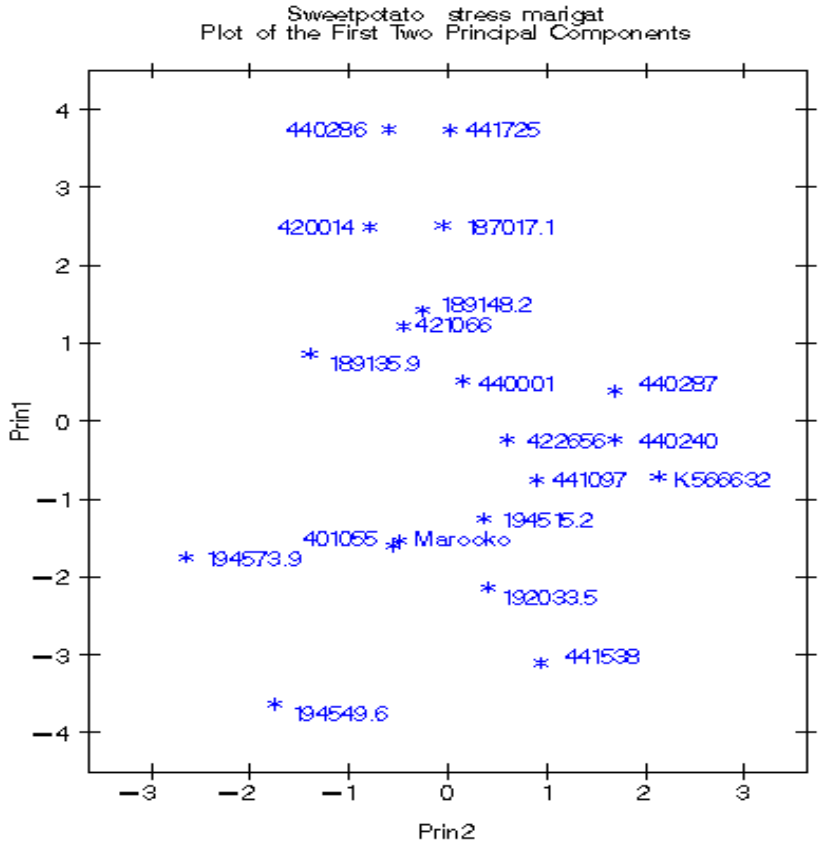


Figure 6. 6 Biplot based on first two principal component axes (PC1 and 2) of 20 sweetpotato genotypes evaluated in Marigat

6.8 Discussion

6.8.1 Biomass yield component

Most of the agronomic traits evaluated for all the genotypes were severely affected by the available moisture content. Although the effect on number of plants harvested were not severe, the foliage and commercial root yield decreased significantly with water stress conditions. Genotypes 189135.9, 194573.9 and 441725 recorded high commercial root yield under severer moisture conditions in both sites while 440240 and 194549.6 had the lowest yield. Although sweetpotato can survive moisture stress

conditions, commercial root yields are significantly reduced (Laurie *et al*., 2009). Genotypes 194515.2 and 422656 had the highest foliage fresh yield under irrigation as well as high ability to produce high storage root yield under low moisture availability. Genotype 440286 experienced a huge reduction in vine production as well as root production emphasizing the fact that leaf expansion was severely reduced for light interception under moisture stress condition. Genotypes 401055 and 189135.9 had a higher mean number of commercial roots than the tolerant check at both sites under moisture stress condition. The number of non-commercial roots is important in sweetpotato production since it is positively correlated to the root yield (Lowe and Wilson, 1974). Selection for genotypes with higher number of non-commercial storage roots will allow piece meal harvesting; as the presence of small roots at the time of harvest indicates that there is continued potential for production (Ndolo *et al*., 1995).

6.8.2 Beta carotene

The ß-carotene range observed in deep orange and orange fleshed roots were similar to that found for other orange-fleshed varieties (6.7-128 mg/100g fresh weight) by Van Jaarsveld *et al*., (2004) for the variety Resisto (13.2 to 19.4 mg/100g, FW). The efficacy of the ß-carotene-rich orange-fleshed sweetpotato variety Resisto in improving the vitamin A status has recently been demonstrated in South African primary school children (Van Jaarsveld *et al*., 2005). Considering 12µg of ß-carotene to be equivalent to 1µg of retinal (IOM, 2001) and assuming 70% retention after boiling, 100g of the orange and deep orange roots evaluated in this study can provide between 50 and 200% of the RDI of vitamin A for children under five years old (450

µg RE/ day; FAO/WHO, 2002) and 100g of the intermediate orange roots can provide between 24 and 101% of this recommendation. The variation of the carotenoid concentrations may be explained by the color intensity of the primary or secondary colors of the fresh storage roots and the proportion the secondary color of the fresh storage roots.

6.8.3 Stress indices and genotype tolerance to drought

Stress index (STI), geometrical mean productivity index (GMP) and mean productivity index (MP) were positively correlated with yield under both conditions, suggesting that these parameters are suitable to screen drought tolerant, high yielding genotypes in both rain fed and irrigated conditions. Similarly Fernandez (1992); Mohammadi *et al*., 2003), Golabadi *et al*., (2006); Sio-SeMardeh (2006) and Mohammadi *et al*., (2010), found these parameters to be suitable for discriminating the best genotypes under stress and irrigated conditions.

In stress condition, storage root yield showed negative association with TOL and SSI. Similar observations were made by Gholipouri *et al*., 2009 and Bansal and Sinha (1991), in wheat grain yield. Therefore, TOL and SSI indices are suitable factors to identify sweetpotato genotypes with low yield and tolerant to drought because under stress yield decreased with increasing SSI. The genotypes with the lowest SI at Kiboko were 441725, 401055, 189135.9, 194515.2 and 440001 and 187017.1, 189135.9, 440287, 194549.6 and 440286 at Marigat and the same genotypes had the lowest SSI value. Therefore these genotypes had low drought susceptibility and high yield stability in both conditions Genotype. 440001 and

422656 for Marigat and genotypes 440286 and 189148.2 for Kiboko with SSI values higher than one were identified as high drought susceptible and having poor yielding ability.. Similar results were reported by Golabadi *et al*., (2006) and Talebi *et al*. (2009), who showed that SSI can be a more useful index in discriminating better genotypes under rain fed condition.

In the present study SSI and TOL were negatively correlated with Ys at both sites. Larger TOL and SSI values represent relatively more sensitivity to stress, thus smaller TOL and SSI values are favored for selecting genotypes with high yield potential under non-stressed conditions and low yield under stressed conditions (Fernandez, 1992).

In this study, genotypes 441725, 401055, 189135.9, 194515.2 and 440001 at Kiboko and 187017.1, 189135.9, 440287, 194549.6 and 440286 for Marigat had the lowest SSI value and therefore these genotypes had low drought susceptibility and high yield stability in both conditions.Genotypes440001 and 422656 at Marigat and genotypes 440286 and 189148.2 at Kiboko with SSI values higher than one were identified as high drought susceptible and poor yield stability genotypes.

6.8.4 Bi-plot analysis

Principal component analysis (PCA) was performed to assess the relationships between all indices at once. The results obtained from bi-plots confirmed correlation analyses. Thomas *et al*., (1996) observed that some 25 accessions of meadow fescue from seven countries investigated in four experiments could be distinguished based

on a bi-plot display. The observed relations were also in agreement with those reported by Fernandez (1992) in mungbean, Farshadfar and Sutka (2002) in maize and Golabadi *et al*., (2006) in durum wheat. In the present study, genotypes 420014,440286, 189148.2, 440287 and 44097 for Kiboko and genotypes 440286, 420014, 421006 and 189135.9 and 441725 for Marigat were identified as genotypes with good performance and high drought tolerant that could be grown in these areas

6.9 Conclusion

Moisture stress severely affected the agronomic performance of the genotypes evaluated Genotypes 420014, 440287 421066, 194573.9, 192033.3, 187017.1, 441724 and 189135 had high values for beta carotene and total root yield compared with the tolerant check. The same genotypes were observed to have the highest values of STI in both sites and could be considered tolerant genotypes. The genotypes that had low STI values like 422656, 440240, 440001 and 401055 were susceptible to water stress.

CHAPTER SEVEN

The evaluation of morphological traits and physiological processes responsible for drought tolerance in selected orange-fleshed sweetpotato genotypes

Abstract

Different cultivars may respond differently to limited quantities of soil water. There is need to rapidly screen sweetpotato genotypes for early identification of those that show drought tolerant traits. The experiment was conducted with an aim of identifying sweetpotato traits associated with water stress. The experiment was conducted in in pots placed in the greenhouse at the Kenya Plant Health Inspectorate Service, Quarantine Station, Muguga (located at1° 11' 0" South, 36° 39' 0" East at an altitude of about 1950m above sea level). The pot experiment was set up in a completely randomized design with five genotypes 194573.9, 421066, 189148.2, 441725, 194515.15 and one tolerant check Marooko, two water levels (stressed and unstressed) with three replications. A total of 216 pots were used, 108 for each treatment with each genotype grown in six pots per replication. Marooko was used as a tolerant check. Data was taken on soil moisture content of the soil by pot weight measurement; Relative water content of the leaves; leaf and stem growth characteristics; Morpho-physiological responses and relationship between relative parameters and available soil water. Statistical analyses were performed using the GLM procedure of SAS (SAS 1999).Under stress condition most of the genotypes had lower values for leaf number and leaf area than the well watered controls, indicating that drought induced premature leaves senescence and shedding. Among the six genotypes evaluated genotypes 421066 and 189148.2 had their leaf areas least

affected by moisture stress. Moisture stress severely reduced the total biomass production in all the genotypes. Genotypes 189148.2 and 194573.9 registered high biomass production although below that of the check. Least biomass production under stress treatment was observed for genotype 421066. Early loss of leaves upon the imposition of stress treatment were observed for genotype 189148.2 which begun to decline at fraction of available soil water (FASW) of 0.89. This suggests that the plant expansion process for sweetpotato defined by leaf number, leaf area is sensitive to water deficits. Genotypes 194573.9 and 189148.2 had biomass partitioning that favored root system development.

7.0 INTRODUCTION

Sweetpotato is a rich source of carbohydrates, vitamins and certain minerals and one of the most efficient plants in food production per unit area. The crop is widely grown in all SSA countries, where it serves the role of a classic food security crop and is often harvested as “piecemeal” over a period of several months. It is grown over a broad range of environments and cultural practices and is commonly grown in low-input agriculture systems (Prakash 1994). Drought is a very common a biotic stress condition, thus economically important crops with high levels of drought tolerance are of great value. Under field conditions, drought severity, timing and duration vary from year to year and a cultivar, which is successful in one year, might fail in another year. The unpredictable and variable forms in which drought stress manifests complicates the selection of superior plant material as well as the breeding programs. Significant potential exists for the improvement of crop productivity by selecting plants that are better equipped to cope with unfavorable environmental

conditions, such as drought. Plant water stress, often caused by drought, can have major impacts on plant growth and development. It is the main cause of lower yields and possible crop failure. Early recognition of water stress symptoms is critical to maintaining the growth of the crop. Sweetpotato is normally propagated from vine cuttings, and the development of adventitious roots is expected to be sensitive to soil moisture deficits immediately after planting. An adequate moisture supply is probably essential for promoting rapid and uniform root development and good stand establishment. During vegetative development of plants even minor stress can reduce the rate of leaf expansion and the leaf area at later stages of development. Although no published information on the effect of soil moisture content on cutting establishment could be found, various publications refer to the negative effect of water stress on growth and yield of sweetpotato. During vegetative development the leaf area index increases with increase in soil moisture (Enyi, 1977; Indira and Ramanujam, 1985; Chowdhury and Ravi, 1988).The storage root initiation period is the most sensitive to moisture deficit due to its effect on storage root number (Indira and Kabeerathumma, 1988; Nair and Nair, 1995; Ravi and Indira, 1996). Moisture deficits during the storage root initiation period induce liginification of adventitious root and hampers growth (Ravi and Indira, 1996).One approach to improve crop performance is to select for genotypes that have improved yield during water deficit conditions. The ability of some plants to maintain a higher yield under drought than others is of great value. Average losses of some major crop plants due to environmental stresses may amount to 50-80% of their genetically determined productivity. The highest proportion of yield losses can be directly attributed to drought. The drought related responses in plants are often of complex nature and

result from genomic re-organization and alterations in gene expression. Water stress occurs when roots cannot supply enough to satisfy evaporative demand of water transpiring from leaves. Plant genetics also can influence root growth and development, and subsequently water uptake, influencing location of roots relative to water in the soil (Batcherlor, 1998). Different crops have different water requirements and respond differently to water stress. Sensitivity to water stress varies from one growth stage to another. Yields of sweetpotato are affected by the amount of available water and the timing and distribution of its supply. It has been observed that drought approximately 40 days following planting causes the greatest reduction in yields (Bouwkamp, 1985). It seems that if sufficient moisture is supplied to a sweetpotato plant until it becomes well established, the plant is better able to withstand dry conditions later in the season. The plants can tolerate considerable periods of drought but yields are significantly reduced if water shortages occur 50 to 60 days after planting or when storage root initiation begins (Kay, 1985). Numerous studies indicate that the magnitude of yield reduction as a result of water stress depends to a lager extent on the growth stage at which it occurs (Ekanayake *et al*., 1988).

The plant is sensitive to water deficits, particularly during the establishment period including vine development and storage root initiation (Indira and Kabeerathumma, 1988). Sweetpotato is considered to be moderately drought tolerant (Valenzuela *et al.,* 2000). However, drought is often a major environmental constraint for sweetpotato production in areas where it is grown under rain fed conditions (Anselmo *et al*., 1998). Different cultivars may respond differently to limited

quantities of soil water. Sweetpotato needs adequate water at planting and for several weeks thereafter, but can tolerate moderate drought in the 2nd and 3rd month of growth (mid-season drought during storage root formation), and fairly severe drought in the 4th or 5th month (terminal drought) (Martin, 1988). Mid-season drought, during storage root thickening may reduce the number of storage roots produced, whereas terminal drought causes smaller storage roots. The various drought coping mechanisms that includes drought escape, avoidance and tolerance or a range of combinations of these may have different impacts on plant performance and yield maintenance under moisture stress conditions. Selection for good cultivar performance (growth rate; root development) under drought conditions is considered to be of major importance. There is need to evaluate sweetpotato genotypes for early identification of those that show drought tolerant traits for further testing under field conditions. The objectives of the experiment was to identify and evaluate traits associated with water stress in sweetpotato genotypes during growth period; Evaluate physical plant growth performance of sweetpotato genotypes under water stress condition during growth period and rate the sweetpotato genotypes for adaptation under water stress condition during plant growth under greenhouse condition.

7.1 Materials and Methods

7.1.1 Planting material and propagation

Planting material consisted of five orange-fleshed genotypes randomly selected from previous field drought screening trials and one drought tolerant local check Marooko (Table 7.1). Initiation and multiplication of the 6 genotypes was done as outlined in section 3.2.

Table 7. 1 Genotypes randomly selected for evaluation under greenhouse condition at PQS Muguga

Clone	Primary color	Secondary color	Beta-carotene mg/100g,FW	Vitamin A (µgRE/100g, FW
194573.9	Intermediateorange	Intermediate	4.92	4100
441725	Deep orange	Intermediate	11.03	919.2
189148.2	Intermediate	Intermediate	7.23	602.5
421066	Intermediate	Intermediate	4.92	410
194515.15	Pale yellow orange	Intermediate	1.38	115
Marooko	Cream	-	0.03	2.5

7.1.2 Experimental site and design

This experiment was conducted in the green house at Kenya Plant Health Inspectorate Service, Quarantine station, Muguga (located at1° 11' 0" South, 36° 39' 0" East at an altitude of about 1950m above sea level). The experiment design was completely randomized design with six genotypes among them a drought tolerant check and two water levels (stressed and unstressed) and three replications. During the establishment of the plants, the soil moisture was maintained at about 80% field capacity by watering all the pots. At 4 weeks after transplanting planting soil moisture in all pots was raised to 80%-90% pot water holding capacity (WHC). Thereafter, half of the pots received no more water while the rest were watered daily to maintain the soil moisture at 80%-90% WHC.

7.1.3 Planting details

Planting material of the six genotypes (among them a local check), and the check were obtained from nodal cuttings which were initially grown in Murashige and Skoog growth media (MS). These were later transferred to sterilized vermiculate soil in polythene bags in the screen house for further multiplication and bulking for 5 weeks before transplanting to 20 l plastic pot. The pots were filled with sterilized soil obtained from KEPHIS Muguga; The soil had gravimetric soil water content of 22.40 % and field capacity of 38.12 %. The plant cuttings with lower leaves removed were planted with 2 nodes below the surface area and 3 nodes above the soil surface to ensure uniformity of development.

a) b)

Figure 7. 1 Visible effect of water treatment (non-irrigated and irrigated treatment) on (a) genotype 441725 and (b) genotype194573.9 on morphology of sweetpotato genotypes under greenhouse growth conditions

The soil, a clay loam was first pulverized, cleaned of small pieces of stones and large plant residues. This was then heated in a soil boiler to 100ºC for 2 hours to get rid of soil pathogens and other pests. The empty plastic pots each measuring16 cm x 24 cm of gage 500 with a capacity of 20 kg were weighed individually and their empty weight recorded. The pots were then filled with 20kg of the sterilized soil; six pots for each treatment combination. These were left standing for 14 days to allow soil moisture to stabilize. Three soil samples (about 100 g each) were weighed and oven dried to a constant weight at 105ºC. The constant weights were then used to calculate the mean moisture content of the soil using the following formula:

MC= FW-ODW/ODW X 100, where: MC= Moisture content (%), FW= Fresh weight of soil (g), ODW= Oven dry weight of the soil (g).

To determine of soil field capacity 3 filled pots were selected and water was added gently but repeatedly for over 3 hours or so, until water started dripping from below. The pots were then covered firmly with polythene paper to avoid any evaporation for 48 hours. The weight of the pots at 100% field capacity was determined. The moisture content of the soil at field capacity was determined from three soil samples each 100g that were taken from the middle of each pot. These were dried to a constant weight at 105ºC. The constant weights were recorded and the following formula used to calculate the moisture content of the soil at field capacity:

MC (Moisture content (%) of the soil at field capacity = Weight of WS-weight of ODS/weight of ODSx100. The two values of moisture content were then used to

compute for the amount of water to add to the watered pots in order to maintain the soil at 80-90% field capacity

7.1.4 Data collected

7.1.4.1 Soil moisture content of the pots

The soil moisture was estimated by pot weight measurements. Water loss through transpiration was determined by weighing the pots every two days. The difference in weights between two consecutive measurements was considered as the water lost through transpiration. Water lost was returned through irrigation to the watered pots.

7.1.4.2 Relative water content of the leaves

The second or third leaf from the youngest leaf on the main stem, which was fully formed, was sampled from each treatment every 2 weeks at 11.00-13.00 h. These were quickly weighed to obtain the fresh weight then placed in distilled de-ionized water in a petri dish and left at 20°C in dim light for 24hours. The leaf weight was obtained after drying water from the surface of the leaves using absorbent paper. Thereafter the leaves were dried at 100°C to a constant weight to obtain the dry weight. RWC was computed as:

RWC%= [(FW-DW)/ (TW-DW)] x100.(Koide et al, 1989)

Where:

FW= fresh weight of the leaf;

TW= the turgid weight,

DW= the dry weight of the leaf.

The RWC of drought-stressed plants was divided by that of watered plants to give the RWC ratio.

7.1.4.3 Plant growth parameters

Main stem length (cm/ plant). This was recorded after every two weeks by measuring the plants in each treatment from the surface of the soil in the pot to the tip of the tallest leaf

Internodes' length (cm/plant)

Internode diameter (mm/ plant) were determined every 2 weeks using vernier caliper

Leaf growth parameters this was determined every 2 weeks

Leaf Area, Leaf length (L) and width (W) at the widest part for leaf numbers 5, 6 and 7 (numbering from the bottom along the main stem were measured and the product L x W used to compute for Leaf area (cm^2 /plant).

The number of leaves/plant. This was determined by counting the number of fully expanded leaves on each plant in all the treatments.

Leaf fresh weight (g/ plant).This was determined at harvest. The plants were cut at the base and then separated into leaves and stems. All the leaves were weighed to obtain leaf fresh weight per plant.

Root dry weight (g /plant)

Plant roots from each treatment were oven dried at 80°C for 72hrs.after which their weights were determined using a precision balance.

Total biomass (g/plant). This was determined by adding the total dry weight of the leaves, vines and roots.

Leaf dry matter content (g per plant)

The leaves were separated from the stem and dried at 100°C for 48 hours and then weighed again to obtain the dry weight.

Specific leaf area (SLA) (cm^2/ g)

This was calculated as leaf area divided by the leaf dry weight. The SLA of drought-stressed plants was then divided by that of watered plants to give the SLA ratio.

7.1.4.4 Final soil water content (g) per plant at time of harvest

This was determined at harvest by weighing each pot. Soil samples were taken from the pots at a depth of 30 cm using a soil auger. The soil samples were then dried at 105°C for 48 hours and the gravimetric soil water content (GW) determined and expressed on a dry weight basis: GW= FWT- DWT/ DWT Where: GW referred to

the gravimetric soil water content, FWT referred to the fresh weight of soil and DWT referred to the dry weight of soil.

7.1.4.5 The plant available soil water

This was expressed as the fraction of available soil water (FASW) for each pot in the drought-stressed plants. FASW at day i for each pot was calculated as:(FASW= GWat dayi- GW_{end} / GW100% - GW_{end}; where:GW_{end} referred to the gravimetric soil water content at the end of the experiment when plants wilted and GW80% refers to the gravimetric soil water content at 80% WHC.

7.1.5 Statistical analysis

Statistical analyses were performed using the general linear model(GLM) procedure of SAS (SAS 1999). Analyses of variance were done for leaf area, plant biomass, specific leaf area, relative water content, leaf number, internode length, Internode diameter leaf fresh and dry weight and specific leaf area. Differences at the P<Level was used as a test of significance and means separated using Tukey's t-test. When the effects of various treatments were found to be significant, post hoc comparisons were carried out using Bonferroni's method (NIST/SEMATECH, 2010).

The relationships between relative parameters, i.e. SLA ratio, RWC ratio, and fraction of available soil water (FASW) were developed using a linear plateau regression using the nonlinear procedure of SAS: Relative parameter = 1 if FASW > FASWt

Relative parameter = 1 + A × (FASW - FASWt) if FASW < FASWt

Where A is the slope of the linear decline, and FASWt is the FASW threshold at which the relative parameter began to decline.

R^2 values were calculated as: R^2= 1- SSE/CSE, where SSE is the sum of squares of the residue and CSE is the total corrected sum of squares

7.2 Results

7.2.1 Leaf growth and stem elongation

There were significant interactions between water treatments and genotypes for most of the parameters observed after every two weeks throughout the period of growth except internode length. This suggests that the general responses of the genotypes to the water treatments were statistically similar (Table 7.2). For parameters taken at harvest significant interaction for the treatment at 1% level were observed for leaf fresh weight, leaf dry weight root dry weight and total biomass (Appendices 8 and 9).

7.2.2 Internal vine diameter

In all cultivars increase in internal diameter grew significantly slower after water was withheld (Table 5). Internode diameter was slightly reduced in genotype 189148.2 and 194515.15 under stress condition although not significantly different from the check. Greatest reduction under the same treatment was observed for genotype 421066 (Table 6.2). Genotypes 441725 and 194573.9 showed a remarkable increase in internal diameter throughout the growth period under controlled condition. This ranged from 1.94 to 2.42mm (Table 6.2).

Table 7. 2 The internal vine diameter (cm) of 6 genotypes grown in a greenhouse at the Plant Quarantine Station, Muguga, Kenya

	Stress								No stress							
	Weeks after planting								Weeks after planting							
Genotype	2	4	6	8	10	12	14	16	2	4	6	8	10	12	14	16
441725	1.94	2.03	2.04	1.99	2.14	2.16	2.14	2.10	2.25	2.61	2.72	2.84	2.88	2.87	2.87	2.93
421006	1.94	1.97	2.09	2.18	2.33	2.33	2.35	2.34	2.23	2.32	2.28	2.51	2.56	2.50	2.58	2.61
194573.9	2.20	2.23	2.19	2.33	2.29	2.32	2.31	2.42	2.41	2.68	2.51	2.64	2.93	2.76	2.80	2.78
Marooko	2.33	2.27	2.39	2.35	2.33	2.33	2.33	2.32	2.25	2.50	2.56	2.54	2.75	2.72	2.76	2.73
189148.2	2.07	2.15	2.15	2.18	2.33	2.36	2.37	2.32	2.16	2.33	2.38	2.67	2.54	2.58	2.51	2.76
194515.5	2.20	2.17	2.20	2.32	2.28	2.27	2.34	2.34	2.17	2.33	2.45	2.50	2.48	2.54	2.60	2.63

LSD(0.05): Week= 0.11; Genotype= 0.09; treatment= 0.05; Genotype X treatment= 0.13

7.2.3 Stem Length

The reduction of stem length varied between well watered and to drought stress treatments. A gradual increase in stem length throughout the test period was observed for all the genotypes grown under irrigated treatment. Highest increase in stem length under the same treatment was observed for genotypes 194573.9, 189148.2 and 194573.9 and this ranged from 194.7 to 274 cm. (Table 7.3). An increase in stem length was observed in194573.9 and 421066 and the length of their stems ranged from 187.2cm to 217.1 cm. The greatest reduction in stem length was observed for genotype 194515.15.

Table 7. 3 Length of main stem (cm) of 6 genotypes grown in a greenhouse at the Plant Quarantine Station, Muguga, Kenya

	Stress								No stress							
	Weeks after planting								Weeks after planting							
Genotype	**2**	**4**	**6**	**8**	**10**	**12**	**14**	**16**	**2**	**4**	**6**	**8**	**10**	**12**	**14**	**16**
441725	161.2	162.7	172.5	178.6	177.6	169.5	167.2	158.3	171.4	180.2	186.3	208.7	218.1	226.7	227.1	236.2
421006	187.2	196.5	214.1	271.8	211.9	203	193.7	189.9	183	196.8	220.6	237.3	245.1	256.5	267.9	274
194573.9	189.7	199.2	203.5	211.3	219.1	224.9	217.1	210.1	194.7	201.2	212.8	219.2	238.3	243.5	251.7	256.2
Marooko	162.7	174.9	180.4	195.6	197.9	191.6	180.4	173.3	181.2	187.5	197.9	207.9	216.6	223.9	240	246.2
189148.2	168.3	173	177.3	181.8	192.3	185.6	180.2	174.5	178.9	187.4	217.9	228.9	236.5	245.9	250.2	254.1
194515.5	173.3	181.4	190.2	202.9	210.3	215.2	220.2	228.2	173.3	181.4	190.2	202.9	210.3	215.2	230.2	228.2

LSD(0.05): Week= 11.3; Genotype= 9.64; treatment= 5.56; week X treatment= 15.74; Genotype X treatment= 0.13

7.2.4 Number of leaves per plant

Leaf number for all the genotypes showed a decreasing trend four weeks after imposing the stress treatment. Genotypes that were observed to have least reduction in number of leaves under stress treatment were 441725 and 189148.2. Highest reductions in number of leaves under the same treatment were noted for genotypes 421066 and 194515.15. Under irrigated treatment all the genotypes exhibited gradual increases in number of leaves throughout the test period. This was 15.3 times more than those in stressed treatment. Outstanding genotypes that produced the highest number of leaves when well watered were 441725, and 412006 and this was significantly higher than that of Marooko (Table 7.4). The number of leaves in watered treatment increased overtime, while those of water stress treatment decreased.

Table 7. 4 Number of leaves in 6 genotypes evaluated at two water levels under greenhouse at the Plant Quarantine Station, Muguga, Kenya

	Stress								No stress							
	Weeks after planting								Weeks after planting							
Genotype	**2**	**4**	**6**	**8**	**10**	**12**	**14**	**16**	**2**	**4**	**6**	**8**	**10**	**12**	**14**	**16**
441725	158.3	159.9	151.3	131	104.2	91.6	78.3	42.3	171.9	167.1	198	227.5	276.4	356	532.3	633.6
421006	161.1	167.2	152.8	149.5	98.1	82.2	42.7	25.7	153.3	175	198.9	239.6	278.6	376.2	569.1	565.2
194573.9	174.5	169.1	155.8	134.8	110.4	92	49.7	30.7	157.9	179	197.9	226.2	265.4	299.7	391.4	420.4
Marooko	180.9	169.6	157.2	126.5	85.7	55.7	28.4	17.7	183.3	197.8	230.2	243.9	296.3	408.5	620	586
189148.2	192.2	185.8	176.6	176.8	137.1	94.1	82.8	60.4	165.9	185.4	213.1	257.3	299.1	368.3	499.4	558
194515.5	164.4	163.9	155.8	145.8	100.5	76.9	45.3	33.5	141.1	170.9	191.2	212.2	246.4	323.4	437.1	473.3

LSD(0.05): Treatment= 3.60; Week X treatment= 131.2

7.2.5 Leaf area

Leaf area increased in three genotypes 441725, 421006 and 194573.9 between 2nd and 4th week after onset of water stress treatment and thereafter decreased in all the genotypes. Conversely leaf area increased in well watered treatment up to 14 weeks. Stress treatment gradually reduced the leaf area for all the genotypes 6 weeks after imposing the treatment. Least reduction in leaf area was observed for genotypes 194573.9 and 421066. Genotype 194515.15 was observed to have the highest reduction in leaf area. For the irrigated treatment a gradual increase in leaf area was observed for all the genotypes throughout the testing period. Best performing genotypes under this treatment were noted for genotypes 421066 and 194573.9 (table 7.5).

Table 7. 5 Effect of water on leaf area (cm²/plant) of 6 genotypes grown in a greenhouse at the Plant Quarantine Station, Muguga, Kenya

	Stress								No stress							
	Weeks after planting								Weeks after planting							
Genotype	**2**	**4**	**6**	**8**	**10**	**12**	**14**	**16**	**2**	**4**	**6**	**8**	**10**	**12**	**14**	**16**
441725	162.2	153	146.8	135.3	121	118.3	97.7	95.7	163.5	175.9	183.6	194.4	229	235.3	248.8	240.3
421006	151.1	156.8	148.7	145.4	139.6	131.8	128.6	121.8	169	172.3	217.3	221.6	224.7	231.3	244.2	246.8
194573.9	157.5	174.6	167.8	159.2	147.7	135.7	128.7	120.1	171.8	173.6	186.6	228	237	252.9	261.2	265.7
Marooko	162.2	168.6	158	151.5	149.6	140.6	135.6	125.5	184.1	188.4	195.7	212.9	218.3	224.6	238.3	240.8
189148.2	171.7	157.7	150.7	150.7	132.7	122.3	117.7	112.3	170.6	182.2	186.8	214.1	224.9	236.5	240.9	249.4
194515.5	162.9	155.7	149	149.5	120.4	116.3	94.4	78.4	162.9	155.7	149	149.5	120.4	116.3	94.4	78.4

LSD(0.05): Week= 7.20; Genotype= 6.23; treatment= 3.60; week X treatment; Genotype X treatment= 8.81

7.2.6 Dry matter production and partitioning

There were no significant interaction between genotype and water levels on leaf dry weight, specific leaf weight and root dry weight. Stress severely reduced dry matter production in all the genotypes. Under severer stress treatment genotypes 189148.2 and 194573.9 recorded highest leaf fresh and dry weight although below that of Marooko (Table 7.6). Specific leaf area is an indicator of tolerance to drought in several crops and has been suggested as a selection criterion for breeding programs targeting low rainfall areas. Lower specific leaf area is due to thicker or more dense leaves. This contributes to long leaf survival, nutrient retention and protection from dessication (Mooney and Dunn 1970). Marooko had the highest specific leaf area followed 189148.2 and 194573.9. This implied that these genotypes had thick leaves, a trait that indicated tolerance to drought (Table 7.6).

There was significant root weight reduction under stress treatment for all the genotypes tested. Under the same treatment genotypes 194573.9 registered higher root weight of 9.86 that was above that of the check (7.32). Genotype 421066 exhibited the least root weight although production was higher under controlled treatment (Table 7.6).

The biomass produced under water stress was 370% to 470% lower than that under well watered condition. Genotypes 189148.2 and 194573.9 had high biomass production although below that of the check. Least biomass production under stress treatment was observed in genotype 421066 (Table 7.6)

Table 7. 6 Mean leaf fresh and dry weight (g /plant), specific leaf area(cm²/g), root dry weight (g /plat), total biomass (g /plant) for sweetpotato genotypes evaluated under in the greenhouse conditions under two water stress levels at Plant Quarantine station, Muguga, Kenya

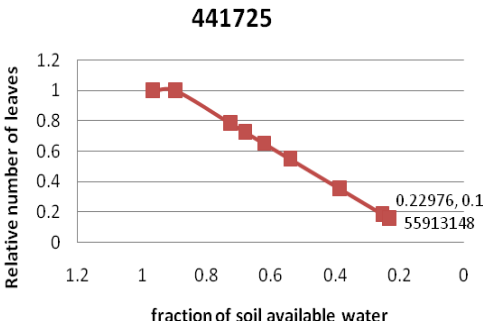
	Leaf fresh weight (g/plant)		Leaf dry weight (g/plant)		Specific leaf area (cm²/g)		Root dry weight (g/plant)		Total biomass (g/plant)	
Genotype	**Stress**	**No stress**	**Stress**	**No stress**	**Stress**	**No stress**	**Stress**	**No stress**	**Stress**	**No stress**
441725	19.17	108.40	5.23	15.68	0.20	0.45	5.23	15.68	40.55	165.79
421006	12.77	98.00	3.78	13.22	0.11	0.40	3.78	13.22	29.49	137.72
194573.9	29.91	139.85	9.86	27.81	0.25	0.53	9.86	27.81	64.36	215.77
Marooko	35.00	156.03	7.32	29.45	0.29	0.65	7.32	29.45	73.82	272.11
189148.2	24.66	130.09	7.58	22.81	0.24	0.58	7.58	22.81	50.39	191.42
194515.15	17.72	94.69	5.69	7.53	0.23	0.39	5.69	7.53	33.26	125.85
$LSD_{(0.05)}$	**22.69**		**7.75**		**0.12**		**7.75**		**27.63**	

7.3 Plant characteristics and soil moisture extraction

7.3.1 Leaf number per plant, Leaf Area per plant

The leaf number per plant and leaf area per plant in drought stressed treatment relative to the plants in the watered treatment showed significant variation at point of decline with respect to the fraction of soil available water across the genotypes. Relative number of leaves remained close to one until the fraction of available soil water (FASW) declined between 0.97-0.73 when it declined linearly (Figure 7.2). Genotypes 194515.15 and 421066 were observed to be less sensitive to moisture stress by maintaining relative number of leaves closer to 1 until FASW fell between range of 0.80- 0.73 which was not different from that of the check Marooko (0.77). No clear decline trend for relative leaf area was observed for genotypes 441725, 421066 and 189148.2. The relative leaf area for genotypes 194515.15 and 194573.9 remained close to 1.0 until the fraction of available soil water (FASW) fell below the range of 0.59 –7.97 when it began to decline linearly (Figure 7.3). Most sensitive genotype to moisture stress with respect to relative leaf area was observed for genotype 194573.9, the decline occurred at a much higher FASW value of 0.84 compared with that of the check that occurred at a value of 0.72.

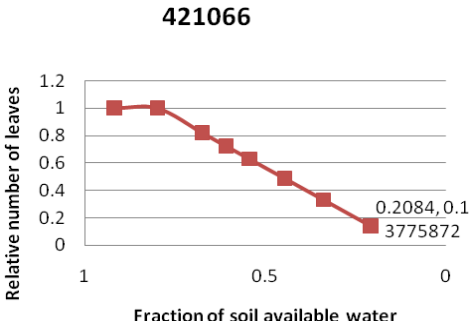
Leaf Number



FASWt=0.80(0.65-0.95)

A= 1.46(0.95-1.96)

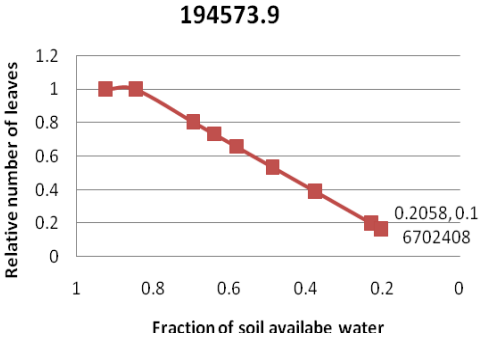
R^2= 0.97



FASWt=0.80(0.65-0.95)

A= 1.46(0.95-1.96)

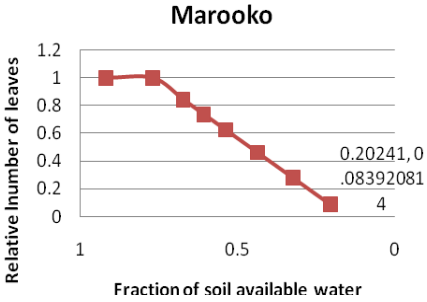
R^2= 0.97



FASWt=0.75(0.56-0.95)

A=0.36(0.18-0.54)

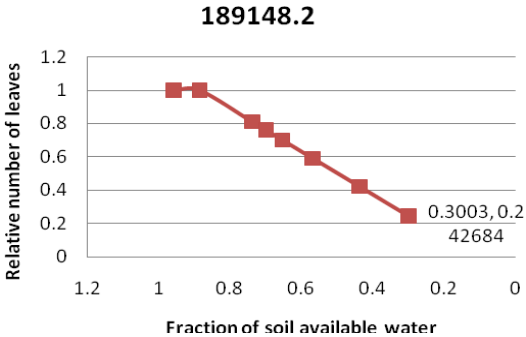
R^2= 0.99



FASWt= 0.67(0.42-0.93)

A=0.26 (0.08-0.45)

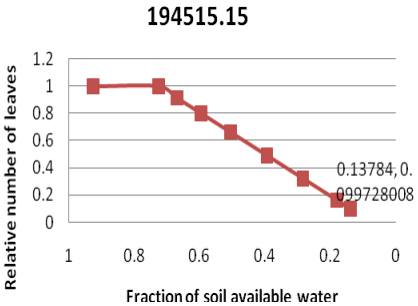
R^2= 0.99



FASWt=0.85(0.69-0.99)

A=1.30(0.87-1.73)

R^2= 0.98



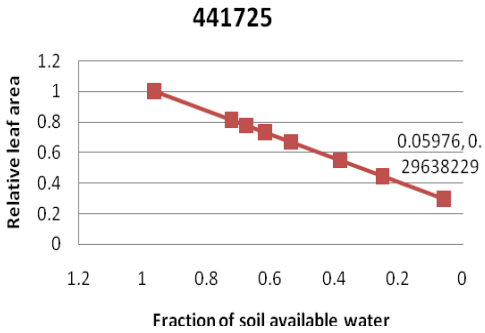
FASWt= 0.77(0.53-1.0)

A=1.6 (0.69-0.89)

R^2= 0.93

Figure 7. 2 The relative number of leaves as a function of soil available water for sweetpotato genotypes grown in the greenhouse

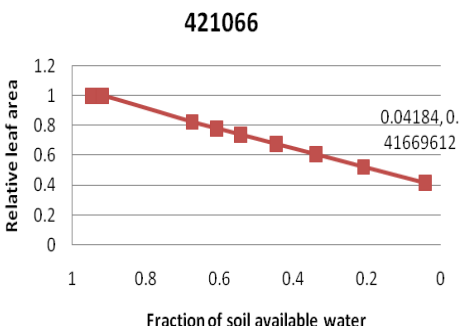
Leaf Area



FASWt=0.97 (0.70-1.23)

A= 0.78((0.40-1.15)

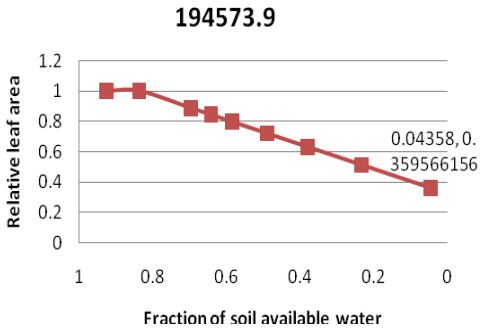
R²= 0.99



FASWt=0.95(0.68-1.22)

A= 0.64(0.32-0.96)

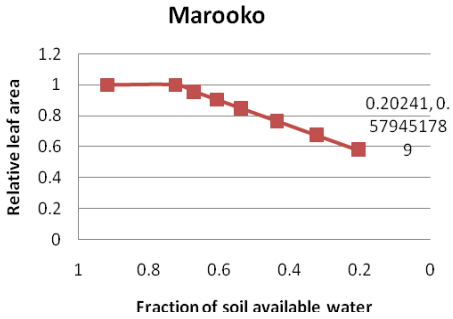
R²= 0.79



FASWt=0.84(0.60-1.074)

A=0.81(0.39-1.23)

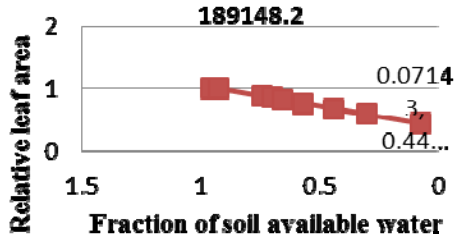
R²= 0.99



FASWt= 0.72(0.599-0.85)

A=0.81 (0.54-1.07)

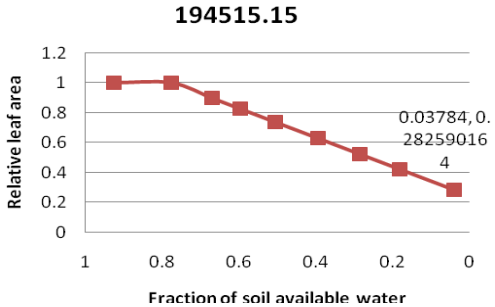
R²= 0.99



FASWt= 0.92(0.63-1.12)

A= 0.70(0.27-1.11)

R²= 0.99



FASWt=0.80(0.69-0.91)

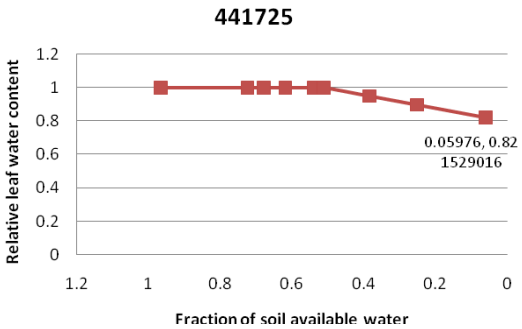
A= 0.97(0.74-1.19)

R²= 0.99

Figure 7. 3 The relative leaf area as a function of soil available water for sweetpotato genotypes grown in the greenhouse

7.3.2 Relative water content (RWC)

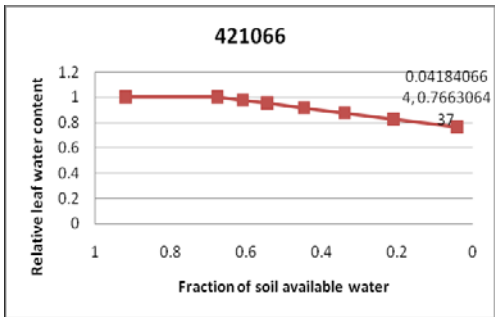
Interaction between the genotypes and water levels for relative water content varied across the genotypes. Late decline at a fraction of soil available water of 0.51 were observed for genotypes 441725, 189148.2 and 194515.15, indicating their ability to maintain high leaf turgidity for a longer period of time under stress condition. Genotype 194573.9 was observed to be sensitive to stress as it showed an earlier decline relative to the check at a fraction of soil available water of 0.73 (Figure 7.4)



FASWt=0.51 (0.30-0.73)

A= 0.40(0.121-0.67)

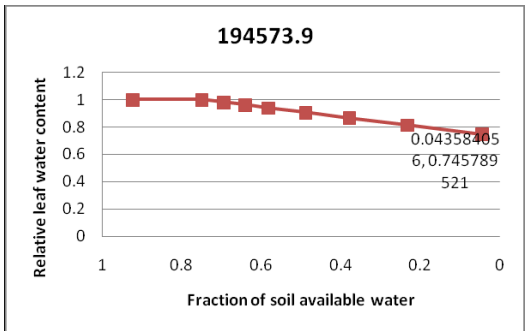
R^2= 0.99



FASWt=0.68 (0.42-0.94)

A= 0.37(0.71-0.63)

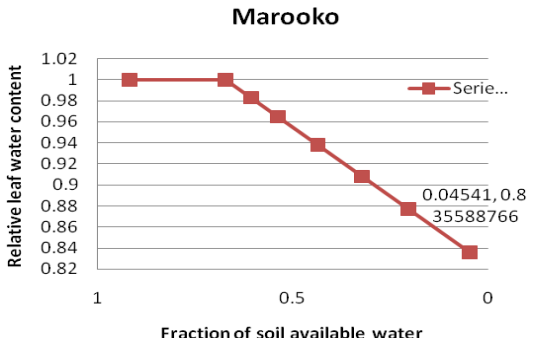
R^2= 0.99



FASWt=0.75(0.56-0.95)

A=0.36(0.176-0.54)

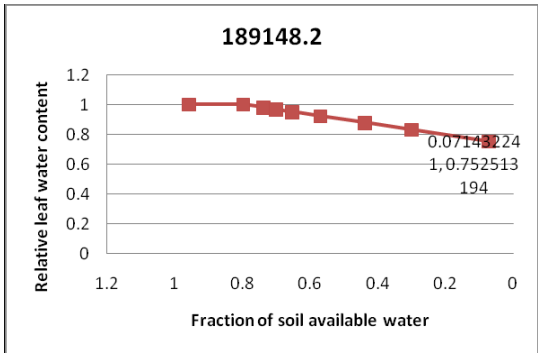
R^2= 0.99



FASWt= 0.67(0.42-0.93)

A=0.26 (0.08-0.45)

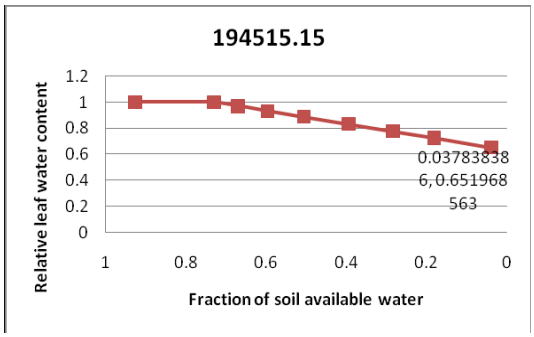
R^2= 0.99



FASWt= 0.80(0.64-0.96)

A= 0.34(0.20-0.49)

R^2= 0.99



FASWt=0.73(0.33-0.68)

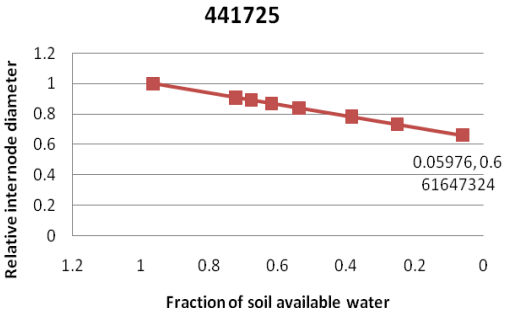
A= 0.50(0.33-0.68)

R^2=0.99

Figure 7. 4 The relative leaf water content as a function of soil available water for sweetpotato genotypes grown in the greenhouse

7.3.3 Vine growth characteristics and soil water extraction

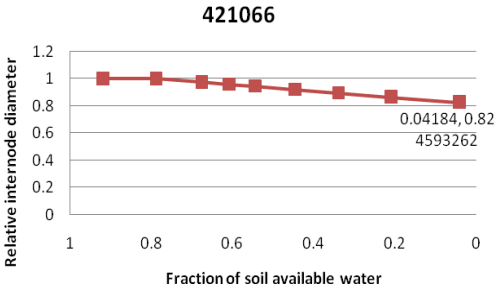
Relative internode diameter, main stem length and internode length as a plateau function of the fraction of available soil water varied across the genotypes. Internode diameter of the drought stressed plants relative to the watered ones for genotypes 194573.9 and 194515.15 begun to decline at a fraction of soil available water of 0.64- 0.733 indicating their ability to maintain increase in diameter under prolonged moisture stress condition (Figure 7.5). The same trend was observed for main stem growth and internode length increase. However genotypes 441725 and 194515.15 showed and outstanding ability to increase in stem growth and internode length as water deficit intensified with FASW threshold of 0.51-0.58 for main stem length and 0.26-0.68 for internal diameter (Figure 7.6 and Figure 7.7).



FASWt= 0.37 (0.01-0.74)

A= 0.97((0.46-1.47)

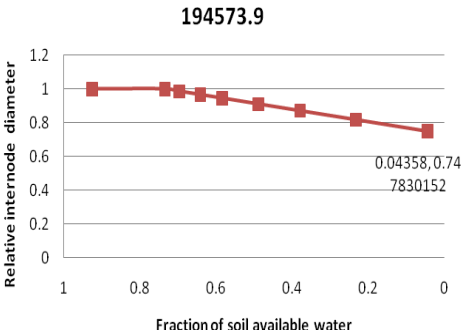
R^2= 0.66



FASWt=0.79(0.54-1.04)

A= 0.24(0.10-0.37)

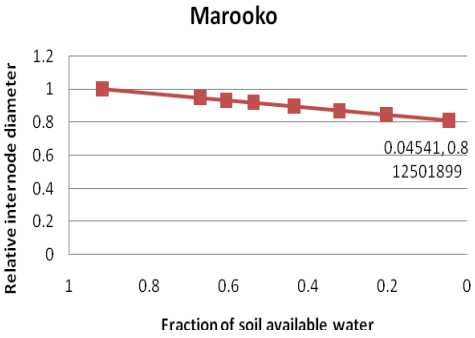
R^2= 0.99



FASWt=0.73(0.54-0.93)

A=0.37(0.17-0.56)

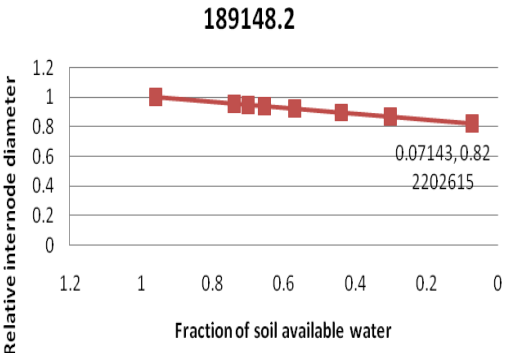
R^2= 0.99



FASWt= 0.92(0.40-1.43)

A= 0.21(0.02-0.41)

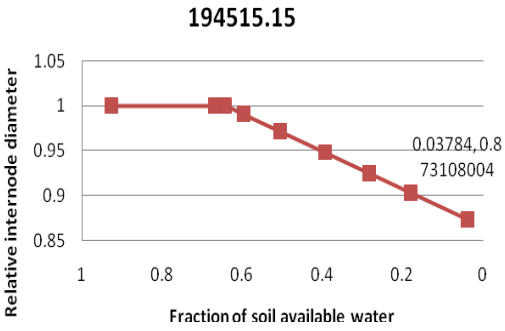
R^2= 0.99



FASWt= 0.96(0.20 - 2.12)

A= 0.20(0.28-0.68)

R^2= 0.34

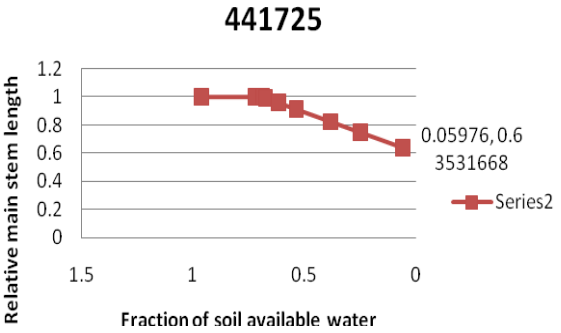


FASWt=0.64(0.31-0.97)

A= 0.21(0.02-0.40)

R^2= 0.99

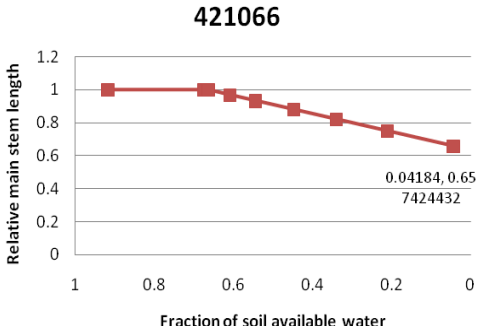
Figure 7. 5 The relative internode diameter as a function of soil available water for sweetpotato genotypes grown in the greenhouse



FASWt=0.58 (0.38-0.78)

A= 0.69((0.57-0.81)

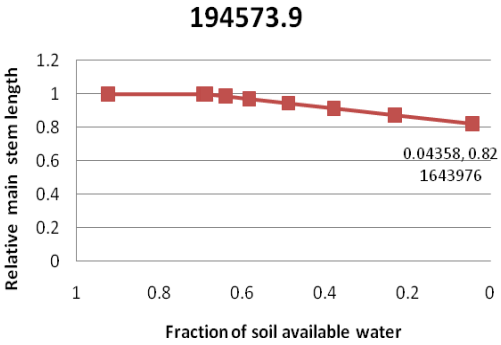
R^2= 0.99



FASWt= 0.67 (0.56-0.77)

A= 0.56 (0.39-0.71)

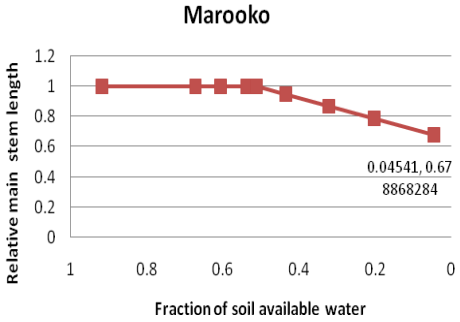
R^2= 0.99



FASWt=0.69(0.21-0.35)

A=0.28(0.21-0.35)

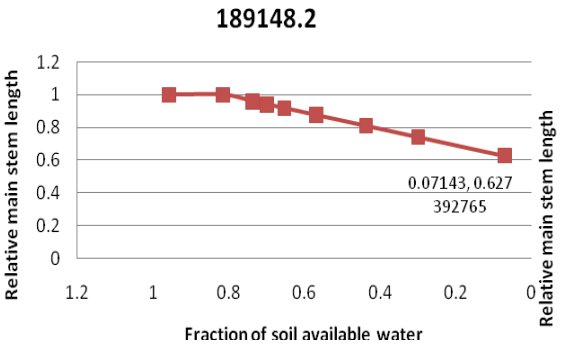
R^2= 0.99



FASWt= 0.51(0.43-0.60)

A=0.69 (0.49-0.89)

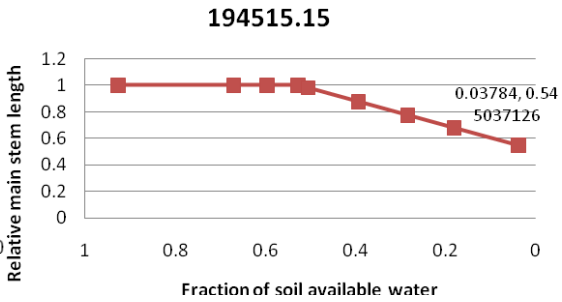
R^2= 0.99



FASWt=0.53(0.36-0.69)

A= 0.93(0.41-1.45)

R^2= 0.99

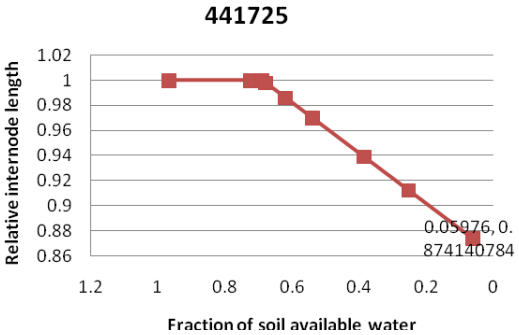


FASWt= 0.53(0.36-0.69)

A=0.93(0.41-1.45)

R^2=0.99

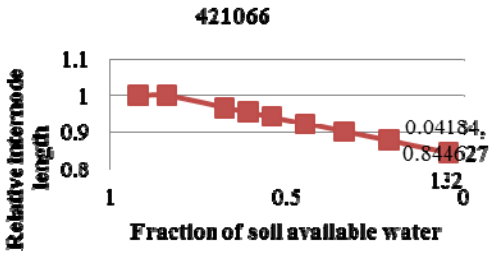
Figure 7. 6 The relative main stem length as a function of fraction of soil available water for sweetpotato genotypes grown in the greenhouse



FASWt=0.69(0.47-0.90)

A= 0.20((0.074-0.33)

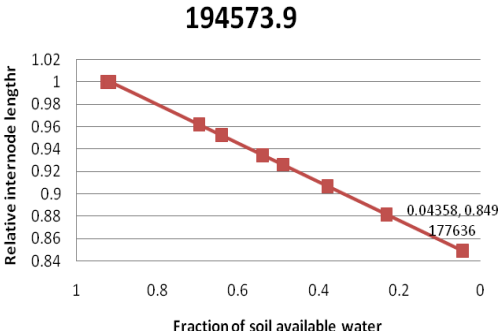
R²=0.99



FASWt=0.84(0.52-1.16)

A= 0.20(0.06-0.33)

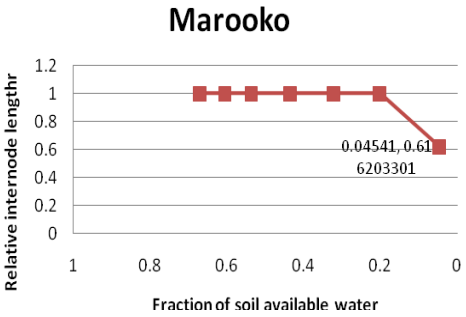
R²= (0.99)



FASWt=0.92(0.45-1.34)

A=0.17(0.02-0.33)

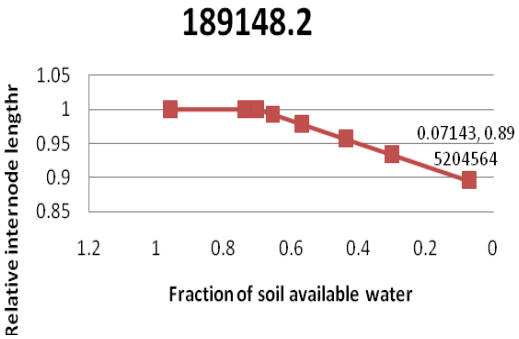
R²= 0.99



FASWt= 0.26(0.146-0.38)

A=0.84 (0.23-1.46)

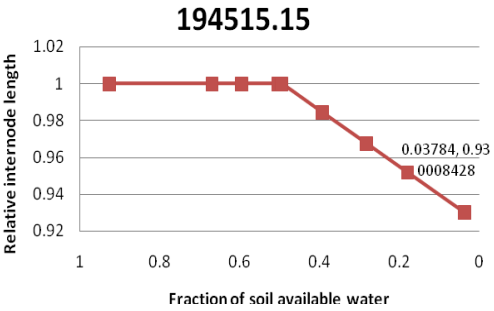
R²= 0.99



FASWt= 0.70(0.30-0.37)

A= 0.17(0.0321-0.075)

R²= 0.99



FASWt=0.50(0.21-0.51)

A= 0.15(0.21-0.51)

R²= 0.99

Figure 7. 7 The relative internode length as a function of fraction of soil available water for sweetpotato genotypes grown in the greenhouse

7.4 Discussion

7.4.1 Leaf area number and specific leaf area

Development of optimal leaf area is important to photosynthesis and dry matter yield. Leaf growth is one of the first physiological processes affected by changes in plant water status under drought. A decrease in leaf expansion rate usually precedes any reduction in stomatal conductance or photosynthesis. Water deficit mostly reduced leaf growth and in turn the leaf area, this is in agreement with observation made in other species of plant like *Populus* (Wullschleger *et al*., 2005), soybean (Zhang *et al*., 2004) and many other species (Farooq *et al*., 2009).Stress can alter leaf structure considerably. Leaves from stressed plants usually reach apparently smaller final sizes and their cytological structure can be altered in comparison to controls (Heckenberger *et al*., 1998; Granier and Tardieau, 1998). The dynamic of the stress interacts with the dynamic of the development of structure and function in growing tissues, resulting in very different responses to stress in leaves of different developmental situations (Roggatz *et al*., 1999).

7.4.2 Stem growth

Plant growth usually decreases, as soil water availability becomes more limited due to turgor loss in expanded cells (Kirnak *et al*., 2001). Reduction in internal diameter observed under stress treatment was in agreement with the findings of Kirnak *et al*., 2001) who showed that water stress reduced both stem height and internode diameter in eggplants by 46 % and 51 % under 40 % field capacity compared to the control (100% field capacity). Water stress greatly suppresses cell expansion and cell growth due to the low turgor pressure. Osmotic regulation can enable the maintenance of cell

turgor for survival or to assist plant growth under severe drought conditions (Shao *et al*., 2008). The reduction in plant height was associated with a decline in the cell enlargement and more leaf senescence (Bhatt and Srinivasa Rao, 2005).

7.4.3 Biomass partitioning

Severe drought negatively affected the accumulation of fresh and dry weight for all the genotypes. Severe drought induced premature leaves senescence and shedding that resulted to fewer leaf numbers for most of the genotypes. Leaf dry matter reflects a fundamental trade off in plant functioning between a rapid production of biomass (high specific leaf area, low leaf dry matter content) and an efficient conservation of nutrients (low specific leaf area, high leaf dry matter content, Garnier *et al*.2001). In the controls, genotype 194573.9 and 189148.2 produced higher leaf dry matter content, specific leaf area although slightly lower than that of the check; similar observation was made for the same genotypes under stress condition.

Under stress condition most of the genotypes had lower values for leaf number and leaf area than the well watered controls, indicating that drought induced premature leaves senescence and shedding. Among the six genotypes evaluated genotypes 421066 and 189148.2 had their leaf areas least affected by moisture stress. This could be ascribed to their low stomatal conductance, which enabled the plants to control water status restrictively when water uptake by the root was curtailed as soil dried. Great reduction in the length and width of the leaf and accordingly reduction in the area of the leaf, reduction in the plant height and internal diameter, all

contribute to the reduction of plant's evaporation area and consequently reduction in the produced dry matter.

Soil moisture changes not only affect the plant biomass dry matter weight but also the distribution of assimilates to the roots and shoots (Amdt *et al*., 2001) In this experiment genotypes 194573.9 and 189148.2 had biomass partitioning that favored root system development. This has been observed to be beneficial as it allows an adequate water supply longer during the dry period (Tuomela *et al.,* 2001). A higher root:shoot ratio in dry sites has been observed to be beneficial as it allows adequate water supply longer during the dry season (Tuomela *et al*.,2001). Genotype 421066 was observed to have the least root biomass partitioning under stress condition.

Plant dry weight was reduced by watered deficit by almost 2-folds, which could be attributed to the large reductions of leaf area. Leaf area is important in light interception and hence dry matter production (Jones, 1992).In addition, plants under drought stressed conditions tended to allocate more dry matter to the roots than those in watered conditions as shown by the higher root to shoot ratios in in all the genotypes.

7.4.4 Fraction of available soil water and relative growth

Early loss of leaves upon the imposition of stress treatment were observed for genotype 189148.2 which begun to decline at FASW of 0.89. This suggests that the plant expansion process for sweetpotato defined by leaf number, leaf area is sensitive to water deficits. This observation is opposite to that observed in other crops like in

pea (*Pisum sativum* L.), tomato (*Lycopersicon esculentum*; sorghum (*Sorghum bicolor* (L.) Moench), (Rosenthal *et al*. 1987; Lecoeur and Sinclair 1996; Sobeih *et al*., 2004), where higher threshold ranges of 0.40-0.45 were noted while for sunflower (*Helianthus annuus* L.), the thresholdwas in the range of 0.5-0.8 (Sadras *et al*., 1993).

Relative water content (RWC) provides a measure of the leaf water status. The well watered plants maintained a RWC above 85% which is reported to be the range for sweetpotato plants that is well watered (Ramirez, 2009). Stress development within the leaves for all the genotypes coincided with the fraction of available soil moisture (FASW) range 0.43-0.93. Leaf expansion and stem elongation began to decline at higher FASW range (0.36-0.69) than RWC. It appears that the reaction of the expansive processes could have been triggered by causes other than changes in RWC.

7.5 Conclusion

All the genotypes showed variations in adaptive responses to water deficit despite having differences in individual leaf size, leaf number, stem and root growth characteristics. The genotypes responded to water deficit mainly by large reduction in leaf area attributed to reduction in expansive processes i.e. individual leaf expansion and stem elongation, and leaf appearance. Severe drought reduced accumulation of fresh and dry weight for all the genotypes. Severe drought induced premature leaves senescence and shedding that resulted to fewer leaves in most of the genotypes. Early loss of leaves upon the imposition of water stress were observed

in genotype 189148.2 which begun to decline at fraction of available soil water (FASW) of 0.89. Among the 6 sweetpotato genotypes evaluated 421066 and 194515.15 had their leaf areas least affected by moisture stress. Genotypes 194573.9 and 189148.2 had biomass partitioning that favored root system development under moisture stress conditions allowing adequate water supply for a longer time during the dry spells. Least biomass production under stress treatment was observed in genotype 421066. This suggests that the plant expansion process for sweetpotato defined by leaf number, leaf area is sensitive to water deficits.

CHAPTER EIGHT

8.0 GENERAL CONCLUSIONS

In vitro screening method using PEG (6000) was found to be an efficient and simple enough to be used for evaluation of drought tolerance of a large number of sweetpotato genotypes in a very short time. It can also be used for identification and selection of tolerant and sensitive genotypes needed for improvement.

At Kiboko genotypes 420014, 440286, 189148.2, 440287 and 441097 for Kiboko, while at Marigat genotypes 440286, 420014, 421006 and 189135.9 and 441725 showed high levels of tolerance. Genotypes 189135.9, 194573.9 and 441725 had higher commercial root yield under severe moisture conditions Marigat and Kiboko. Genotypes 420014, 440287 421066, 194573.9, 192033.3, 187017.1, 441724 and 189135 had high beta carotene, a precursor for vitamin A.

The β-carotene content was associated with storage root flesh color. It was also found that the intensity of the orange-flesh color was negatively related with dry matter content but positively related to beta carotene. In this screening trial variation in root yield among the genotypes was either due to the difference in the number of storage roots per plant or size of individual roots or difference in bulking rate.

Yield potential (Yp) and stress yield (Ys) had highly significant positive correlation coefficients with Stress Tolerance Index (STI), Mean Productivity (MP) and Geometric Mean Productivity (GMP). These indices can be used for screening drought tolerance in sweetpotato genotypes. Severe drought reduced fresh and dry

weight, the number of leaves/plant and increased root: shoot ratio, increased the number of unmarketable storage roots. Soil moisture changes not only affect the plant dry biomass but also the distribution of assimilates to the roots and shoots.

8.1 Recommendations

It is recommended that finger printing be done for the genotypes screened and evaluated to identify duplicate accessions to create core sub-sets for the 20 genotypes evaluated and facilitate the selection of parents that are drought tolerant and have broad genetic base for breeding program.

It is also recommended that the best six genotypes identified from this study namely 420014, 440286, 421006, 189135.9, 441725 and 189148.2 be entered for NPT trials managed by KEPHIS to facilitate their official release to farmers.

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APPENDICES

Appendix 1 Sweetpotato genotypes with contrasting drought tolerance, beta-carotene and mineral content levels received from Lima, Peru

	CIP Number	Genotype Name	Female Parent	Male Parent	Form	Number Sent	Genus
1	187003.1	NACIONAL	RCB IT-57	PC	In-vitro	2	Ipomoea
2	187016.2	COSTANERO	YORUMBA DLP 339	PC_SALT 87	In-vitro	2	Ipomoea
3	187017.1	SALYBORO	RCB IF- 49	PC_SALT 87	In-vitro	2	Ipomoea
4	189121.14		YM89.071	PC	In-vitro	2	Ipomoea
5	189123.68		YM89.074	PC	In-vitro	2	Ipomoea
6	189135.9		YM89.110	PC	In-vitro	2	Ipomoea
7	189140.32		YM89.117	PC	In-vitro	2	Ipomoea
8	189141.4		YM89.118	PC	In-vitro	2	Ipomoea
9	189148.18		YM89.133	PC	In-vitro	2	Ipomoea
10	189148.21		YM89.133	PC	In-vitro	2	Ipomoea
11	189148.65		YM89.133	PC	In-vitro	2	Ipomoea
12	189150.1		YM89.146	PC	In-vitro	2	Ipomoea
13	189151.38		YM89.150	PC	In-vitro	2	Ipomoea
14	189165.37		YM89.239	PC	In-vitro	2	Ipomoea
15	190083.9		SR90.015	PC	In-vitro	2	Ipomoea
16	190094.28		SR90.322	PC	In-vitro	2	Ipomoea

Appendix 1 cont.

	CIP Number	Genotype Name	Female Parent	Male Parent	Form	Number Sent	Genus
17	190094.52		SR90.322	PC	In-vitro	2	Ipomoea
18	192033.5		NCSU 240	PC92_5 NACIONAL	In-vitro	2	Ipomoea
19	194515.15		SR93.048	PC	In-vitro	2	Ipomoea
20	194521.2		SR93.062	PC	In-vitro	2	Ipomoea
21	194539.36		SR93.103	PC	In-vitro	2	Ipomoea
22	194541.45		SR94.161	PC	In-vitro	2	Ipomoea
23	194549.6		SR94.226	PC	In-vitro	2	Ipomoea
24	194555.7		SR93.260	PC	In-vitro	2	Ipomoea
25	194569.1		SR94.294	PC	In-vitro	2	Ipomoea
26	194573.9		SR94.437	PC	In-vitro	2	Ipomoea
27	400011	Santo Amaro			In-vitro	2	Ipomoea
28	401055	Camote Blanco			In-vitro	2	Ipomoea
29	401430	Morada			In-vitro	2	Ipomoea
30	420001	Paramongui.Naranja Oscuro			In-vitro	2	Ipomoea
31	420014	Jonathan	Nemañete (Sd16-80)	DC 79	In-vitro	2	Ipomoea
32	420027	Zapallo			In-vitro	2	Ipomoea
33	420064	Paramonguino			In-vitro	2	Ipomoea
34	421066	Paramonguino NP-47			In-vitro	2	Ipomoea
35	421111	Mochero			In-vitro	2	Ipomoea
36	422656	Huambachero			In-vitro	2	Ipomoea
37	440001	Resisto	W-72	OP	In-vitro	2	Ipomoea
38	440008	W - 213			In-vitro	2	Ipomoea

Appendix 1 cont.

	CIP Number	Genotype Name	Female Parent	Male Parent	Form	Number	Genus
39	440017	W - 222			In-vitro	2	Ipomoea
40	440019	W - 224			In-vitro	2	Ipomoea
41	440021	W - 226			In-vitro	2	Ipomoea
42	440023	W - 228			In-vitro	2	Ipomoea
43	440024	Yanshu 1	NANCY HALL	OKINAWA 100	In-vitro	2	Ipomoea
44	440025	Xushu 18			In-vitro	2	Ipomoea
45	440027	Ningshu 1	HENJIN	LIZIXIANG	In-vitro	2	Ipomoea
46	440029	Feng Shou Bai	PENGWEI	LIZIXIANG	In-vitro	2	Ipomoea
47	440031	Jewel	CENTENNIAL	NUGGET	In-vitro	2	Ipomoea
48	440034	Mohc			In-vitro	2	Ipomoea
49	440050	Pepa			In-vitro	2	Ipomoea
50	440093	NCSU 1560			In-vitro	2	Ipomoea
51	440104	Porto Rico			In-vitro	2	Ipomoea
52	440131	Naveto			In-vitro	2	Ipomoea
53	440132	Beauregard	L8-21	PC	In-vitro	2	Ipomoea
54	440166	Tanzania			In-vitro	2	Ipomoea
55	440167	Wagabolige			In-vitro	2	Ipomoea
56	440170	Kemb 37			In-vitro	2	Ipomoea
57	440240	Kokei No. 14			In-vitro	2	Ipomoea
58	440283	BIS 50			In-vitro	2	Ipomoea
59	440286	VSP 1			In-vitro	2	Ipomoea
60	440287	VSP 3			In-vitro	2	Ipomoea
61	440328	AVRDC-CN 1840-284			In-vitro	2	Ipomoea
62	440362	WV 5 (ACC 172)			In-vitro	2	Ipomoea
63	440378	85022-12			In-vitro	2	Ipomoea

Appendix 1 cont.

	CIP Number	Genotype Name	Female Parent	Male Parent	Form	Number	Genus
64	440394	AVRDC-CN 1842-195			In-vitro	2	Ipomoea
65	440396	BNAS White			In-vitro	2	Ipomoea
66	440429	Blesbok			In-vitro	2	Ipomoea
67	440643	Red Variety			In-vitro	2	Ipomoea
68	441097	Ck - Sono			In-vitro	2	Ipomoea
69	441538	Tenian			In-vitro	2	Ipomoea
70	441724	Cuitzeo			In-vitro	2	Ipomoea
71	441725	Tucumana Mantecosa			In-vitro	2	Ipomoea
72	441755	IB 90.10.20			In-vitro	2	Ipomoea
73	441768	SPK 004			In-vitro	2	Ipomoea

Appendix 2 Genotypes screened in the tissue lab using PEG and 1st rapid screening at KARI, Kiboko

	CIP Number	Genotype Name	Female Parent	Male Parent
1	187016.2	COSTANERO	DLP 339	PC_SALT 87
2	187017.1	SALYBORO	RCB IF- 49	PC_SALT 87
3	189123.68		YM89.074	PC
4	189135.9		YM89.110	PC
5	189140.32		YM89.117	PC
6	189148.21		YM89.133	PC
7	189148.65		YM89.133	PC
8	189150.1		YM89.146	PC
9	189151.38		YM89.150	PC
10	192033.5		NCSU 240	PC92_5 CIONAL
11	194515.15		SR93.048	PC
12	194521.2		SR93.062	PC
13	194539.36		SR93.103	PC
14	194541.45		SR94.161	PC
15	194549.6		SR94.226	PC
16	194555.7		SR93.260	PC
17	194569.1		SR94.294	PC
18	194573.9		SR94.437	PC
19	400011	Santo Amaro		
29	401055	Camote Blanco		
21	420001	Paramongui.Naranja Oscuro		
22	420014	Jonathan	Nemañete (Sd16-80)	DC 79
23	420027	Zapallo		
24	420064	Paramonguino		
25	421066	Paramonguino NP-47		
26	421111	Mochero		
27	422656	Huambachero		
28	440001	Resisto	W-72	OP
29	440017	W - 222		

Appendix 2 cont.

	CIP Number	Genotype Name	Female Parent	Male Parent
30	440023	W - 228		
31	440024	Yanshu 1	NANCY HALL	OKINAWA 100
32	440025	Xushu 18		
33	440027	Ningshu 1	HENJIN	LIZIXIANG
34	440031	Jewel	CENTENNIAL	NUGGET
35	440034	Mohc		
36	440050	Pepa		
37	440104	Porto Rico		
38	440131	Naveto		
39	440132	Beauregard	L8-21	
40	440166	Tanzania		
41	440167	Wagabolige		
42	440170	Kemb 37		
43	440240	Kokei No. 14		
44	440286	VSP 1		
45	440287	VSP 3		
46	440328	AVRDC-CN 1840-284		
47	440378	85022-12		
48	440394	AVRDC-CN 1842-195		
49	440396	BNAS White		
50	440429	Blesbok		
51	440643	Red Variety		
52	441097	Ck - Sono		
53	441538	Tenian		
54	441724	Cuitzeo		
55	441725	Tucumana Mantecosa		
56	441755	IB 90.10.20		
57	441768	SPK 004		
58	Marooko	Local check		
59	K566632	Local check		

Appendix 3 Summarized analysis of variance table showing mean square values for various variables measured during the in vitro drought screening of sweetpotato genotypes evaluated at Plant Quarantine station, Muguga

Source of variation	Root length (cm)	Root dry weight (g)	Shoot length (cm)	Shoot fresh weight (g)	Shoot dry weight (g)	Leaf area (cm2)
Genotype	907.9**	20.88**	135.22**	14.19**	3.52**	27.24**
Salt level	1889.3**	10.33**	195.03**	45.53**	7.07**	90.59**
genotype* salt	907.9**	1.77**	18.52**	9.50**	8.02**	7.96**

**=significant at P < 0.001; * Significant at P< 0.005

Appendix 4 Nutrient analysis for soil samples taken from Kiboko experimental screening sitesbefore planting during 2007 long rains

	Nutrient amount	
Parameter	**Value**	**inference**
Soil pH	7.31	Alkaline
Acidity Exchange me (%)	-	-
Total Nitrogen (%)	0.06	Low
Organic Carbon (%)	1.04	Low
Phosphorus (ppm)	73	High
Potassium (me %)	0.69	adequate
Calcium me (%)	5.5	adequate
Magnesium (me %)	2.60	adequate
Manganese (me %)	0.38	adequate
Copper (ppm)	1.76	adequate
Iron (ppm)	23.8	adequate
Zinc (ppm)	7.15	Low
Sodium (me %)	0.56	adequate
El. Condu.(mS/cm)	0.40	adequate

Appendix 5 Soil analysis test for Kiboko experimental field during 2008 short rain season

Soil nutrient	Before planting	After planting	Class
Soil pH	8.10	7.93	Medium Alkaline
Total Nitrogen %	0.09	0.11	Low
Org, Carbon %	0.35	0.54	Low
Phosphorus ppm	55	40	High
Potassium me %	0.80	0.70	Adequate
Calcium me %	7.8	5.8	Adequate
Magnesium me %	5.70	6.31	High
Manganese me %	0.52	0.54	Adequate
Copper ppm	6.19	5.53	Adequate
Iron ppm	31.4	32.1	Adequate
Zinc ppm	8.89	13.9	Adequate
Sodium me %	0.86	0.54	Adequate
Elect. Cond. ms/cm	0.55	0.40	Adequate

Appendix 6 Soil analysis test for Marigat experimental field during 2008 short rain season

Soil nutrient	before planting		after planting	
Soil pH	7.75	Medium Alkaline	7.35	Slightly alkaline
Total Nitrogen (%)	0.07	Low	0.09	Low
Org, Carbon (%)	0.27	Low	0.47	Low
Phosphorus (ppm)	16	Adequate	20	High
Potassium me (%)	1.94	High	1.84	High
Calcium me (%)	7.6	Adequate	7.6	Adequate
Magnesium me (%)	7.24	High	6.37	High
Manganese me (%)	0.77	Adequate	0.92	Adequate
Copper (ppm)	2.81	Adequate	4.14	Adequate
Iron (ppm)	54	Adequate	70.4	Adequate
Zinc (ppm)	21.1	Adequate	17.8	Adequate
Sodium me (%)	0.30	Adequate	0.34	Adequate
Elect. Cond. ms/cm	0.35	Adequate	0.60	Adequate

Appendix 7 F values and their level of significant for Foliage vigor (FLVIG), plant establishment (POEst), Vine fresh yield (VFRESH yield), Dry matter vine yield (DMVines), number of plants with roots(PLTwRoots), number of commercial roots (NCRoots), number of non-commercial roots (NCRoots), total number of roots(TNRoots), average number of roots per plant (AVRplt), yield of commercial roots (YieldCR), yield of non-commercial roots (YNCroots), root fresh yield (RFRESH), and weevil of sweetpotato genotypes evaluated at Kiboko and Marigat, Kenya

Source of variation	df	FLVIG	POEst	VFRESH yield	DMVines	PLTwRoots	NCRoots	NNCRoots	TNRoots	AVRplt	Yield CR	YNCroots	RFRESH	Weevil
Site	1	0.04ns	17.57**	113.04**	19.93**	1.40ns	2.61ns	1.97ns	0.00ns	10.69ns	2.17ns	34.85**	6.92ns	0.15ns
Clone	19	3.52**	3.91**	1.38ns	2.57ns	2.92ns	2.14ns	3.14ns	3.32ns	2.57ns	1.50ns	2.40ns	1.92ns	2.57ns
Site x clone	19	2.04ns	3.67**	0.54ns	0.96ns	2.04ns	1.14ns	1.39ns	1.60ns	1.62ns	1.18ns	1.82ns	1.07ns	1.44ns
Management	1	421.04**	129.67**	88.77**	59.66**	154.85**	48.03**	31.40**	72.97**	35.27**	50.91**	69.42**	93.52**	627.63**
Site x management	1	24.51**	66.89**	31.58**	0.36ns	54.27**	13.98ns	14.29**	26.32**	10.78ns	8.21ns	11.66ns	18.66**	4.86ns
Clone x management	19	3.55**	3.05ns	0.96ns	1.24ns	0.88ns	1.43ns	1.92ns	1.93ns	1.44ns	1.34ns	2.11ns	1.26ns	2.49ns
Site X clone X management	19	1.86ns	2.14ns	0.63ns	0.93ns	0.93ns	0.58ns	0.56ns	0.66ns	0.73ns	0.68ns	1.09ns	1.07ns	1.48ns

ns: not significant; ** significant at > 0.001

Appendix 8 Sum of squares for internal diameter (INTD), internode length (INTL), Leaf Area, Leaf number (LFNO) and Main stem length (MSTL) of 6 genotypes evaluated at Plant Quarantine station, Muguga, Kenya

Source of variation	df	INTD	INTL	LFAFREA	LFNO	MSTL
Week	7	0.50379**	16.08	1105.1**	71213.	9137.9**
Genotype	5	0.23099**	48.90	2357.0**	11511.	17501.9**
Treatment	1	9.04995**	33.13	375897.3**	2936525**.	108218.3**
week.Genotype	35	0.01451	14.22	179.3	12276.	65.1
week.Treatment	7	0.08238	15.54	21273.5**	319842**.	3919.5**
Genotype.Treatment	5	0.39264**	11.03	1243.5**	15488.	3825.6**
week.Genotype.Treatment	35	0.01698	14.46	255.9	12357.	183.5
Residual	192	0.05269	15.03	239.5	39836.	573.1

** Significant at 1%

Appendix 9 Mean sum of squares for Leaf fresh and dry weight, specific leaf weight, soil moisture content at harvest, root dry weight and total biomass of 6 genotypes evaluated at Plant Quarantine station, Muguga

Source of variation		Leaf fresh weight	Leaf dry weight	Specific Leaf Weight	Moisture content at harvest	Root dry weight	T/Biomass
Genotype	5	975.36**	1606.2	0.218**	127.37	162.66**	7581.2**
Treatment	1	8901.20**	86410.5**	4.25	101155.89**	1483.02**	167321.9**
Genotype.Treatment	5	461.22**	424.0	0.05	59.28	76.81	2122.8

** Significant at 1%