Breeding Sweetpotato for Improved Yield and Related Traits and Resistance to Sweetpotato Virus Disease in Eastern Tanzania

By

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Thesis Abstract

Sweetpotato production contributes significantly to food security and incomes of subsistence farmers in Tanzania. However, productivity of the crop is constrained by several biotic, abiotic and socio-economic factors. Amongst the biotic constraints, the sweetpotato virus disease (SPVD) causes significant yield losses in the country. Improved cultivars and landraces that are grown succumb to SPVD. Both chemical and biological control methods are not fully effective against SPVD. The use of resistant varieties remains the most effective and cheapest method for subsistence farmers. Therefore, breeding for SPVD resistance and high yields is an important consideration to develop and release improved sweetpotato varieties with end users preferences. Therefore, the objectives of the study were to: 1) assess the present sweetpotato farming systems, farmers' preferences, production constraints and breeding priorities in eastern Tanzania, 2) determine genetic variation among diverse sweetpotato germplasm with regards to yield, dry matter content and SPVD resistance and to identify suitable clones for breeding, 3) investigate the genetic diversity of 48 Tanzanian sweetpotato genotypes using nine selected polymorphic simple sequence repeat (SSR) markers and to determine genetic relationship and select unique parents for breeding, 4) determine the general combining ability (GCA) and specific combining ability (SCA) effects of selected sweetpotato clones for the number of storage roots, fresh storage root yield, dry matter content (DMC) and resistance to sweetpotato virus disease (SPVD) for further selection and breeding, and 5) determine the magnitude of genotype-by-environment and stability for yield and yield related traits and SPVD resistance among newly developed sweetpotato clones in eastern Tanzania.

Participatory rural appraisal study was conducted involving 138 and 149 farmers sampled for household interviews and focus group discussion, respectively at Gairo, Kilosa and Kilombero districts of Morogoro Region and Mkuranga district of the Coast Region of Tanzania. More than 94% of the respondents depended on crop farming for their livelihoods. Farmers preferred sweetpotato varieties with high yields, high dry matter content, tolerance to diseases and early maturing. Sweetpotato virus disease and pests, drought, unavailability of markets, lack of transport, low prices, inadequate extension services and post-harvest losses were identified by farmers being the most important production constraints. Improved extension service delivery, SPVD tolerant cultivars and reliable and coordinated market systems of sweetpotato were the most immediate needs for improved sweetpotato production and productivity.

Field experiments consisting 144 sweetpotato genotypes were conducted at two sites in Tanzania using a 12x12 simple lattice design in 2013 to screen genotypes for yield, dry matter content and sweetpotato virus disease resistance and to identify suitable clones for breeding. The genotypes differed in time to 50% flowering, number of roots per plant, root yield, dry matter content and resistance to SPVD. Seven clones including Simama, Ukerewe, Mataya, Resisto, 03-03, Ex-Msimbi-1 and Gairo were selected as potential parents for sweetpotato breeding for high storage root yield and related traits or SPVD resistance.

Nine polymorphic simple sequence repeat markers (SSR) were used to determine genetic relationship among 48 Tanzanian sweetpotato genotypes to identify unique parents useful for future breeding. The SSR markers were highly polymorphic and allocated the genotypes into three major genetic clusters. Ex-Ramadhani, Kibakuli, Mkombozi, Mjomba, Ex-Halima-3 and Kabuchenji were identified as genetically unrelated and complementary genotypes and recommended for future breeding programmes.

Eight genotypes contrasting for their yield, dry matter content or SPVD resistance were selected and crossed using an 8x8 half diallel mating design. The families were evaluated in the field using a 6x6 triple lattice design at Sugarcane Research Institute (SRI) at Kibaha, Kilombero Agricultural Training and Research Institute (KATRIN) and Sokoine University of Agriculture (SUA) in Tanzania. There were highly significant differences among families (P< 0.001) for all studied traits across sites. Clonal parents with highest general combining ability (GCA) were 03-03 and Resisto for storage root yield, Ukerewe for dry matter content (DMC) and Ex-Msimbu-1 which displayed negative and significant GCA effect for SPVD resistance. Therefore, the parents Resisto, Ukerewe and Ex-Msimbu-1 could be used for future sweetpotato breeding programmes to improve yield, DMC or resistance to SPVD. The following crosses were best combiners displaying positive and significant SCA effects: Mataya x Gairo and Simama x Gairo for number of roots per plant, Mataya x Ex-Msimbu-1 and 03-03 x Ex-Msimbu-1 for root yield and, Mataya x 03-03, 03-03 x Ukerewe and Resisto x SPKBH008 for DMC, and Mataya x SPKBH008 and Mataya x Gairo had negative and significant SCA effect for resistance to SPVD. The selected parents and crosses were the best candidates to develop improved sweetpotato varieties with high root yield, DMC or SPVD resistance.

The magnitude of genotype-by-environment interaction for yield and related traits and SPVD resistance of 26 selected sweetpotato clones was investigated across six diverse environments; namely Gairo, Kilombero Agricultural Training Research Institute (KATRIN), Sokoine University

of Agriculture (SUA), Sugarcane Research Institute (SRI), Chambezi and Mkuranga. The Additive Main Effect and Multiplicative Interaction (AMMI) and genotype and genotype-by-environment interaction (GGE) biplot analyses were used to determine the GxE interaction and stability of the genotypes. The genotypes were ranked differently for yield and related traits and SPVD resistance. AMMI and GGE biplot analyses identified the following genotypes: G5, G11, G23, G9, G7, G18 and G17 being high yielding and resistant to SPVD which could be further evaluated in multi-environment yield trials (MEYTs) in eastern Tanzania. Also, the genotypes G22 and G3 were isolated as high yielding and resistant to SPVD but specifically suited to Chambezi and Gairo. Test environments sufficiently discriminated the candidate genotypes for the traits studied. MEYTs are required for selection and recommendation of high yielding, SPVD resistant and stable sweetpotato clones for eastern Tanzanian or similar environments.

Overall, the study identified valuable sweetpotato parents and families with high combining ability for number and yield of storage roots, dry matter content and SPVD resistance from which new clones can be selected for future evaluation and release as new cultivars.

Declaration

I, Stephan Eliuth Ngailo, declare that:

1. The research reported in this thesis, except where otherwise indicated, is my original research.

2. This thesis has not been submitted for any degree or examination at any other University.

3. This thesis does not contain other persons' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from other persons.

4. This thesis does not contain other persons' writing, unless specifically acknowledged as being sourced from other researchers. Where other written sources have been quoted, then:

    a. Their words have been re-written but the general information attributed to them has been referenced.

    b. Where their exact words have been used, then their writing has been placed in italics and inside quotation marks, and referenced.

5. This thesis does not contain text, graphics or tables copied and pasted from the Internet, unless specifically acknowledged, and the source being detailed in the thesis and in the references sections.

Signed ……………………………………………………………………………………………

Stephan Eliuth Ngailo

As the candidate's supervisors, we agree to the submission of this thesis:

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Prof. Hussein Shimelis (Supervisor)

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Dr. Julia Sibiya (Co-Supervisor)

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Oversight of names of individuals or institutions that contributed to making this study a success is not deliberate and is sincerely regretted and apologized.

May God bless you ALL and reward you abundantly. AMEN.

Dedication

I dedicate this thesis to:

Almighty God for His mercies and protection.

My beloved late son Lugano.

My wife, Mary and children, Amani, Rehema and Joyce, for their support, understanding and sacrifice, without which I would have lacked the strength to continue.

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My late parents, Eliuth Ngailo and Alphoncina Ngailo, who brought me to this wonderful world.

Table of contents

Publications pertaining to this thesis

Chapter 1

Ngailo, S.E., Shimelis, H., Sibiya, J. and K. Mtunda. 2013. Sweetpotato breeding for resistance to sweetpotato virus disease and improved yield: progresses and challenges. African Journal of Agricultural Research 8(25):3202-3215.

Chapter 2

Ngailo, S.E., Shimelis, H., Sibiya, J. and K. Mtunda. 2015. Assessment of sweetpotato farming systems, production constraints and breeding priorities in eastern Tanzania. South African Journal of Plant and Soil. doi.org/10.1080/02571862.2015.1079932

Chapter 3

Ngailo, S.E., Shimelis, H., Sibiya, J. and K. Mtunda. 2015. Screening of Tanzanian sweetpotato germplasm for yield and related traits and resistance to sweetpotato virus disease. Acta Agriculturae Scandinavica, Section B - Plant and Soil doi.org/10.1080/09064710.2015.1063684.

Chapter 4

Ngailo, S.E., Shimelis, H., Sibiya, J., Amelework, B. and K. Mtunda. 2016. Genetic diversity assessment of Tanzanian sweetpotato genotypes using simple sequence repeat markers. South African Journal of Botany 102:40-45.

Thesis introduction

Importance of sweetpotato

Sweetpotato (*Ipomoea batatas* L., 2n = 6x =90) is an important root crop grown in more than 100 countries worldwide (Osiru et al., 2009; Lou et al., 2010). It is the seventh most important food crop globally. In developing countries sweetpotato is the fifth important food security crop after rice, wheat, maize and cassava (Cervantes-Flores et al., 2010). According to FAOSTAT (2015) the average sweetpotato production from 1999 to 2013 was 120 million tonnes per annum worldwide, of which 79% was produced by China (Table 1). In sub-Saharan Africa (SSA), it is cultivated in an area of about 3.22 million hectares with an annual production of 14.65 million tonnes (Table 1) which is about 12% of the world total production (FAOSTAT, 2015). Within sub-Saharan Africa 66% of sweetpotato production is concentrated in East Africa, where it is the basic subsistence crop (FAOSTAT, 2015).

Table 1. Sweetpotato production for some selected countries/regions from 1999–2013

Region/Country	Average area harvested in ha	Average production in tonnes	Productivity (tonnes/ha)
World	8 800 798	119 530 437	13.58
Africa	3 216 819	14 652 992	4.56
China	4 388 052	93 778 201	21.37
Burundi	122 817	832 195	6.78
Kenya	63 840	706 186	11.06
Nigeria	997 800	2 995 733	3.00
Rwanda	146 451	935 021	6.38
Uganda	576 919	2 606 827	4.52
Tanzania	480 815	1 596 267	3.32

Source: FAOSTAT, 2015.

Sweetpotato is grown for food, feed and income generation in many countries in SSA (Fugile, 2007; Low et al., 2009). It is an important food security crop, often crucial during famine due to its

excellent drought tolerance and rapid production of storage roots (Kapinga et al., 2003; Mukhopadhyay et al., 2011). It is a crucial crop in rural and marginalized communities including many HIV affected and women-headed households in eastern and central Africa (Johanson and Ives, 2001). The per capita consumption in SSA ranges between 85–160 kg year^{-1} (Johanson and Ives, 2001). It has supported more people per unit area than any other crop (Okada et al., 2002).

In Tanzania, sweetpotato is an important crop widely grown in almost all agro-ecological zones (Kulembeka et al., 2005; Masumba et al., 2005). In the country, it ranks fifth in terms of food production after maize, cassava, rice and sorghum. It is the second most important root crop after cassava (Table 2).

Table 2. Area and production of primary crops in Tanzania from 1999–2013

Crop	Average area harvested in ha	Average production in tonnes
Maize	2 731 616	3 815 196
Paddy/ rice	704 691	1 392 176
Sorghum	705 479	685 542
Cassava	848 110	5 127 036
Sweetpotato	480 814	1 596 267
Potatoes	128 981	892 200
Bananas	390 978	2 262 260

Source: FAOSTAT, 2015.

Sweetpotato has high productivity per unit area. It performs well in infertile soils and it is relatively drought tolerant (Tairo et al., 2005). It is grown in different cropping systems and patterns in different agro-ecologies in Tanzania. It is either monocropped or intercropped with maize, coconut, banana, cassava, pigeon peas or sunflower (Mukhopadhyay et al., 2011). Farmers mainly grow diverse landraces disseminated informally through farmer to farmer exchange of vines during planting time (Ndunguru et al., 2009). The crop has flexible planting and harvesting periods such that it can be harvested within 4 months of planting, and roots store well when left in the ground for a period of six to twelve months (Kapinga et al., 1995; Karyeija et al., 1998). In addition to serving as an important complementary food crop, sweetpotato supplements household income through formal and informal trading at both rural and urban markets, thereby

contributing to the alleviation of widespread food shortages and poverty for the majority of rural communities who are dependent on this crop (Mwanga and Ssemakula, 2011).

Despite the importance of sweetpotato and its wide adaptability in Tanzania the current crop yields are quite low. In the country sweetpotato yields ranges from 3–6 t ha^{-1}, which is lower than the potential yields recorded from experimental trials varying from 15 to 27 t ha^{-1} (Sebastiani et al., 2007; FAOSTAT, 2015).

Constraints to sweetpotato production

Biotic constraints

The production of sweetpotato is affected by several biotic constraints such as viral diseases, insect pests and weeds (Ndunguru et al., 2009). Important diseases and insects are sweetpotato virus diseases and sweetpotato weevils, respectively. Sweetpotato virus disease (SPVD) caused by the dual infection and synergistic interaction of sweetpotato chlorotic stunt virus and sweetpotato feathery mottle virus is cosmopolitan (Mukasa et al., 2006). It is the most devastating disease causing reduction in plant growth and root yields and quality (Gibson, 2005; Kapinga et al., 2009). Also SPVD limits the length of time the roots can be kept in the ground and shorten the storage duration of the harvested crop (Engoru et al., 2005; Tsakama et al., 2010). The damage caused by SPVD ranges from 50-100% (Gibson et al., 1998). A sweetpotato weevils, *Cylas punctcollis* and *Cylas brunneu*s, are also major sweetpotato production constraints (Stathers et al., 2003; Munyiza et al., 2007). The weevils tunnel and feed on vines and roots thereby reducing the quality and yield of the crop (Mullen, 1984; Stathers et al., 1999). According to Stanthers et al. (1999), yield losses from weevil infestation can be as high as 100%. Moreover, infestation levels are the highest under dry conditions due to many cracks which appear when the soil dries (Muyinza et al., 2007). Other biotic constraints such as millipedes, *Alternaria* leaf spot, stem blight, black rot, *Fusarium* rot, bacterial rot, nematodes and vertebrate pests such as rats also affect sweetpotato production (Fugile, 2007; Namanda et al., 2011). In addition, weeds may cause severe yield loses when high rainfall occurs early in the growing season (Harrison and Jackson, 2011). Seem et al. (2003) reported that time of weed infestation was critical. They reported that, the critical period of weed competition was from 2-6 weeks after planting. Al-Tikriti (1966) cited in Harrison and Jackson (2011), reported a yield loss of over 90% in weedy sweetpotato plots compared to weeded ones. Destruction of the crop by stray animals such as cattle and goats has also been reported in east Africa (Namanda et al., 2011).

Abiotic constraints

Abiotic constraints which significantly affect sweetpotato production include low soil fertility and drought (Fugile, 2007; Namanda et al., 2011). Declining soil fertility constrains sweetpotato production as its replenishment is limited by unaffordable high prices of inorganic fertilizers (Elliott and Hoffman, 2010). Moreover, most soils under smallholder farmers' condition are degraded and depleted making applied fertilizers less effective. Continuous cropping without addition of organic and inorganic manures has led to a decline in soil fertility and consequently a decline in productivity (Saleh and Zahor, 2007).

Drought is a significant abiotic constraint that limits the productivity of sweetpotato affecting both the quality and quantity of yields (Cattivelli et al., 2008; Namanda et al., 2011). In a participatory rural appraisal, Oduro (2013) reported that drought was among the highly ranked constraints in sweetpotato production in Ghana. Although it is documented that sweetpotato is drought tolerant, prolonged and frequent dry spells and erratic rainfall cause substantial yield reduction (Johanson and Ives, 2001). An et al. (2003) reported lower sweetpotato yields under hot-dry season compared to cool-wet season; however, the response varied with genotypes. Drought not only affects crop growth and development, but also root yield, dry matter content and composition, and pests and disease incidences (Ekanayake and Collins, 2004; Masumba et al., 2005). Besides low dry matter content and susceptibility to viral diseases, the newly introduced orange fleshed sweetpotato (OFSP) are unable to withstand drought, which leads to low productivity and unacceptability to farmers (Mwanga and Ssemakula, 2011). Sweetpotato varieties less tolerant to drought significantly retard the efforts invested by farmers making them unpopular and subsequently rejected. Gibson (2005) reported that the participatory sweetpotato breeding and selection trials were ruined by drought and farmers rejected the less drought tolerant varieties. Therefore, drought significantly affects and lowers sweetpotato production and productivity.

Socio-economic constraints

There are several socio-economic constraints which affect sweetpotato production. These include inadequate availability of high yielding, disease resistant planting materials, poor or no fertilization and weeding and lack of post-harvest technologies (Kulembeka et al., 2005; Tairo et al., 2005; Ndunguru et al., 2009). The use of infected, low yielding planting materials significantly contributes to persistence of sweetpotato viral diseases (Namanda et al., 2011). Inadequate extension services limits dissemination and adoption of improved husbandry practices. Consequently, farmers continue growing informally disseminated inferior planting materials,

which lead not only to persistence of diseases but also negatively affect productivity of the crop (Fugile, 2007; Namanda et al., 2011). Similarly, poor linkage between farmers and other stakeholders coupled with undeveloped and fragmented infrastructures in rural areas, significantly lowers the productivity of the crop (Kapinga and Carey, 2003; Waddington et al., 2010). Further, inadequate post-harvest technologies such as storage facilities and processing technologies severely affect investment, production and sustainability of the crop (Fugile, 2007; Waddington et al., 2010). Den (1991) cited in Rahman et al. (2003) reported root crops losses of 20-40% due to lack of appropriate storage and processing technologies.

Low production of sweetpotato is also contributed by lack of high yielding varieties with farmers'-preferred traits (Karuri et al., 2009). High yielding and farmers-preferred varieties are the bases for increased productivity and sustainable development of the crop. Presently, most farmers use local landraces. Though adapted to local agro-ecologies, the landraces are low yielding and late maturing (Masumba et al., 2005). Also, sweetpotato is one of the most under-exploited crop and breeding initiatives are at a relatively early stage compared to other crops such as maize, rice and cassava (Gasura et al., 2010). Several attempts have been made to use exotic varieties in various agro-ecologies to improve low productivity and circumvent pest and disease damage (Kapinga et al., 2009; Gasura et al., 2010). However, the exotic varieties have shown relatively poor performance compared to landraces which are well adapted to the farming systems (Gasura et al., 2010). Mwanga and Ssemakula (2011) reported almost 100% failure of the newly introduced orange-fleshed sweetpotato in Uganda. Similar studies in Tanzania indicated that, some of the introductions were rejected by farmers due to low dry matter content, low yields and poor production of vines during recurrent droughts (Kulembeka et al., 2005). A relatively similar performance of the local unimproved and introduced improved varieties for both yields and adaptability to different agro-ecologies have been reported (Mbwaga et al., 2007). This underpins the need for sweetpotato breeding to develop and release cultivars with high yielding, resistant to prevailing diseases and with preferred traits such as high dry matter content.

Problem statement and justification

Sweetpotato production significantly contributes to food security and incomes of subsistence farmers in Tanzania. Both improved cultivars and landraces that are grown succumb to several viral diseases, including the most devastating sweetpotato virus disease (SPVD). Sweetpotato virus disease is amongst the major constraints to sweetpotato production and causes significant

yield losses in the country. Continued use of susceptible varieties, absence of high yielding and early maturing resistant varieties, and lack of effective control measures to SPVD contribute to low yields and disease build up, development and persistence. Both chemical and biological control methods are not effective against viral diseases. Therefore, use of resistant varieties remains the most effective and cheapest method for small-scale farmers. Developing new sweetpotato clones through genetic recombination of local germplasm and exotic ones with desirable genetic variations and attributes is helpful for breeding. This requires a complementary genetic analyses and continuous selection of useful traits such as high yields and resistance to SPVD. The use of local genetic resources is necessary since they are well-adapted to local agro-ecologies and possess farmers-preferred traits. In the past, there are limited genetic studies on breeding of sweetpotato for resistance to SPVD in Tanzania. Development of sweetpotato cultivars with farmers-preferred traits and SPVD resistance is an overriding consideration to ensure food security and incomes to small scale farmers. Therefore, this study aimed at developing sweetpotato varieties with improved yield and related traits and resistance to SPVD for increased productivity and acceptability by farmers. The following trials were conducted encompassing five objectives.

Objectives

Overall objective

The main objective of this study was to contribute to the development of improved sweetpotato varieties with improved yield and related traits and resistant to SPVD for increased productivity and acceptability by farmers in Tanzania.

Specific objectives

The specific objectives of the study were:

1. To assess the present sweetpotato farming systems, farmers' preferences, production constraints and breeding priorities in eastern Tanzania

2. To determine genetic variation among diverse sweetpotato germplasm with regards to yield, dry matter content and sweetpotato virus disease (SPVD) resistance and to identify suitable clones for breeding.

3. To investigate the genetic diversity of 48 Tanzanian sweetpotato genotypes using nine selected polymorphic simple sequence repeat (SSR) markers to determine genetic relationship

4. To determine the general combining ability (GCA) and specific combining ability (SCA) effects of selected sweetpotato clones for the number of storage roots, fresh storage root yield, dry matter content (DMC) and resistance to sweetpotato virus disease (SPVD) for further selection and breeding.

5. To determine the magnitude of genotype-by-environment and stability for yield and yield related traits and sweetpotato virus disease (SPVD) resistance among newly developed sweetpotato clones in eastern Tanzania.

Thesis outline

This thesis consists of six distinct chapters (Table 3) reflecting a number of activities related to the above-mentioned objectives. Chapters 2 to 6 are written in the form of discrete research chapters, each following the format of a stand-alone research paper (whether or not the chapter has already been published). The referencing system used in the chapters of this thesis is based on the Journal of Crop Science system. This is the most recommended thesis format adopted by the University of KwaZulu-Natal. As such, there is some unavoidable repetition of references and some introductory information between chapters. Chapter 1 has been published in African Journal of Agricultural Research, while Chapter 2 is in press in the South African Journal of Plant and Soil. Chapter 3 has been published in the Acta Agriculturae Scandinavica, Section B - Soil & Plant Science and Chapter 4 has been published in the South African Journal of Botany.

Table 3. Thesis outline

Chapter	Title
-	Thesis introduction
1	A review of the literature
2	Assessment of sweetpotato farming systems, production constraints and breeding priorities in eastern Tanzania
3	Screening of Tanzanian sweetpotato germplasm for yield and related traits and resistance to sweetpotato virus disease
4	Genetic diversity assessment of Tanzanian sweetpotato genotypes using simple sequence repeat markers
5	Combining ability of sweetpotato clones for storage root yield and related traits and resistance to sweetpotato virus disease
6	Genotype-by-environment interaction of yield and related traits and resistance to sweetpotato virus disease among selected sweetpotato clones
7	An overview of research findings

References

An, L.V., B.E. Frankow-Lindberg, and J.E. Lindberg. 2003. Effect of harvesting interval and defoliation on yield and chemical composition of leaves, stems and tubers of sweetpotato (*Ipomoea batatas* L. (Lam.)) plant parts. Field Crops Research 82:49-58.

Cattivelli, L., F. Rizza, F.W. Badeck, E. Mazzucotelli, A.M. Mastrangelo, E. Francia, C. Mare`, A. Tondelli, and A.M. Stanca. 2008. Drought tolerance improvement in crop plants: An integrated view from breeding to genomics. Field Crops Research 105:1-14.

Cervantes-Flores, J., B. Sosinski, K. Pecota, R. Mwanga, G. Catignani, V. Truong, R. Watkins, M. Ulmer, and G. Yencho. 2010. Identification of quantitative trait loci for dry-matter, starch, and β-carotene content in sweetpotato. Molecular Breeding:1-16.

Ekanayake, I.J. and W. Collins. 2004. Effect of irrigation on sweetpotato root carbohydrates and nitrogenous compounds. Food, Agriculture and Environment 2:243-248.

Elliott, K.A. and M. Hoffman. 2010. Pulling Agricultural Innovation into the Market together: Working paper. Massachhusetts, Washington, DC: Center for Global Development.

Engoru, P., J. Mugisha, and B. Bashaasha. 2005. Tuber utilization options among sweetpotato producers in eastern Uganda. African Crop Science Journal 7:715-719.

FAOSTAT. 2015. Food and Agricultural Organization, Agricultural data. Crops and products domain available at http.faostat.fao.org/ [Online]. Rome: FAO. [Accessed 12th October 2015].

Fugile, K.O. 2007. Priorities for sweetpotato research in developing countries: Results of a survey. HortiScience 42:1200-1206.

Gasura, E., A.B. Mashingaidze, and S.B. Mukasa. 2010. Genetic variability for tuber yield, quality, and virus disease complex traits in Uganda sweetpotato germplasm. African Crop Science Journal 16:147-160.

Gibson, R.W. 2005. Working with farmers to control sweetpotato virus disease in East Africa: Crop protection programme. UK: Natural resource institute.

Gibson, R.W., I. Mpembe, T. Alicai, E.E. Carey, R.O.M. Mwanga, S.E. Seal, and H.J. Vetten. 1998. Symptoms, aetiology and serological analysis of sweetpotato virus disease in Uganda. Plant Pathology 47:95-102.

Harrison, H.F., Jr. and D.M. Jackson. 2011. Response of two sweetpotato cultivars to weed interference. Crop Protection 30:1291-1296.

Johanson, A. and C.L. Ives. 2001. An inventory of agricultural biotechnology for the Eastern and Central Africa region. Michigan, USA: Institute of International Agriculture.

Kapinga, R.E., J. Ndunguru, G. Mulokozi, and S. Tumwegamire. 2009. Impact of common sweetpotato viruses on total carotenoids and root yields of an orange-fleshed sweetpotato in Tanzania. Scientia Horticulturae 122:1-5.

Kapinga, R.E., D. Zhang, B. Lemaga, M. Andrade, R.O.M. Mwanga, S. Laurie, P. Ndoho, and E. Kanju. 2003. Sweetpotato improvement in sub-saharan africa. *in:* kapinga, r., kingamkono, r., msabaha, M., Ndunguru, J., Lemaga, B. and G. Tusiime. (eds.) *The Thirteenth Triennial Symposium of the International Society for Tropical Root Crops.* AICC, Arusha: International Society for Tropical Root Crops (ISTRC).

Kapinga, R.E. and E.E. Carey. 2003. Present status of sweetpotato breeding for eastern and southern Africa. *In:* Rees, D., Q.V. Oirschot, and R. Kapinga. (eds.) Sweetpotato post-harvest assessment. Experience from East Africa. University of Greenwich.

Kapinga, R.E., P.T. Ewell, S.C. Jeremiah, and R. Kileo. 1995. Sweetpotato in Tanzanian farming and food systems: Implications for research, Internation potato Center (CIP) Sub-Saharan Africa Regional Office, Nairobi and Ministry of Agriculture, Dar es Salaam, Tanzania.

Karuri, H.W., E.M. Ateka, R. Amata, A.B. Nyende, and A.W.T. Muigai. 2009. Characterization of Kenyan sweetpotato genotypes for SPVD resistance and high dry matter content using simple sequence repeat markers. African Journal of Biotechnology 8:2169-2175.

Karyeija, R., R. Gibson, and J. Valkonen. 1998. The significance of sweetpotato feathery mottle virus in subsistence sweetpotato production in Africa. Plant Disease 82:4-15.

Kulembeka, H., C. Rugutu, E. Kanju, B. Chirimi, E. Rwiza, and R. Amour. 2005. The agronomic performance and acceptability of orange fleshed sweetpotato varieties in the lake zone of Tanzania. African Crop Science Journal 12:229-240.

Lou, H.R., M.S. Maria, J. Benavides, D.P. Zhang, Y. Zhang, and M. Ghislain. 2010. Rapid genetic transformation of sweetpotato *(Ipomeea batatas* (L.) Lam) via organogenesis African Journal of Biotechnology 5:1851-1857.

Low, J., J. Lynam, B. Lemaga, C. Crissman, I. Barker, G. Thiele, S. Namanda, C. Wheatley, and M. Andrade. 2009. Sweetpotato in Sub-Saharan Africa. *In:* Loebenstein, G. and G. Thottappilly. (eds.) The sweetpotato. Springer Netherlands.

Masumba, E., H. Kulembeka, S. Tollano, and M. Yongolo. 2005. Participatory evaluation of improved sweetpotato varieties in eastern Tanzania. African Crop Science Journal 12:259-265.

Mbwaga, Z., M. Mataa, and M. Msabaha. 2007. Quality and yield stability of orange fleshed sweetpotato *(Ipomoea batatas)* varieties grown in different agro-ecologies. *The Eighth African Crop Science Society Conference.* El-minia, Egypt: African Crop Science Soceity.

Mukasa, S.B., P.R. Rubaihayo, and J.P.T. Valkonen. 2006. Interactions between a crinivirus, an ipomovirus and a potyvirus in co-infected sweetpotato plants. Plant Pathology 55:458-467.

Mukhopadhyay, S., A. Chattopadhyay, I. Chakraborty, and I. Bhattacharya. 2011. Crops that feed the world 5. Sweetpotato. Sweetpotato for income and food security. Food Security 3:283-305.

Mullen, M.A. 1984. Influence of sweetpotato weevil infestation on the yields of twelve sweetpotato lines. Journal of Agricultural Entomology 1:227-230.

Munyiza, H., P. Stevenson , R. Mwanga, H. Talwana, J. Murumu, and B. Odongo. 2007. The relationship between stem base and root damage by *Cylass* spp. on sweetpotato. African Crop Science Journal 8:955-957.

Mwanga, R. and G. Ssemakula. 2011. Orange-fleshed sweetpotato for food, health and wealth in Uganda. International Journal of Agricultural Sustainability 9:42-49.

Namanda, S., R. Gibson, and K. Sindi. 2011. Sweetpotato seed systems in Uganda, Tanzania, and Rwanda. Journal of Sustainable Agriculture 35:870-884.

Ndunguru, J., R. Kapinga, P. Sseruwagi, B. Sayi, R. Mwanga, S. Tumwegamire, and C. Rugutu. 2009. Assessing the sweetpotato virus disease and its associated vectors in northwestern Tanzania and central Uganda. African Journal of Agricultural Research 4:334-343.

Oduro, V. 2013. Genetic Control of Sugars, Cry Matter, and Beta-Carotene in Sweetpotato *(Ipomoea batatas* [L.] Lam*).* University of Ghana.

Okada, Y., M. Nishiguchi, A. Saito, T. Kimura, M. Mori, K. Hanada, J. Sakai, Y. Matsuda, and T. Murata. 2002. Inheritance and stability of the virus-resistant gene in the progeny of transgenic sweetpotato. Plant Breeding 121:249-253.

Osiru, M.O., O.M. Olanya, E. Adipala, R. Kapinga, and B. Lemaga. 2009. Yield stability analysis of *Ipomoea batatas* L. cultivars in diverse environments. Australian Journal of Crop Science 3:213-220.

Rahman, S.M.M., C. Wheatley, and S.K. Raksh. 2003. Selection of sweetpotato variety for high starch extraction. International Journal of Food Properties 6:419–430.

Saleh, H. and O. Zahor. 2007. Farmers' perception and varieties acceptability of orange-fleshed sweetpotato in Zanzibar. *In:* Kapinga, R., R. Kingamkono, M. Msabaha, J. Ndunguru, B. Lemaga,and G. Tusiime. (eds.) *Proceedings of the Thirteenth Triennial Symposium of the International Society of Tropical Root Crops.* AICC, Arusha: International Society of Tropical Root Crops (ISTRC).

Sebastiani, S.K., A. Mgonja, F. Urio, and T. Ndondi. 2007. Agronomic and economic benefits of sweetpotato *(Ipomoea batatas*) response to application of nitrogen and phosphorus fertilizer in the northern highlands of Tanzania. *The Eighth African Crop Science Society Conference.* El-minia, Egypt: African Crop Science Society.

Seem, J.E., N.G. Creamer, and D.W. Monks. 2003. Critical weed-free period for Beauregard sweetpotato (*Ipomoea batatas*). Weed Technology 17:686-695.

Stathers, T.E., D. Rees, D. Jeffries, S. Kabi, N. Smith, L. Mbilinyi, K. Kiozya, S. Jeremiah, M. Nyango, and C. Moss. 1999. Investigating the potential of cultivar differences in susceptibility to sweetpotato weevil as a means of control. Crop Post-harvest Programme. UK: DFID.

Stathers, T.E., D. Rees, S. Kabi, L. Mbilinyi, N. Smith, K. Kiozya, S. Jeremiah, A. Nyango, and D. Jeffries. 2003. Sweetpotato infestation by *Cylas* spp. in East Africa: I. Cultivar differences in field infestation and the role of plant factors. International Journal of Pest Management 49:131-140.

Tairo, F., S.B. Mukasa, R.A.C. Jones, A. Kullaya, P.R. Rubaihayo, and J.P.T. Valkonen. 2005. Unravelling the genetic diversity of the three main viruses involved in Sweetpotato virus disease (SPVD), and its practical implications. Molecular Plant Pathology 6:199-211.

Tsakama, M., A.M. Mwangwela, T.A. Manani, and N.M. Mahungu. 2010. Physiochemical and pasting properties of starch extracted from eleven sweetpotato varieties. African Journal of Food Science and Technology 1:90-98.

Waddington, S., X. Li, J. Dixon, G. Hyman, and M. De Vicente. 2010. Getting the focus right: production constraints for six major food crops in Asian and African farming systems. Food Security 2:27-48.

Chapter one

1. A Review of the Literature

Abstract

Sweetpotato is one of the main staple food crops for millions of subsistence farmers in Africa. Biotic and abiotic stresses and socio-economic challenges are the major production constraints of the crop. Amongst biotic constraints, the sweetpotato virus disease (SPVD) is the most devastating causing yield reduction ranging from 50-98%. Both improved cultivars and landraces that are presently grown succumb to SPVD and several viral diseases. The yield losses caused by SPVD have significant negative impact on food security and income for the rural poor in eastern Tanzania. Continued use of susceptible varieties, absence of high yielding and early maturing resistant varieties, and lack of effective control measures to SPVD contribute to low yields and disease build up, development and persistence. Both chemical and biological control methods are not effective against viral diseases. The use of resistant varieties remains the most effective and cheapest method for small-scale farmers. Breeding for resistance against SPVD remains the most important component to improve yield and reduce the impact of SPVD. Reduced flowering and fertility, self- or cross-incompatibility are the major challenges of conventional breeding in sweetpotato breeding. The use of new breeding techniques such as marker-assisted selection and genetic engineering could have complementary roles in sweetpotato breeding. This review provides theoretical basis on breeding sweetpotato for SPVD resistance and improved yields.

Keywords: Breeding, resistance, SPVD, Sweetpotato, viral disease, yield

1.1. Introduction

Sweetpotato (*Ipomoea batatas* (L.) Lam.; 2n=6x=90) is a perennial plant cultivated as an annual crop. It is a dicotyledonous and belongs to morning glory family Convolvulaceae (Huaman, 1992; Martin, 1970). Principally, sweetpotato is grown for its storage roots for food security and income (Diaz et al., 1996; Tairo et al., 2004). It has supported more people per square unit than any other crop (Okada et al., 2002). The genus *Ipomoea* consists of about 600 to 700 species including sweetpotato (Cao et al., 2009; Vaeasey et al., 2008). The series Batatas consists of 13 species closely related to cultivated sweetpotato (Diaz et al., 1996; Huang and Sun, 2000; Orjeda et al., 1990; Srisuwan et al., 2006). Further, section Batatas consists of three cytogenetic groups, namely; group A, B and X; while A and X are self- and cross- compatible, group B where sweetpotato belongs is self-incompatible but cross-compatible (Diaz et al., 1996; Kobayashi et al., 1993; Kowyama et al., 2000; Nishiyama et al., 1975). Central America has been documented as the origin and the primary centre of diversity of the currently cultivated sweetpotato (Gichuki et al., 2003; Low et al., 2009; Srisuwan et al., 2006; Zhang et al., 2000). On the other hand, East Africa is one of the secondary centres for sweetpotato diversity (Gichuki et al., 2003). Sweetpotato is believed to be introduced to Africa by Portuguese during 16th and 17th century (Gichuki et al., 2003; Zhang et al., 2000).

Sweetpotato is grown from 48N to 40°S of the equator with altitudes ranging from 0 to 3000 m above sea level (Low et al., 2009; Troung et al., 2011; Vaeasey et al., 2008; Woolfe, 1992). The crop requires ambient day and night temperatures of 15°C to 33°C for optimum growth and root development. Temperature above 25°C is considered optimal for maximum growth (Woolfe, 1992). However, temperatures below 12°C and above 35°C retard sweetpotato growth (Kuo, 1991). Dry matter production increases with increasing temperatures from 20°C to 30°C, but declines at temperatures beyond 30°C (Kuo, 1991). The crop grows best with a well distributed annual rainfall of 600-1600mm (Low et al., 2009). Excess rainfall at early stage of establishment may aggravate weed problem resulting in low yield (Harrison and Jackson, 2011). The crop is extensively grown under rain-fed conditions and is relatively drought tolerant. However, prolonged and frequent dry spells or drought and erratic rainfall cause substantial yield reduction (Low et al., 2009; Schafleitner et al., 2010). Sweetpotato requires well-drained soil with a pH of 5.5 to 6.5 (Woolfe, 1992). It also requires full sun light; however, it can tolerate a 30-50% reduction of full solar radiation (Troung et al., 2011).

Flowering ability is an essential aspect in sweetpotato breeding and determines the potential for crop improvement through breeding (Gasura et al., 2010). Sweetpotato flower contains both male and female reproductive organs for sexual reproduction (Jones, 1980). The flowers are born solitarily and grow vertically upward from the leaf axis (Huaman, 1992). Each flower has five united sepals and five petals joined together to form a funnel-shaped corolla tube (Huaman, 1992; Jones, 1980). The tube is usually lavender coloured and is the most conspicuous part of the flower (Jones, 1980). Five stamens with varying heights are attached to the base of the corolla tube (Jones, 1980). In most cultivars the two longest stamens are about the same length as the style. The filaments vary in length and are hairy and, anthers are either white or yellow or pink and contain numerous pollen grains on their surfaces (Huaman, 1992). The ovary consists of two carpel, each containing one locule (Mont et al., 1993; Orjeda et al., 1991). Each locule contains either one or two ovules, with a maximum of four ovules per ovary (Huaman, 1992; Jones, 1980).

Despite that sweetpotato flowers mostly under short day length, long day and day neutral cultivars exist (Jones, 1980; Troung et al., 2011). However, most sweetpotato cultivars are sensitive to day length. Hence, some genotypes flower readily at any season while others only when days are short (Jones, 1980). Short days promote flowering and growth of storage root (Martin, 1988). Still others do not flower under any normal conditions. Those that do not flower can be induced to flower by grafting on other *Ipomoea* species (Chiona, 2009). Sweetpotato cultivars differ in their flowering ability, some do not flower, others produce very few flowers or flower profusely depending on the genotypes and environmental influences (Huaman, 1992; Jones, 1980). On the other hand, non-flowering genotypes pose challenges in exploiting their genes via the conventional breeding programmes.

The flowers open soon after daybreak and wither depending on prevailing environmental conditions (Jones, 1980). Flowers open longer on cool and cloudy days compared to hot and sunny days. Pollination can be facilitated either by insects or hand. In either case, the male pollen grain lands on the stigma, initiating fertilization. The pollen germinates few minutes to 3 or 4 hours after pollination (Jones, 1980; Kowyama et al., 2000; Martin and Cabanillas, 1966). The pollen tube grows down the style until it meets the female gametophyte in 8 hours after pollination (Jones, 1980; Martin and Cabanillas, 1966). Pollen may be rejected shortly after contacting the stigmatic surface resulting in pollen germination failure (Kowyama et al., 2000). With normal fertilization and embryo development up to four seeds can be produced per ovary (Jones, 1980; Mont et al., 1993). However, successful fertilization is uncertain, possibly due to embryo and fruit abortions (Mont et al., 1993). Gasura et al. (2010) reported higher fertilization successes for

flowers pollinated in early than late hours of the day. Additionally, insect pollination produce more seeds compared to hand pollination (Gasura et al., 2010; Nishiyama et al., 1975). The low fertility or fertilization failure could be due to incompatibility contributed by hexaploid genome of the crop. Besides incompatibility, other environmental and management practices also affect the amount of seeds produced in the ovary. Weed management and controlled application of nitrogen fertilizer improve seed setting (Jones, 1980).

The sweetpotato fruit is a capsule containing one to four seeds (Huaman, 1992). The seeds are black and about 3 mm long; also they are flat on one side and convex on the other (Chiona, 2009; Huaman, 1992). The seeds remain viable for many years with extended dormancy period probably due to thick, hard and impermeable testa (Chiona, 2009; Huaman, 1992). This has implication on seed germination. Therefore, mechanical or chemical scarification is necessary for improved germination (Ernest et al., 1994; Huaman, 1992). Nevertheless, the production sweetpotato is constrained by several biotic, abiotic and socio-economic factors (Thottappilly and Loebenstein, 2009). Amongst the most important biotic constraints are sweetpotato virus diseases. The objective of this paper was to highlight the progresses and challenges of breeding sweetpotato towards improved yield and SPVD resistance. Further, the potential and limitations of non-conventional breeding techniques for sweetpotato improvement have been reviewed.

1.2. Constraints to sweetpotato production

1.2.1. Biotic constraints

The production of sweetpotato is affected by several biotic constraints such as viral diseases, insect pests and weeds (Harrison and Jackson, 2011; Lou et al., 2010; Ndunguru et al., 2009; Schafleitner et al., 2010). Diseases and insects of paramount importance are sweetpotato virus diseases and sweetpotato weevils, respectively (Kivuva et al., 2014b). Sweetpotato virus disease (SPVD) caused by the dual infection and synergistic interaction of sweetpotato chlorotic stunt virus and sweetpotato feathery mottle virus is distributed worldwide (Gibson et al., 1998; Mukasa et al., 2006). It is the most devastating disease causing reduction in plant growth and storage root yields (Gibson, 2005; Gibson et al., 2004; Gibson et al., 1997; Kapinga et al., 2009; Karyeija et al., 2000). Also SPVD limits the length of time the roots can be kept in the ground and shorten the storage duration of the harvested crop (Engoru et al., 2005; Tsakama et al., 2010). The damage caused by SPVD ranges from 50-98% (Gibson et al., 1998; Njeru et al., 2004; Tairo et

al., 2004). On the other hand, sweetpotato weevils, *Cylas* spp., is another major sweetpotato production constraint (Kapinga et al., 2003b; Korada et al., 2010; Munyiza et al., 2007; Stathers et al., 2003). The weevils tunnel and feed on vines and storage roots thereby reducing the quality and yield of the crop (Mullen, 1984; Stathers et al., 1999). According to Stanthers et al. (1999), yield losses from weevils' infestation can be as high as 100%. Moreover, infestation levels are highest under dry conditions due to many cracks which appear when the soil dries (Muyinza et al., 2007). Other biotic constraints such as millipedes, *Alternaria* leaf spot, stem blight, black rot, *Fusarium* rot, bacterial rot, nematodes and vertebrate pests such as rats are also a threat to sweetpotato production (Ebregt et al., 2004; Johanson and Ives, 2001; Kapinga et al., 1995). In addition, weeds may cause severe yield loses when high rainfall occurs early in the growing season (Harrison and Jackson, 2011).

1.2.2. Abiotic constraints

Abiotic constraints which significantly affect sweetpotato production include low soil fertility and drought (Kapinga et al., 1995; Mihale et al., 2009; Mwololo et al., 2007; Pareek et al., 2010). Declining soil fertility constrains sweetpotato production as its replenishment is limited by unaffordable high prices of inorganic fertilizers (Elliott and Hoffman, 2010; Mudiope et al., 2000). Moreover, degraded and depleted soils make applied fertilizers less effective. Continuous cropping without addition of organic and inorganic manures has led to a decline in soil fertility and consequently a decline in productivity (Saleh and Zahor, 2007).

Drought is a significant abiotic constraint limiting the productivity of not only sweetpotato but also many other crops and affects both the quality and quantity of yield (Balouchi, 2010; Cattivelli et al., 2008; Collins et al., 2008). Kivuva et al. (2014b) reported that, 28% of 345 farmers interviewed identified drought as a major constraint in sweetpotato production in Kenya. Although it is documented that sweetpotato is drought tolerant, prolonged and frequent dry spells and erratic rainfall cause substantial yield reduction (Johanson and Ives, 2001; Liwenga and Kangalawe, 2009; Schafleitner et al., 2010). Drought not only affects crop growth and development, but also root yield, dry matter content and composition, and pests and disease incidences (Ekanayake and Collins, 2004; Masumba et al., 2005; Mcharo and Carey, 2001). Mwololo et al. (2007) reported an increased incidence and severity of sweetpotato viral diseases in the event of drought. For instance, besides low dry matter content and susceptibility to viral diseases, the newly introduced orange fleshed sweetpotato (OFSP) were unable to withstand drought, which

leads to low productivity and unacceptability to farmers (Mwanga and Ssemakula, 2011). Sweetpotato varieties less tolerant to drought significantly retard the efforts invested by farmers making them unpopular and subsequently rejected. Gibson (2005) reported that the participatory sweetpotato breeding and selection trials were ruined by drought and farmers rejected the less drought tolerant varieties. Therefore, together with other constraints, the production of sweetpotato is also significantly affected by drought leading to low productivity.

1.2.3. Socio-economic constraints

There are several socio-economic constraints which affect sweetpotato production. These include inadequate availability of high yielding, disease resistant planting materials, poor or no fertilization and weeding, and lack of post-harvest technologies (Kulembeka et al., 2005; Mpagalile et al., 2003; Mudiope et al., 2000; Mwololo et al., 2007; Ndunguru et al., 2009; Rees et al., 1998; Schafleitner et al., 2010; Tairo et al., 2005). The use of infected, low yielding planting materials contributes significantly to persistence of sweetpotato viral diseases (Mwololo et al., 2007; Opiyo et al., 2010). Inadequate extension services limits dissemination and adoption of improved husbandry practices. Consequently, farmers continue growing informally disseminated inferior planting materials, which lead not only to persistence of diseases but also negatively affect productivity and profit of the crop (Kapinga and Carey, 2003; Fugile, 2007). Similarly, poor linkage between farmers and other stakeholders coupled with undeveloped and fragmented infrastructures in rural areas significantly lowers the productivity of the crop (Kapinga and Carey, 2003; Waddington et al., 2010). Further, inadequate post-harvest technologies such as storage facilities and processing technologies severely affect investment, production and sustainability of the crop (Fugile, 2007; Hu et al., 2011; Mpagalile et al., 2003; Waddington et al., 2010).

Also, lack of high yielding sweetpotato varieties with farmers' preferred traits contributes to low production (Karuri et al., 2009). High yielding and farmers' preferred varieties are the bases for increased productivity and sustainable development of the crop. Presently, most farmers use local landraces. Though adapted to local agro-ecologies, the landraces are low yielding and late maturing (Gibson et al., 1998; Masumba et al., 2005). Likewise, sweetpotato is one of the most under-exploited crop and breeding initiatives are at a relatively early stage compared to other crops such as maize, rice and cassava (Gasura et al., 2010; Kriegner et al., 2003). In the past, attempts were made to use exotic varieties in various agro-ecologies to address low productivity and circumvent pest and disease damages (Gasura et al., 2010; Kapinga et al., 2009).

Nevertheless, the exotic varieties have shown relatively poor performance compared to landraces which are well adapted to the farming systems (Gasura et al., 2010). Mwanga et al. (2007) and Mwanga and Ssemakula (2011) reported almost 100% failure of the newly introduced orange-fleshed sweetpotato in Uganda. Similar studies in Tanzania indicated that, some of the introductions were rejected by farmers due to low root yields and dry matter content, and poor production of vines during recurrent droughts (Kulembeka et al., 2005; Masumba et al., 2003). On the other hand, relatively similar performance of the local unimproved and introduced improved varieties for both yields and adaptability to different agro-ecologies have been reported (Mbwaga et al., 2007). This underpins the need for further sweetpotato research and development.

1.3. Sweetpotato virus diseases

Sweetpotato is invariably affected by bacteria, fungal and viral diseases, and nematode (Clark et al., 2009; Thottappilly and Loebenstein, 2009). Different diseases attack the crop at different stages of growth, from pre-harvest to post harvest (Dje and Diallo, 2005). The levels of damages due to diseases and pests depend on the causal agent, intensity of infestation, variety and prevailing environmental conditions (Thottappilly and Loebenstein, 2009). Viral diseases cause substantial yield losses in farmers' fields (Wambugu, 2003).

Viral diseases are amongst the important biotic constraints in sweetpotato production (Gutiérrez et al., 2003; Wambugu, 2003). They are the most devastating and occur in all sweetpotato growing areas (Mwololo et al., 2007; Ndunguru et al., 2009; Tairo et al., 2004). The most important sweetpotato virus diseases include sweetpotato feathery mottle virus (SPFMV), sweetpotato chlorotic stunting virus (SPCSV), sweetpotato mild mottle virus (SPMMV) and sweetpotato chlorotic fleck virus (SPCFV) (Feng et al., 2000; Tairo et al., 2004). Sweetpotato mild speckling virus (SPMSV), sweetpotato virus *G* (SPVG) and sweetpotato latent virus (SPLV) have also been reported to affect sweetpotato (Feng et al., 2000; Ndunguru and Kapinga, 2007). These viruses not only adversely affect sweetpotato yields and quality but also decrease plant resistance to insect pests (Bryan et al., 2003; Feng et al., 2000; Yang, 2010). An infection by single virus strain causes little yield losses compared to co- or multiple-infections that cause the complex sweetpotato virus disease (SPVD) (Ames de Icochea and Ames, 1997; Karyeija et al., 2000).

Sweetpotato virus disease (SPVD) severely affects sweetpotato production (Gutiérrez et al., 2003; Kokkinos et al., 2006). It is caused by dual infection and synergistic interaction of sweetpotato chlorotic stunting virus (SPCSV); family *Closteroviridae*, genus *Crinivirus* and

sweetpotato feathery mottle virus (SPFMV); family *Potyviridae* genus *Potyvirus* (Karyeija et al., 1998; Kreuze et al., 2009; Untiveros et al., 2008). Sweetpotato feathery mottle virus is non-persistently transmitted by aphids while sweetpotato chlorotic stunting virus is semi-persistently transmitted by the whitefly [*Bemisia tabaci*] (IsHak et al., 2003; Kokkinos et al., 2006; Untiveros et al., 2008). In some incidences, co-infection of sweetpotato chlorotic stunting virus and sweetpotato mild mottle virus (SPMMV) occurs (IsHak et al., 2003; Mukasa et al., 2006). Further, not only dual co-infection but also triple infections occur resulting into most severe disease symptoms and yield losses (Gibson et al., 2004; Kapinga et al., 2009; Mukasa et al., 2006; Tairo et al., 2005). The symptoms and damage of co-infection are more severe and devastating than individual viral disease (Feng et al., 2000; Karyeija et al., 2000; Mukasa et al., 2006). The SPVD symptoms and damages are subject to its incidences and severity.

The incidences and severity of SPVD are highly variable. They vary between and within agro-ecologies, between varieties and growth stages of plants (Gasura and Mukasa, 2010; Gibson et al., 2000; Kapinga et al., 2009; Mwololo et al., 2007). The disease is characterized by stunted growth, chlorotic and malformed leaves, and ultimately reduced yields (Gibson et al., 2004; Gutiérrez et al., 2003; Untiveros et al., 2008). The SPVD infection causes yield losses as high as 98% (Feng et al., 2000; Gibson et al., 2000; Gutiérrez et al., 2003; Mukasa et al., 2006). Bryan et al. (2003) reported a decrease in root diameter and yield due to presence of SPFMV and other potyviruses. The disease not only decreases yields, but also lowers quality and resistance to other pathogen (Bryan et al., 2003; Domola et al., 2008). In severe incidences, SPVD can lead to abandonment of elite cultivars (Bryan et al., 2003; Gasura and Mukasa, 2010; Rukarwa et al., 2010).

The SPVD is persistent in farmers' fields due to several predisposing factors. Lack of knowledge among farmers, predominantly use of aged vegetative propagating materials, susceptible landraces, and high temperatures favour development, spread and expression of the disease (Ateka et al., 2004; Kreuze, 2002; Mwololo et al., 2007; Ndunguru et al., 2009; Tairo et al., 2004; van den Bosch et al., 2007). Also, the use of healthy-looking vines collected from the previous to the succeeding cropping cycles contributes to the spread of the disease (Opiyo et al., 2010; Rukarwa et al., 2010). Bryan et al. (2003) reported early development of disease symptoms from transplants infected with viruses compared to uninfected transplants which consequently led to decline in yield and root quality. Aritua et al. (2007) reported high virus incidences in bimodal rains compared to unimodal rain in a year. On the other hand, Ndunguru et al. (2007) found lower incidences and severity of SPVD in cooler compared to warmer agro-ecologies and where the

crop was grown in only one season per year. Further, prolonged, hot and dry spells provide natural breaks in the transfer of viruses between crop cycles (Aritua et al., 2007; Ndunguru et al., 2007). In endeavour to reduce the incidences and effects of SPVD, several strategies such as phytosanitation and breeding for resistant cultivars have been recommended (Tairo et al., 2004; Valverde et al., 2007).

1.4. Strategies to control SPVD

Adequate management of plant disease is amongst the prerequisite for stable and profitable crop production for ascertained food security. Plant viruses are a major problem in the cultivation of many crops. There is no effective and complete control method against the disease to date. The control of viral diseases remains difficult in subsistence cropping systems (Rukarwa et al., 2010). Both chemical and biological control methods are not effective against viral diseases (Dje and Diallo, 2005; Garcïa-Arenal and McDonald, 2003; Maule et al., 2007). Several strategies such as cultural practices, phytosanitary measures, control of vectors and deployment of genetic resistance to prevent or limit the extent of damage have been recommended (Maule et al., 2007; van den Bosch et al., 2007). On the other hand, control of SPVD has been mainly by use of clean and virus-free planting materials and resistant varieties (Aritua et al., 1998; Gibson et al., 2000). The use of clean and disease free planting materials, sanitation and other cultural practices effectively contribute to the control of the disease (Miano et al., 2008; Tairo et al., 2005). Karyeija et al. (1998) and Thottappilly and Loebenstein (2009) suggested that, use of virus-free and certified planting materials are likely to significantly reduce the effects of SPVD. However, deployment of genetic resistance to virus disease is viewed as the most effective and sustainable approach for managing SPVD (Garcïa-Arenal and McDonald, 2003; Maule et al., 2007).

1.4.1. Cultural practices to control SPVD

Virus infected plants cannot be cured and the only way to adequately protect the crops is the use of resistant cultivars (Kreuze, 2002). The use of resistant varieties is cheap, easy, safe, effective and environmentally friendly (Byamukama et al., 2002; Garcïa-Arenal and McDonald, 2003; Okada et al., 2001; Valverde et al., 2007). The impact of SPVD in farmers' fields has been reduced by the use of resistant cultivars and landraces (Miano et al., 2008). However, the local landraces are highly variable in their resistance to SPVD. Most varieties are resistant to SPFMV but this resistance breaks down in the event of co-infection with SPCSV resulting in redundant resistance (Gasura and Mukasa, 2010; Tairo et al., 2004; van den Bosch et al., 2007). Further, the

sweetpotato grown by farmers are landraces with build-up of viruses resulting from several generations of vegetative propagation (Low et al., 2009; Miano et al., 2008). In general, resistant varieties are rarely available in addition to being low yielders and late maturing (Abidin et al., 2005; Gibson et al., 2004; Miano et al., 2008). Therefore, improving virus resistance through development and deployment of SPVD resistant and high yielding varieties would improve production, productivity and ensure food security for subsistence farmers.

Improved phytosanitation offers considerable benefits for controlling SPVD (Muturi et al., 2007). Phytosanitary measures includes quarantine, sanitation, use of virus-free vegetative propagules for all new plantings and roguing of diseased plants from within plantings (Thresh, 2003). Roguing, the removal of all plants showing disease symptoms has been reported to decrease the population of whitefly, a vector responsible in spreading SPVD (Karyeija et al., 1998; Muturi et al., 2007; Valverde et al., 2007). Also, Ndunguru et al. (2009) and van den Bosch et al. (2007) reported that, roguing of infected plants may form an effective way of minimizing SPVD incidence and its damage to sweetpotato production. Gibson et al. (2000) and Gibson et al. (2004) found that, Tanzanian and Ugandan farmers controlled SPVD by using symptomless plants to establish new crop and destroying all infected plants. On the other hand, control of vegetation closer to sweetpotato fields is likely to significantly reduce vectors' population thereby reducing incidences of SPVD. Muturi et al. (2007) reported drastic increase in whitefly populations in experimental plots surrounded by maize plants. Contrastingly, Gutiérrez et al. (2003) used maize as an integrated pest management to control whitefly and aphid population to reduce virus transmission. Further, avoidance of introducing new infections in a new field by isolating new plots from SPVD-affected ones can effectively reduce spread and incidences of SPVD (Domola et al., 2008; Gibson et al., 2004). Moreover, Gibson et al. (1998) recommended enforcement of phytosanitary controls to prevent introduction of new and severe viral strains between regions. Aritua et al. (1999) suggested widerspread cultivation of resistant varieties could limit infections to susceptible ones grown in nearby fields.

Another approach to circumvent the damage caused by viral infection is the production and use virus-free plants through shoot tip culture (Feng et al., 2000; Okada et al., 2002; Rukarwa et al., 2010). The use of health planting materials contributes significantly to the control of viral diseases including SPVD. The approach is effective in eliminating sweetpotato viruses. Recently, Kivuva et al. (2015) reported use of clean seed and high yielding varieties being amongst the strategies to address SPVD and low productivity constraints. Hannington et al. (2002) reported that, inadequate quantities of clean planting materials was amongst the causes of persistent low yields

of sweetpotato in farmers' fields in Kenya. According to Feng et al. (2000) and Gutiérrez et al. (2003), the use of virus-free sweetpotato is likely to restore cultivar's original yield, quality and improve resistance to other pathogens and insects. Further, the use of virus-free sweetpotato planting materials has been recommended to be among the most effective way to circumvent losses caused by viruses (Opiyo et al., 2010). Aritua et al. (2003) reported that farmers in Uganda selected cuttings from new unaffected crops to control SPVD thereby reducing disease incidences and yield losses. Nevertheless, the use of clean and virus-free planting materials is economically viable provided there is effective and efficient system for production, multiplication and distribution of planting materials (Carey et al., 1999; Feng et al., 2000). However, commercialization of sweetpotato production is a major challenge in many developing countries particularly in Sub-Saharan Africa as the crop is mainly grown for household subsistence (Valverde et al., 2007). The capacity of public institutes to sustainably produce and multiply clean and virus-free planting materials for low income farmers in these countries is uncertain. Research institutes are financially constrained and farmers lack purchasing power to multiply and distribute, and purchase improved healthy planting materials, respectively (Kapinga et al., 2003a; Mtunda et al., 2003). Rukarwa et al. (2010) reported that, inadequacy of production, multiplication and distribution of certified virus-free planting materials was a major setback in sweetpotato production in Uganda. Therefore, economic and infrastructure constraints are likely to significantly limit establishment and development of clean and virus-free planting material schemes.

1.4.2. Control of SPVD vectors

The viruses including SPFMV and SPCSV, the major components of SPVD are transmitted by aphids and whiteflies, respectively. The control of these vectors is likely to contribute significantly to the control of SPVD. The control of the vectors may involve varied practices such use of chemicals, eradication of weeds and other virus sources (Hull, 1994; Thresh, 2003). However, the control of vector populations under field conditions has proven to be difficult and seldom used in sweetpotato (van den Bosch et al., 2007). Ames et al. (1997) pointed out that controlling whiteflies is not usually an effective means of limiting the incidence of the viruses they transmit. Also, Ndunguru et al. (2009) reported the absence of correlation between number of whiteflies and SPVD severity. Further, the control of insect vectors may not be economically viable as sweetpotato is not well commercialized and is largely grown by subsistence farmers (Rukarwa et al., 2010).

1.4.3. Deployment of SPVD resistant germplasm

Sweetpotato is primarily propagated using stem cuttings. Botanically, true seeds have been exclusively used for breeding programmes (Gaba and Singer, 2009; Sihachakr et al., 1997). In farmers' fields sweetpotato seeds or seedlings have not been considered as a source of diversity (Gibson et al., 2000). In sweetpotato improvement programmes genetic variation has largely been enhanced through conventional hybridization. The approach has some limitations due to biological nature of the crop (Shin et al., 2011; Yi et al., 2007). Genetic improvement of sweetpotato has been challenging due to their heterozygous genetic constitution, polyploidy, self-incompatibility and cross-incompatibility (Mwanga et al., 2002b; Okada et al., 2002; Zhang et al., 2000). Sweetpotato has hexaploid number of chromosomes (2n = 6x = 90) (Kowyama et al., 2000; Magoon et al., 1970; Martin and Ortiz, 1967; Nishiyama et al., 1975; Orjeda et al., 1990). This large number of chromosomes has implications on meiotic irregularity. Sexual compatibility barriers associated with hexaploidy nature restricts hybridization within the species (Diaz et al., 1996; Jones, 1980). The barriers are either genetic or cytogenetic or physiological and their interactions. Also, its genetic improvement is largely limited by sterility and incompatibility (Jones, 1980; Kowyama et al., 2000; Martin, 1968; Martin, 1970; Ting and Kehr, 1953). Relatively few genetic studies on sweetpotato could be largely be due to reproductive barriers from self-incompatibility, high levels of cross-incompatibility, polyploidy and reduced or absence of flowering in some genotypes (Cao et al., 2009; Chang et al., 2009; Magoon et al., 1970; Martin and Ortiz, 1967; Okada et al., 2002; Shin et al., 2011). Incompatibility is caused by pre- and post-fertilization barriers (Kobayashi et al., 1993; Kowyama et al., 1980; Martin, 1970; Martin and Ortiz, 1967). The system of SI in sweetpotato and other species in genus *Ipomoea* is homomorphic sporophytic incompatibility controlled by a single multiple alleles at S-locus (Diaz et al., 1996; Kowyama et al., 1980; Kowyama et al., 2000; Martin, 1968; Tomita et al., 2004). This system causes complete failure of pollen germination on the stigma after self-fertilization (Kowyama et al., 2000; Martin, 1970; Tomita et al., 2004). Martin (1968) suggested presence of duplicated incompatibility loci with epistatic interaction. On the other hand, Kowyama et al. (1980) suggested presence of either dominance or independence or competitive relationships among multi-alleles controlling sporophytic incompatibility.

Self-incompatibility prevents self-fertilization and promotes cross-fertilization (Byers and Meagher, 1992; Tseng et al., 2002). However, cross-fertilization is not guaranteed due to cross-incompatibility (Martin, 1970; Tseng et al., 2002). According to Diaz et al. (1996), complex genetic, cytogenetic and physiological interactions, greatly influence interbreeding in the section *Batatas*.

It plays a role in maintaining genetic diversity but limits genetic improvement due to cross-incompatibility (Nishiyama et al., 1975; Tomita et al., 2004). Despite the SI gene, high degree of cross-incompatibility and other barriers such as male sterility (Elameen et al., 2011; Liu, 2011), genetic improvement of sweetpotato by either conventional or biotechnology means are necessary.

1.4.4. Conventional sweetpotato breeding for SPVD resistance

Breeding for virus resistant cultivars has been recommended as the long-term solution to sustainably control SPVD and other viral diseases (Domola et al., 2008). However, breeding for SPVD resistance has not been an easy endeavour. Lack of resistant, high yielding and locally adapted varieties have given farmers limited alternatives to susceptible high yielding local varieties or landraces (Gibson et al., 2000). Therefore, incorporation of resistance genes into susceptible but high yielding landraces is a preferred strategy for managing not only SPVD but also other crop diseases. This is the direct and effective strategy for long term control of viral diseases (Carey et al., 1999; Fraile et al., 2011; Hull, 1994; Mihovilovich et al., 2000). Jones et al. (1986) recommended that, "no matter which insect species infecting the plant, genetic resistance should be considered as the possible solution; even intermediate level of resistance can be of significant economic importance". Efficient and effective breeding systems are likely to effectively contribute to the release of superior and resistant cultivars to control SPVD (Gibson et al., 2004; Gibson et al., 2000). Progress on breeding for SPVD resistance has been made in several countries including Uganda, United States, Japan, China, Taiwan and Peru (Carey et al., 1999; Lebot, 2010; Mwanga et al., 2002b; Tairo et al., 2005).

Emphasis in developing resistance to SPVD has largely focused on resistance to SPFMV, an important component of SPVD (Mwanga et al., 2002b; Valverde et al., 2007). This resistance breaks down in co- or multi-infections with either SPCSV or SPMMV or both. Breakdown of resistance by different strains or highly virulent viruses leaves the resistance redundant (Kreuze et al., 2009; Miano et al., 2008). This implies that, resistant cultivars developed such as in Peru and other parts of the world might be of little value in other environments due to presence of different viral strains. The international potato center (CIP) identified some clones resistant to SPFMV after exhaustive germplasm screening; however, the selections succumbed to the SPVD in Uganda (Karyeija et al., 1998). Further, Gibson et al. (1998), Karyeija et al. (1998) and Mwanga et al. (2002b) reported that, resistant varieties in West Africa and Peru succumbed viral diseases in East Africa, possibly due to different strains of viruses. Even in the same region, resistant

cultivars still succumbed to SPVD (Tairo et al., 2005). Therefore, this underpins the use of local germplasm in breeding for SPVD resistant varieties than heavily depending on exotic introductions (Gasura et al., 2010). The resistance of landraces could have been attributed by co-evolutionary processes which led to accumulation of resistance genes in the host population due to dynamic pathogen population (host-parasite co-evolution) (Anderson et al., 2011; Fraile et al., 2011; Ghazvini and Tekauz, 2007). Plants have diverse mechanisms to survive and adapt to broad range of biotic and abiotic stresses. Ulukan (2009) pointed out that most field crops have in-built protection mechanism against diseases, pests and vermin. Oduro (2013) reported lower yields in exotic parents than their progenies due to high viral incidences. Therefore, there is a need to identify and use local germplasm in breeding for SPVD resistant varieties (Gasura et al., 2010; Gibson et al., 1998). Despite its contribution in genetic deployment for disease resistance, conventional hybridization in sweetpotato is constrained by its sterility, incompatibility and hexaploidy nature. Biotechnology or genetic engineering offers great potential for improving disease, pest or stress resistance in sweetpotato (Liu, 2011).

1.4.5. Sweetpotato genetic engineering

Efficient methods to control the sweetpotato virus disease are not available and conventional breeding for resistance has limited success. Breeding for resistance through genetic engineering offers an alternative solution for the control of SPVD. For more than two decades non-conventional approaches have shown the potential to accelerate crop improvement. Plant tissue culture, regeneration techniques and development of transgenic plants are valuable tools for sweetpotato improvement and development (Liu, 2011; Nyaboga et al., 2008; Yang, 2010; Yi et al., 2007). Some of the valued added traits through genetic engineering include plant resistance to viral diseases (Jauhar, 2006). Feng et al. (2000) pointed out the potential of genetic engineering in virus resistance breeding. Also, Chang et al. (2009) pointed the value of marker-assisted selection (MAS) to breeders for rapid determination of superior genotypes prior field maturity. For instance, Prakash and Varadarajan (1992) reported successful introduction of foreign marker genes into the genome of sweetpotato through particle bombardment. Otani et al. (2003) and Yi et al. (2007) successful introduced herbicide resistant *bar* gene in sweetpotato cells and pointed the potential of combining it with other agronomically important traits for improvement of new sweetpotato cultivars. Anwar et al. (2011) successfully produced transgenic plants from a diverse group of sweetpotato cultivars that were tolerant to herbicide and indicated the possibility of generating transgenic plants for economically important groups of sweetpotato. Therefore the use

26

of transgenic technology could be an excellent option to protect crops against devastating viral diseases including SPVD via pathogen–derived resistance or non-conventional protection to viral diseases (Hull, 1994; Jauhar, 2006; Kreuze, 2002). Transgenic sweetpotato resistant to SPVD through resistance to SPFMV have been developed in Kenya, China and other parts of the world (Hannington et al., 2002; Okada et al., 2001; Wambugu, 2003). However, the Kenyan transgenic sweetpotato resistant to SPFMV has been controversial Due to fact that, while Wambugu (2003) reported success' Ching (2004) reports "Broken promises; genetically modified sweetpotato project turns sour as the transgenic material did not quite withstand virus challenge in the field all lines tested were susceptible to viral attacks". Further, Hannington et al. (2002) reported that, despite a decade of research in transgenics, sweetpotato farmers did not receive the virus resistant genetic stock due to underdeveloped biosafety systems.

The transgenic resistance uses the viral coat protein (CP) gene to achieve resistance to SPFMV (Kreuze, 2002). The international potato center (CIP) has used cysteine proteinase inhibitor to develop transgenic resistance to both SPFMV and SPCSV (Kreuze, 2002). Nishiguchi et al. (1998) reported no significant difference in transgenic and non-transgenic sweetpotato with regard to morphological and biological characters. Further, reported no significant differences of ELISA values between the inoculated-transgenic and the non-inoculated-virus free plants to SPFMV. Nyaboga et al. (2008) reported increased resistance with less severe symptoms in transgenic plants than the non-transformed lines inoculated with a combination of SPFMV and SPCSV. Also, Okada and Saito (2008) reported that CP gene provided long term protection to transgenic sweetpotato against SPFMV complex infection compared to the control and suggested that the same are likely to acquire resistance to SPFMV in the field. The technology shades some light as the CP gene is likely to be transmitted from one generation to the next (Okada and Saito, 2008). Despite the appropriateness of transgenic resistance in addressing sweetpotato farmers' priorities is doubtful as low productivity is attributed not only by diseases but also several other factors (Clark et al., 2002; Hannington et al., 2002). Further, transgenic approach is useful for a single gene trait while most of economically important traits including disease resistance in sweetpotato are quantitatively inherited (Cervantes-Flores et al., 2010; Jain, 2010; Mwanga et al., 2002a; Mwanga et al., 2002b). Working with Kenyan sweetpotato genotypes, Miano et al. (2008) identified molecular markers associated with SPVD resistance which could be used in breeding. Yang (2010) recommended that, *in vitro* shoot tip tissue culture could contribute significantly to the production of virus-free plantlets for farmers. The use of tissue culture in generating clean propagating materials should be an integral component of any management programme as it

offers the possibility of managing not only virus diseases but also other pathogens and control genetic stability (Clark et al., 2002).

Despite the low transformation efficiency which has limited the successful application of genetic engineering in sweetpotato (Liu, 2011), still the technology has attractive potential of contributing to sweetpotato improvement not only disease resistance but also other agronomically important traits. Further, marker-assisted selection techniques are effective tools for improving disease resistance and quality in sweetpotato (Liu, 2011). Therefore, identification and development of improved cultivars is one of the strategies for increasing productivity and food security; however, this depends on the availability of diverse germplasm coupled with improved and efficient technologies.

1.4.6. Mutation breeding

For more than half a century, mutation breeding, specifically induced mutation has contributed significantly in the development of superior crop varieties (Jain, 2010). Since sweetpotato is clonally propagated, mutation breeding is likely to be an effective approach for crop improvement and breeding for disease resistance (Liu, 2011; Shin et al., 2011; Wang et al., 2007). Maluszynski et al. (1995) and Wang et al. (2007) pointed out the application of *in vitro* mutagenesis techniques in improving vegetatively propagated crops. By *in vitro* selection, desirable mutants with useful agronomic traits such as disease resistance can be isolated within a relatively short period of time (Jain, 2010). Contrary to transgenic approach which is for single gene traits, mutants with multiple traits are possible. Further, mutation breeding in conjunction with genetic engineering is likely to enhance the improvement of sweetpotato not only for disease resistance but also other important agronomic traits (Wang et al., 2007). Further, Jain (2010) commended mutation induction as being flexible, workable and a low-cost alternative to genetically modified organisms (GMOs).

1.5. The genetics of root yield, dry matter and SPVD

Important traits in crops are controlled mostly by quantitative genes which have distinct effects which are described by different gene effects. Gene effects are either additive or non-additive (e Silva et al., 2004; Hill et al., 2008). Most of economically important traits in sweetpotato are quantitatively inherited (Cervantes-Flores et al., 2010; Lin et al., 2007). Knowledge on heritability of quantitative traits is necessary for an efficient genetic improvement in breeding programmes (Maluf et al., 1983).

28

Additive gene action has reported in the inheritance of dry matter content. Shumbusha et al. (2014) reportedpredominance of additive gene action than non-additive action in inheritance of dry matter in Uganda. Similar findings were reportedby Chiona (2009). Also, Oduro (2013) reported that the GCA effect was substantially greater than SCA effect for dry matter. Moreover, GCA effect for root yield was larger than SCA effect indicating the predominance of additive to non-additive gene effects in inheritance of sweetpotato root weight and yield (Chiona, 2009; Oduro, 2013). Likewise, (Musembi et al., 2015) reported the GCA/SCA ratio of 0.51–0.76 for root yield and dry matter percentage, implying additive gene effects were more important than non-additive gene effects in inheritance of these traits. Conversely, the same author reported predominance of non-additive over additive gene effect for inheritance of number of marketable roots.

Unlike resistance to other plant pathogens, resistance to plant viruses is inherited quantitatively (Diaz-Pendon et al., 2004). Studies on inheritance of SPVD resistance are limited due to its hexaploidy characterized by high genetic variability and complex segregation rations of sweetpotato progeny genotypes (Mwanga et al., 2002b; Nishiyama et al., 1975). Previous studies have indicated the potential of improving resistance to SPVD despite limited knowledge on its inheritance which hinders its efficient utilization in breeding programmes. Hahn et al. (1981) and Mwanga et al. (2002b), reported broad-sense heritability of resistance to SPVD ranging from 0.48-0.98 and narrow-sense heritability of 0.31-0.41. Therefore, with these levels of heritability there are potentials for sweetpotato improvement for SPVD resistance through population improvement techniques.

The breeding of vegetatively reproducing crops differs from sexually reproducing crops. In sweetpotato, once the seedlings are established from the true seeds following hybridization, the integrity of its genotype is maintained by vegetative propagation (Tai, 1974). Hence the genetic effects, either additive or dominance are inherited as whole. Genetic effect can either be additive or dominant or epistatic and in rare cases over-dominance. According to Griffing (1956), general combining ability (GCA) and specific combining ability (SCA) are used to estimate gene effects. The GCA is used to estimate the additive genetic effect while SCA estimates the non-additive components. Fraser (1986) in Mihovilovich et al. (2000) pointed out that where virus resistance was controlled by more than one gene, additive effects were found. Similarly, using a diallel mating design, Mwanga et al. (2002b) found significant proportion of GCA effect compared to SCA implying the presence of additive gene action with regard to inheritance to SPVD resistance. Also, Mihovilovich et al. (2000) reported the predominance of additive genetic effect on the

inheritance of resistance to SPFMV, a major component of SPVD. In addition to additive effects, dominance genetic effect also contributed significantly in the inheritance of SPVD (Mwanga et al., 2002b). Despites the efforts made in developing resistant varieties, lack of knowledge and limited information on the nature of inheritance of the resistance hinders its application in sweetpotato breeding (Mihovilovich et al., 2000; Mwanga et al., 2002b; Valverde et al., 2007) necessitating further investigations. Valverde et al. (2007) pointed the need for comprehensive resistance for protection against local strains in the breeding programmes. Consequently, a number of mating designs have been used to estimate these genetic effects for the aforementioned traits and others. This includes polycross, topcross, North Carolina designs and diallel mating designs.

The choice of a good mating design in conventional plant breeding is a key to the successful plant breeding programme (Nduwumuremyi et al., 2013). Different mating designs have been used to estimate genetic effects for different traits in sweetpotato. Ernest et al. (1994) used nine sweetpotato clones in a polycross for high yield and estimation of heritability for number and yield of storage root in Papua New Guinea. Chiona (2009) adopted polycross design for 12 and 30 parents to determine the magnitude of GxE on various traits including dry matter and root yield. Also, Kapila et al. (2010) adopted a 12 parent polycross mating design to develop high yielding orange fleshed sweetpotato in Papua New Guinea. Mihovilovich et al. (2000) used a 7x7 diallel method four model one to estimate combining ability for resistance to sweetpotato feathery mottle virus. Mwanga et al. (2002) and Chiona (2009) used a 5x5 full diallel to determine the inheritance of resistance to SPVD, root yield, dry matter content and bête carotene. Kivuva et al. (2015) adopted a 6x6 half diallel for root yield, dry matter and drought tolerance. Alternatively, Gasura et al. (2010) and Oduro (2013) adopted a 7x6 and 6x5 North Carolina design II studying inheritance of yield and other quality traits. Likewise, Sseruwu (2012) used a 7x9 North Carolina II to study inheritance of Alternaria blight and other root yield components in Uganda. On the other hand, the expression of the genetic effects is substantially influenced by prevailing environments.

1.6. Effects of genotype-by-environment interaction on resistance to SPVD

Crop growth and production are a result of interactions of its genetic potential and environment.

The performance of genotypes is quantified in terms of a wide and specific adaptability and yield stability (Abidin et al., 2005).

Several important and common traits are a composite reflection of multiple genetic and environmental factors (Vuylsteke and van Eeuwijk, 2008). Sweetpotato is grown in diverse

environments across the world (Caliskan et al., 2007). Despite its adaptability to diverse and harsh growing conditions, the crop is very sensitive to environmental variation (Bryan et al., 2003). This influences most of economically important traits which are largely quantitatively inherited and delays selection process in breeding programmes (Lebot, 2010; Ngeve, 1993). Nakitandwe et al. (2005) found that, sweetpotato genotypes grown in multi-location trials performed differently with regard to yield and disease resistance. The GxE interactions could have largely contributed to breakdown of resistance in improved varieties grown in agro-ecologies with high SPVD pressure (Gibson et al., 1998; Karyeija et al., 1998). Osiru et al. (2009) suggested that, knowledge of genotype performance in different agro-ecologies is critical in cultivar development. Since there are differences in virus strains between agro-ecologies or regions, this could cause resistant genotypes in one region to be susceptible in others (Carey et al., 1999; Gibson et al., 1998). Therefore, newly developed cultivars need to be evaluated across target agro-ecologies to ascertain not only their reaction to SPVD but also yield and other related traits (Caliskan et al., 2007; Mwololo et al., 2009). Determination of genotype by environment interaction effects of sweetpotato genotypes is essential prior to variety release (Kivuva et al., 2014a). Moreover, Laurie (2010) suggested that assessing the reaction of new varieties to different environments would facilitate cultivar recommendations. On the other hand, selecting genotypes that interact less with the environments in which they are grown would be beneficial though not an easy endeavour.

1.7. Conclusions

Sweetpotato is a vital staple food crop for most communities in developing world. Unfortunately, the crop is underexploited compared to other crops despite its contribution. Hence its productivity is not encouraging. The low productivity is aggravated by biotic, abiotic and socio-economic factors. Amongst the biotic factors, SPVD is the most important. The effects of SPVD in sweetpotato production are real and devastating. Breeding for resistant cultivars is indispensable to control the disease for ascertained food security and incomes of rural and marginalized communities depending on this subsector. Conventional breeding in combination with non-conventional techniques such as biotechnology, mutation breeding and genetic engineering have significant role in developing new sweetpotato cultivars that are high yielding and resistant to SPVD. Despite the potential of genetic engineering in crop improvement, its application is not promising in developing countries (Jain, 2010). Presently, combination of conventional breeding, mutation breeding and tissue culture has the role in new cultivar development while waiting for

institutionalization of transgenic crops and other GMOs. Lastly, phytosanitary practices have a role in maintaining the newly developed cultivars.

References

Abidin, P.E., F.A. Eeuwijk, P. Stam, P.C. Struik, M. Malosetti, R.O.M. Mwanga, , B. Odongo, M. Hermann, and E.E. Carey. 2005. Adaptation and stability analysis of sweetpotato varieties for low-input systems in Uganda. Plant Breeding 124:491-497.

Ames De Icochea, T. and T. Ames. 1997. Sweetpotato: major pests, diseases, and nutritional disorders, International Potato Center.

Ames, T., N.E.J.M. Smit, A.R. Braun, J.N. O'sullivan, and L.G. Skoglund. 1997. Sweetpotato: Major pests, diseases and nutritional disorders, Lima, Peru, International Potato Center.

Anderson, K.M., Q. Kang, J. Reber, and M.O. Harris. 2011. No fitness cost for wheat's H gene-mediated resistance to Hessian fly (Diptera: Cecidomyiidae). Journal of Economic Entomology 104:1393-1405.

Anwar, N., K. Watanabe, and J. Watanabe. 2011. Transgenic sweetpotato expressing mammalian cytochrome P450. Plant Cell, Tissue and Organ Culture 105:219-231.

Aritua, V., T. Alicai, E. Adipala, E.E. Carey, and R.W. Gibson. 1998. Aspects of resistance to sweetpotato virus disease in sweetpotato. Annals of Applied Biology 132:387-398.

Aritua, V., J.P. Legg, N.E. Smit, and R.W. Gibson. 1999. Effect of local inoculum on the spread of sweetpotato virus disease: limited infection of susceptible cultivars following widespread cultivation of a resistant sweetpotato cultivar. Plant Pathology 48:655-661.

Ateka, E.M., R.W. Njeru, A.G. Kibaru, J.W. Kimenju, E. Barg, R.W. Gibson, and H.J. Vetten. 2004. Identification and distribution of viruses infecting sweetpotato in Kenya. Annals of Applied Biology 144:371-379.

Balouchi, H.R. 2010. Screening wheat parents of mapping population for heat and drought tolerance, detection of wheat genetic variation. International Journal of Biological and Life Sciences 6:56-66.

Bryan, A.D., J.R. Schultheis, Z. Pesic-Vanesbroeck, and G.C. Yencho. 2003. Cultivar decline in sweetpotato: II. Impact of virus infection on yield and storage root quality in 'Beauregard' and 'Hernandez'. Journal of the American Society for Horticultural Science 128:856-863.

Byamukama, E., E. Adipala, R. Gibson, and V. Aritua. 2002. Reaction of sweetpotato clones to virus disease and their yield performance in Uganda. African Crop Science Journal 10:317-324.

Byers, D.L. and T.R. Meagher. 1992. Mate availability in small populations of plant species with homomorphic sporophytic self-incompatibility. Heredity 68:353-359.

Caliskan, M.E., E. Erturk, T. Sogut, E. Boydak, and H. Arioglu. 2007. Genotype x environment interaction and stability analysis of sweetpotato (*Ipomoea batatas*) genotypes. New Zealand Journal of Crop and Horticultural Science 35:87-99.

Cao, Q., A. Zhang, D. Ma, H. Li, Q. Li, and P. Li. 2009. Novel interspecific hybridization between sweetpotato (*Ipomoea batatas* (L.) Lam.) and its two diploid wild relatives. Euphytica 169:345-352.

Carey, E., R. Gibson, S. Fuentes, M. Machmud, R. Mwanga, G. Turyamureeba, L. Zhang, D. Ma, F.A. El-Abbas, and R. El-Bedewy. 1999. The causes and control of virus diseases of sweetpotato in developing countries: Is sweetpotato virus disease the main problem. CIP Program Report, 1997-1998:241-248.

Cattivelli, L., F. Rizza, F.W. Badeck, E. Mazzucotelli, A.M. Mastrangelo, E. Francia, C. Mare`, A. Tondelli, and A.M. Stanca. 2008. Drought tolerance improvement in crop plants: An integrated view from breeding to genomics. Field Crops Research 105:1-14.

Cervantes-Flores, J., B. Sosinski, K. Pecota, R. Mwanga, G. Catignani, V. Truong, R. Watkins, M. Ulmer, and G. Yencho. 2010. Identification of quantitative trait loci for dry-matter, starch, and β-carotene content in sweetpotato. Molecular Breeding:1-16.

Chang, K., H. Lo, Y. Lai, P. Yao, K. Lin, and S. Hwang. 2009. Identification of quantitative trait loci associated with yield-related traits in sweetpotato (*Ipomoea batatas*). Botanical Studies 50:43-55.

Ching, L.L. 2004. Broken promises: GM sweetpotato project turns sour. *A magazine of Green Social Thoughts* St. Louis, MO 63130 WD Press, Synthesis/Regeneration

Chiona, M. 2009. Towards enhancement of β-carotene content of high drymass sweetpotato genotypes in Zambia*.* PhD Thesis. University of KwaZulu Natal.

Clark, C., R. Valverde, S. Fuentes, L. Salazar, and J. Moyer. 2002. Research for improved management of sweetpotato pests and diseases: cultivar decline. Acta Horticulturae 583:103-112.

Clark, C.A., G.J. Holmes, and D.M. Ferrin. 2009. Major fungal and bacterial diseases. *In:* Loebenstein, G. and thottappilly, G. (eds.) The sweetpotato. Springer Netherlands.

Collins, N.C., F. Tardieu, and R. Tuberosa. 2008. Quantitative trait loci and crop performance under abiotic stress: where do we stand? Plant Physiology 147:469–486.

Diaz-Pendon, J.A., V. Truniger, C. Nieto, J. Garcia-Mas, A. Bendahmane, and M. Aranda. 2004. Advances in understanding recessive resistance to plant viruses. Molecular Plant Pathology 5:223-233.

Diaz, J., P. Schmiediche, and D.F. Austin. 1996. Polygon of crossability between eleven species of *Ipomoea*: section Batatas (Convolvulaceae). Euphytica 88:189-200.

Dje, Y. and H.A. Diallo. 2005. Detection of sweetpotato feathery mottle virus in sweetpotato using membrane immunobinding assay. African Journal of Biotechnology 4:717-723.

Domola, M.J., G.J. Thompson, T.A.S. Aveling, S.M. Laurie, H. Strydom, and A.A. Van Den Berg. 2008. Sweetpotato viruses in South Africa and the effect of viral infection on storage root yield. African Plant Protection 14:15-23.

Ebregt, E., P.C. Struik, P.E. Abidin, and B. Odongo. 2004. Farmers' information on sweetpotato production and millipede infestation in north-eastern Uganda. II. Pest incidence and indigenous control strategies. Njas-Wageningen Journal of Life Sciences 54:69-84.

Ekanayake, I.J. and W. Collins. 2004. Effect of irrigation on sweetpotato root carbohydrates and nitrogenous compounds. Food, Agriculture and Environment 2:243-248.

Elameen, A., A. Larsen, S. Klemsdal, S. Fjellheim, L. Sundheim, S. Msolla, E. Masumba, and O. Rognli. 2011. Phenotypic diversity of plant morphological and root descriptor traits within a sweetpotato germplasm collection from Tanzania. Genetic Resources and Crop Evolution 58:397-407.

Elliott, K.A. and M. Hoffman. 2010. Pulling Agricultural Innovation into the Market together: Working paper. Massachhusetts, Washington, DC: Center for Global Development.

Engoru, P., J. Mugisha, and B. Bashaasha. 2005. Tuber utilization options among sweetpotato producers in eastern Uganda. African Crop Science Journal 7:715-719.

Ernest, J., I.E. Wagih, and V. Kesavan. 1994. Genetic evaluation of polycross hybrids of sweetpotatoes. African Crop Science Journal 2:29-34.

e Silva, J.C., N.M. Borralho, and B.M. Potts. 2004. Additive and non-additive genetic parameters from clonally replicated and seedling progenies of Eucalyptus globulus. Theoretical and applied genetics, 108:1113-1119.

Feng, G., G. Yifu, and Z. Pinbo. 2000. Production and deployment of virus-free sweetpotato in China. Crop Protection 19:105-111.

Fraile, A., I. Pagan, G. Anastasio, E. Saez, and F. Garcia-Arenal. 2011. Rapid genetic diversification and high fitness penalties associated with pathogenicity evolution in a plant virus. Molecular Biology and Evolution 28:1425-1437.

Fugile, K. 2007. Priorities for sweetpotato research in developing countries: Results of a survey. American Journal of Potato Research 84:353-365.

Gaba, V. and S. Singer. 2009. Propagation of sweetpotatoes: *In situ* germplasm conservation and conservation by tissue culture. *In:* Loebenstein, Gand G. Thottappilly. (eds.) The Sweetpotato*. Springer Science+Business Media B.V.

Garcĭa-Arenal, F. and B.A. Mcdonald. 2003. An analysis of the durability of resistance to plant viruses. Analytical and Theoretical plant pathology 93:941-952.

Gasura, E., A.B. Mashingaidze, and S.B. Mukasa. 2010. Genetic variability for tuber yield, quality, and virus disease complex traits in Uganda sweetpotato germplasm. African Crop Science Journal 16:147-160.

Gasura, E. and S.B. Mukasa. 2010. Prevalence and implication of sweetpotato recovery from sweetpotato virus disease in Uganda. African Crop Science Journal 18:195-205.

Ghazvini, H. and A. Tekauz. 2007. Reactions of Iranian barley accessions to three predominant pathogens in Manitoba. Canadian Journal of Plant Pathology-Revue Canadienne De Phytopathologie 29:69-78.

Gibson, R.W. 2005. Working with farmers to control sweetpotato virus disease in East Africa: Crop protection programme. UK: Natural resource institute.

Gibson, R.W., V. Aritua, E. Byamukama,I. Mpembe, and J. Kayongo. 2004. Control strategies for sweetpotato virus disease in Africa. Virus Research 100:115-122.

Gibson, R.W., S.C. Jeremiah, V. Aritua, R.P. Msabaha, I. Mpembe, and J. Ndunguru. 2000. Sweetpotato virus disease in Sub Saharan Africa: Evidence that neglect of seedlings in the traditional farming system hinders the development of superior resistant landraces. Journal of Phytopathology 148:441-447.

Gibson, R.W., I. Mpembe, T. Alicai, E.E. Carey, R.O.M. Mwanga, S.E. Seal, and H.J. Vetten. 1998. Symptoms, aetiology and serological analysis of sweetpotato virus disease in Uganda. Plant Pathology 47:95-102.

Gibson, R.W., R.O.M. Mwanga, S. Kasule, I. Mpembe, and E.E. Carey. 1997. Apparent absence of viruses in most symptomless field-grown sweetpotato in Uganda. Annals Applied Biology 130:481-490.

Gichuki, S.T., M. Berenyi, D. Zhang, M. Hermann, J. Schmidt, J. Glössl, and K. Burg. 2003. Genetic diversity in sweetpotato [*Ipomoea batatas* (L.) Lam.] in relationship to geographic sources as assessed with RAPD markers. Genetic Resources and Crop Evolution 50:429-437.

Griffings, B. 1956. Concept of general and specific combining ability in relation to diallel crossing systems. Australian Journal of Biological Sciences 9:463-493.

Gutiérrez, D.L., S. Fuentes, and L.F. Salazar. 2003. Sweetpotato virus disease (SPVD): Distribution, incidence and effect on sweetpotato yield in Peru. Plant Disease 87:297-302.

Hahn, S., E. Terry, and K. Leuschner. 1981. Resistance of sweetpotato to virus complex. HortScience 16:535-537.

Hannington, O., P. Kameri-Mbote, and D. Wafula. 2002. Innovation and policy process: Case of transgenic sweetpotato in Kenya. Economic and Political Weekly 37:2770-2777.

Harrison, H.F., Jr. and D.M. Jackson. 2011. Response of two sweetpotato cultivars to weed interference. Crop Protection 30:1291-1296.

Hill, W.G., M.E. Goddard, and P.M. Visscher. 2008. Data and Theory Point to Mainly Additive Genetic Variance for Complex Traits. PLoS Genetics 4(2): e1000008. doi:10.1371/journal.pgen.1000008

Hu, W., A. Jiang, L. Jin, C. Liu, M. Tian, and Y. Wang. 2011. Effect of heat treatment on quality, thermal and pasting properties of sweetpotato starch during yearlong storage. Journal of the Science of Food and Agriculture 91:1499-1504.

Huaman, Z. 1992. Systematic botany and morphology of the sweetpotato plant. *In:* CIP (ed.). Lima, Peru: CIP.

Huang, J.C. and M. Sun. 2000. Genetic diversity and relationships of sweetpotato and its wild relatives in *Ipomoea* series Batatas (Convolvulaceae) as revealed by inter-simple sequence repeat (ISSR) and restriction analysis of chloroplast DNA. TAG Theoretical and Applied Genetics 100:1050-1060.

Hull, R. 1994. Resistance to plant viruses: Obtaining genes by non-conventional approaches. Euphytica 75:195-205.

Ishak, J.A., J.F. Kreuze, A. Johansson, S.B. Mukasa, F. Tairo, F.M. Abo El-Abbas, and J.P.T. Valkonen. 2003. Some molecular characteristics of three viruses from SPVD-affected sweetpotato plants in Egypt. Archives of Virology 148:2449-2460.

Jain, S.M. 2010. Mutagenesis in crop improvement under the climate change. Romanian Biotechnological Letters 15:89-106.

Jauhar, P.P. 2006. Modern biotechnology as an intergral supplement to conventional plant breeding: The prospects and challenges. Crop Science 46:1841-1859.

Johanson, A. and C.L. Ives. 2001. An inventory of agricultural biotechnology for the Eastern and Central Africa region. Michigan, USA: Institute of International Agriculture.

Jones, A. 1980. Sweetpotato. American Society of Agronomy 46:645-655.

Jones, A., P.D. Dukes, and J.M. Schalk. (eds.). 1986. Sweetpotato breeding, Westport, CT, USA: AVI Publishing Co.

Kapila, R., B. Wera, M. Deros, R. Pawilnga, S. Ivahupa, G. Bagle, T. Okpul, and E. Guaf. 2010. Niugini Agrisaiens. Niugini Agrisaiens:30.

Kapinga, R., J. Ndunguru, G. Mulokozi, and S. Tumwegamire. 2009. Impact of common sweetpotato viruses on total carotenoids and root yields of an orange-fleshed sweetpotato in Tanzania. Scientia Horticulturae 122:1-5.

Kapinga, R., S. Tumwegamire, B. Lemaga, M. Andrade, R. Mwanga, M. Mtunda, P. Ndolo, and J. Nsumba. 2007. Development of farmer based seed systems for healthy planting materials and increased sweetpotato production in East and Southern Africa. *In:* Kapinga, R., R. Kingamkono, M. Msabaha, J. Ndunguru, B. Lemaga, and G. Tusiime. eds. *The Thirteenth triannial Symposium of the International Society for tropical and Root Crops*,

2003a AICC, Arusha, Tanzania. International Society for tropical and Root Crops (ISTRC), 1169-1173.

Kapinga, R., D. Zhang, B. Lemaga, M. Andrade, R.O.M. Mwanga, S. Laurie, P. Ndoho, and E. Kanju. 2003. Sweetpotato improvement in sub-Saharan Africa. *In:* Kapinga, R., R. Kingamkono, M. Msabaha, J. Ndunguru, B. Lemaga, and G. Tusiime. e. (eds.) *The Thirteenth Triennial Symposium of the International Society for Tropical Root Crops.* AICC, Arusha: International Society for Tropical Root Crops (ISTRC).

Kapinga, R.E. and E.E. Carey. 2003. Present status of sweetpotato breeding for eastern and southern Africa. *In:* Rees, D., Q. van Oirschot, and R. Kapinga. (eds.) Sweetpotato post-harvest assessment: Experience from East Africa*.* London, UK: Natural Resource Institute, University of Greenwich.

Kapinga, R.E., P.T. Ewell, S.C. Jeremiah, and R. Kileo. 1995. Sweetpotato in Tanzanian farming and food systems: Implications for research, Internation potato Center (CIP) Sub-Saharan Africa Regional Office, Nairobi and Ministry of Agriculture, Dar es Salaam, Tanzania.

Karuri, H.W., E.M. Ateka, R. Amata, A.B. Nyende, and A.W.T. Muigai. 2009. Characterization of Kenyan sweetpotato genotypes for SPVD resistance and high dry matter content using simple sequence repeat markers. African Journal of Biotechnology 8:2169-2175.

Karyeija, R., R. Gibson, and J.P.T. ValkonenJ. 1998. The significance of sweetpotato feathery mottle virus in subsistence sweetpotato production in Africa. Plant Disease 82:4-15.

Karyeija, R.F.,J.F. Kreuze, R.W. Gibson, and J.P.T. Valkonen. 2000. Synergistic interactions of a potyvirus and a phloem-limited crinivirus in sweetpotato plants. Virology 269:26-36.

Kivuva, B.M., S.M. Githiri, G.C. Yencho, and J. Sibiya. 2014a. Genotype X Environment Interaction for Storage Root Yield in Sweetpotato Under Managed Drought Stress Conditions. Journal of Agricultural Science 6:41-56.

Kivuva, B.M., F.J. Musembi, S.M. Githiri, C.G. Yencho, and J. Sibiya. 2014b. Sssessment of production constraints and farmers'preferences for sweetpotato genotypes. Journal of Plant Breeding and Genetics 2:15-29.

Kobayashi, R.S., S.L. Sinden, and J.C. Bouwkamp. 1993. Ovule culture of sweetpotato (*Ipomoea batatas*) and closely related species. Plant Cell, Tissue and Organ Culture 32:77-82.

Kokkinos, C.D., C.A. Clark, C.E. Mcgregor, and D.R. Labonte. 2006. The effect of sweetpotato virus disease and its viral components on gene expression levels in sweetpotato. Journal of America Society of Horticultural Science 131:657-666.

Korada, R.R., S.K. Naskar, A.R. Prasad, A.L. Prasuna, and K.N. Jyothi. 2010. Differential volatile emision from sweetpotato plant: mechanism of resistance in sweetpotato for weevil *Cylas foricarius* (Fab). Current Science 99:1597-1601.

Kowyama, Y., N. Shimano, and T. Kawase. 1980. Genetic analysis of incompatibility in the diploid Ipomoea species closely related to the sweetpotato. TAG Theoretical and Applied Genetics 58:149-155.

Kowyama, Y., T. Tsuchiya, and K. Kakeda. 2000. Sporophytic self-incompatibility in *Ipomoea trifida*, a close relative of sweetpotato. Annals of Botany 85:191.

Kreuze, J.F. 2002. Molecular studies on the sweetpotato virus disease and its two causal agents*.* PhD Thesis, Swedish University of Agricultural Sciences.

Kreuze, J.F., J.P.T. Valkonen, and M. Ghislain. 2009. Genetic engineering. *In:* Loebenstein, G. and G. Thottappilly. (eds.) The sweetpotato*.* Netherlands: Springer

Kriegner, A., J.C. Cervantes, K. Burg, R.O.M. Mwanga, and D. Zhang. 2003. A genetic linkage map of sweetpotato based on AFLP markers. Molecular Breeding 11:169-185.

Kulembeka, H., C. Rugutu, E. Kanju, B. Chirimi, E. Rwiza, and R. Amour. 2005. The agronomic performance and acceptability of orange fleshed sweetpotato varieties in the lake zone of Tanzania. African Crop Science Journal 12:229-240.

Kuo, C.G. 1991. Conservation and distribution of sweetpotato germplasm. *In:* DODDS, J. H. (ed.) In-vitro methods for conservationof plant genetic resources*.* London, UK: Chapman and Hall.

Lebot, V. 2010. Sweetpotato. *In:* Bradshaw, J.E. (ed.) Root and tuber crops: Handbook of plant breeding*.* London: Springer.

Lin, K., Y.C. Lai, K. Chang, Y. Chen, S.Y. Hwang, and H.F. Lo. 2007. Improving breeding efficiency for quality and yield of sweetpotato. Botanical Studies 48: 283-292.

Liu, Q. 2011. Sweetpotato omics and biotechnology in China. Plant Omics 4:295-301.

Liwenga, E.T. and R.Y.M. Kangalawe. 2009. Climate change/variability and implications on agricultural production and livelihoods in the southern highlands of Tanzania. *In:* Paul,

S.M. and A.E. Majule. (eds.). *Strengthening local agricultural innovations to adapt to climate change in Botswana, Malawi, South Africa and Tanzania.* Dar-es- Salaam, Tanzania: Institute of Resource Assessment, University of Dar es Salaam.

Lou, H.R., M.S. Maria, J. Benavides, D.P. Zhang, Y. Zhang, and M. Ghislain. 2010. Rapid genetic transformation of sweetpotato (*Ipomeea batatas* (L.) Lam) via organogenesis African Journal of Biotechnology 5:1851-1857.

Low, J., J. Lynam, B. Lemaga, C. Crissman, I. Barker, G. Thiele, S. Namanda, C. Wheatley, and M. Andrade. 2009. Sweetpotato in Sub-Saharan Africa. *In:* Loebenstein, G. and Thottappilly, G. (eds.) The sweetpotato. Springer Netherlands.

Magoon, M.L., R. Krishnan, and K. Vijaya Bai. 1970. Cytological evidence on the origin of sweetpotato. TAG Theoretical and Applied Genetics 40:360-366.

Maluszynski, M., B. Ahloowalia, and B. Sigurbjörnsson. 1995. Application of in vivo and in vitro mutation techniques for crop improvement. Euphytica 85:303-315.

Martin, F.W. 1968. The system of self-incompatibility in Ipomoea. Journal of Heredity 59:263.

Martin, F.W. 1970. Self-and interspecific incompatibility in the Convolvulaceae. Botanical Gazette 131:139-144.

Martin, F.W. and E. Cabanillas. 1966. Post-pollen-germination barriers to seed set in sweet-potato. Euphytica 15:404-411.

Martin, F.W. and S. Ortiz. 1967. Anatomy of stigma and style of sweetpotato. New Phytologist 66:109-113.

Masumba, E., R. Kapinga, S.M. Tollan, M. Yongolo, and D.C. Kitundu. 2007. Adaptability and acceptability of new orange-fleshed sweetpotato varieties in selected areas of eastern and central zones of Tanzania. *In:* Kapinga, R., R. Kingamkono, M. Msabaha, J. Ndunguru, B. Lemaga, and G. Tusiime. (eds). *The Thirteenth Triennial Symposium of International Society of Tropical Root Crops* 10-14 November 2003 AICC, Arusha. Tanzania: International Society of Tropical Root Crops (ISTRC), 737-745.

Masumba, E., H. Kulembeka S. Tollano, and M. Yongolo. 2005. Participatory evaluation of improved sweetpotato varieties in Eastern Tanzania. African Crop Science Journal 12:259-265.

Maule, A.J., C. Caranta, and M.I. Boulton. 2007. Sources of natural resistance to plant viruses: Status and prospects. Molecular Plant Pathology 8:223-231.

Mbwaga, Z., M. Mataa, and M. Msabaha. 2007. Quality and yield stability of orange fleshed sweetpotato *(Ipomoea batatas)* varieties grown in different agro-ecologies. *The Eighth African Crop Science Society Conferenc*e*.* El-minia, Egypt: African Crop Science Soceity.

Mcharo, M. and E.E. Carey. 2001. Performance of selected sweetpotato varieties in Kenya. African Crop Science Journal 9:49-57.

Miano, D., D. Labonte, and C. Clark. 2008. Identification of molecular markers associated with sweetpotato resistance to sweetpotato virus disease in Kenya. Euphytica 160:15-24.

Mihale, M., A. Deng, H. Selemani, M. Kamatenesi, A. Kidukuli, and J. Ogendo. 2009. Use of indigenous knowledge in the management of field and storage pests around Lake Victoria basin in Tanzania. African Journal of Environmental Science and Technology 3:251-259.

Mihovilovich, E., H.A. Mendoza, and L.F. Salazar. 2000. Combining ability for resistance to sweetpotato feathery mottle virus. HortScience 35:1319-1320.

Mont, J., M. Iwanaga, G. Orjeda, and K. Watanabe. 1993. Abortion and determination of stages for embryo rescue in crosses between sweetpotato, *Ipomoea batatas* Lam. (2n=6x=90) and its wild relative, *I. trifida* (H. B. K.) G. Don. (2n=2x=30). Sexual Plant Reproduction 6:176-182.

Mpagalile, J., V. Silayo, H. Laswai, W. Ballegu, and C. Kikuu. 2003. Effect of different storage methods on the shelf-life of fresh sweetpotatoes in Gairo, Tanzania. Tropical Root and Tuber Crops 10:500-505.

Mtunda, K.J., E. Kanju, D. Chilosa, and M. Kilima. 2003. Increasing sweetpotato production in Tanzania through multiplication and distribution of improved farmer selected varieties. *Technical Annual Report.* Kibaha: Sugarcane Research Institute.

Mudiope, J., H. Kindness, and V. Haigenemana. 2000. Socio-economic constraints to the production, processing and marketing of Sweetpotato in Kumi district, Uganda. UK: DFID.

Mukasa, S.B., P.R. Rubaihayo, and J.P.T. Valkonen. 2006. Interactions between a crinivirus, an ipomovirus and a potyvirus in co-infected sweetpotato plants. Plant Pathology 55:458-467.

Mullen, M.A. 1984. Influence of sweetpotato weevil infestation on the yields of twelve sweetpotato lines. Journal of Agricultural Entomology 1:227-230.

Munyiza, H., P. Stevenson, R. Mwanga, H. Talwana, J. Murumu, and B. Odongo. 2007. The relationship between stem base and root damage by *Cylass* spp. on sweetpotato. African Crop Science Journal 8:955-957.

Musembi, K., S. Githiri, G. Yencho, and J. Sibiya. 2015. Combining ability and heterosis for yield and drought tolerance traits under managed drought stress in sweetpotato. Euphytica 201:423-440.

Muturi, P.W., J.K. Mwololo, M.W.K. Mburu, R.W. Njeru, N. Kiarie, J.K. Munyua, E.M. Ateka, R.W. Muinga, R.E. Kapinga, and B. Lemaga. 2007. Strategies of maintaining sweetpotato nurseries free from insect vectors that spread sweetpotato virus disease.2071-2074.

Muyinza, H., P. Stevenson, R. Mwanga, H. Talwana, J. Murumu, and B. Odongo. 2007. The realationship between stem base and root damage by Cylas spp. on sweetpotato. African Crop Science Journal 8:955-957.

Mwanga, R., E.E. Carey, J.W. Moyer, D.P. Zhang, and G.C. Yencho. 2002a. Nature of resistance of sweetpotato to sweetpotato virus disease. Acta Horticulturae 583:113-119.

Mwanga, R. and G. Ssemakula. 2011. Orange-fleshed sweetpotatoes for food, health and wealth in Uganda. International Journal of Agricultural Sustainability 9:42-49.

Mwanga, R., G. Yencho, and J.W. Moyer. 2002b. Diallel analysis of sweetpotato for resistance to sweetpotato virus disease. Euphytica 128:237-248.

Mwanga, R.O.M., B. Odongo, C. Niringiye, R. Kapinga, and S. Tumwegamire. 2007. Sweetpotato selection releases: Lessons learnt from Uganda. African Crop Science Journal 15:11-23.

Mwololo, J.K., M.W.K. Mburu, R.W. Njeru, E.M. Ateka, N. Kiarie, J.K. Munyua, R.W. Muinga, R. Kapinga, and B. Lemaga. 2007. Resistance of sweetpotato genotypes to sweetpotato virus disease in Coastal Kenya.2083-2086.

Mwololo, J.K., P.W. Muturi, M.W.K. Mburu, R.W. Njeru, N. Kiarie, J.L. Munyua, E.M. Ateka, R.W. Muinga, R.E. Kapinga, and B. Lemaga, . 2009. Additive main effects and multiplicative interaction analysis of geneotype x environmental interaction among sweetpotato genotypes. Journal of Animal and plant Sciences 2:148-155.

Nakitandwe, J., E. Adipala, R. El-Bedewy, W. Wagoire, and B. Lemaga. 2005. Adaptability of SIFT potato genotypes in different agro-ecologies of Uganda. African Crop Science Journal 13:107-116.

Ndunguru, J. and R. Kapinga. 2007. Viruses and virus-like diseases affecting sweetpotato subsistence farming in southern Tanzania. African Journal of Agricultural Research 2:232-239.

Ndunguru, J., R. Kapinga, P. Sseruwagi, B. Sayi, R. Mwanga, S. Tumwegamire, and C. Rugutu. 2009. Assessing the sweetpotato virus disease and its associated vectors in northwestern Tanzania and central Uganda. African Journal of Agricultural Research 4:334-343.

Nduwumuremyi, A., P. Tongoona, and S. Habimana. 2013. Mating designs: helpful tool for quantitative plant breeding analysis. Journal of Plant Breeding and Genetics 1:117-129.

Ngeve, J.M. 1993. Regression analysis of genotype × environment interaction in sweetpotato. Euphytica 71:231-238.

Nishiguchi, M., M. Mori, Y. Okada, T. Murata, T. Kimura, J. Sakai, K. Hanada, C. Miyazaki, and A. Saito. 1998. Virus resistant transgenic sweetpotato with the CP gene: Current Challenge and perspective of its use. Phytoprotection 79:112-116.

Nishiyama, I., T. Miyazaki, and S. Sakamoto. 1975. Evolutionary autoploidy in the sweetpotato (*Ipomoea batatas* (L.) Lam.) and its progenitors. Euphytica 24:197-208.

Njeru, R.W., M.W.K. Mburu, E. Cheramgoi, R.W. Gibson, Z.M. Kiburi, E. Obudho, and D. Yobera. 2004. Studies on the physiological effects of viruses on sweetpotato yield in Kenya. Annals of Applied Biology 145:71-76.

Nyaboga, E.N., E.M. Ateka, S.T. Gichuki, and W.D. Bulimo. 2008. Reaction of transgenic sweetpotato (*Ipomoea batatas* L.) lines to virus challenge in the glasshouse. Journal of Applied Biosciences 9:362 - 371.

Oduro, V. 2013. Genetic Control of Sugars, Cry Matter, and Beta-Carotene in Sweetpotato (*Ipomoea batatas* [L.] Lam). University of Ghana, Legon.

Okada, Y., M. Nishiguchi, A. Saito, T. Kimura, M. Mori, K. Hanada, J. Sakai, Y. Matsuda, and T. Murata, T. 2002. Inheritance and stability of the virus-resistant gene in the progeny of transgenic sweetpotato. Plant Breeding 121:249-253.

Okada, Y. and A. Saito. 2008. Evaluation of resistance to complex infections of SPFMVs in transgenic sweetpotato. Breeding Science 58:243-250.

Okada, Y., A. Saito, M. Nishiguchi, T. Kimura, M. Mori, K. Hanada, J. Sakai, C. Miyazaki, Y. Matsuda, and T. Murata. 2001. Virus resistance in transgenic sweetpotato [*Ipomoea*

batatas L. (Lam)] expressing the coat protein gene of sweetpotato feathery mottle virus. TAG Theoretical and Applied Genetics 103:743-751.

Opiyo, S.A., E.M. Ateka, P.O. Owuor, L.O.A. Manguro, and D.W. Miano. 2010. Development of a multiplex PCR techniques for simultaneous detection of Sweetpotato feathery mottle virus and Sweetpotato chlorotic stunt virus. Journal of Plant Pathology 92:363-366.

Orjeda, G., R. Freyre, and M. Iwanaga. 1990. Production of 2n pollen in diploid Ipomoea trifida, a putative wild ancestor of sweetpotato. Journal of Heredity 81:462.

Orjeda, G., R. Freyre, and M. Iwanaga. 1991. Use of *Ipomoea trifida* germplasm for sweetpotato improvement. 3. Development of 4x interspecific hybrids between *Ipomoea batatas* (L.) Lam. (2n=6x=90) and *I. trifida* (H.B.K) G. Don. (2n=2x=30) as storage-root initiators for wild species. TAG Theoretical and Applied Genetics 83:159-163.

Otani, M., V. Wakita, and T. Shimada. 2003. Production of herbicide-resistant sweetpotato (*Ipomoea batatas* (L.) Lam) plants by Agrobacterium tumefaciens-mediated transformation. Breeding Science 53:145-148.

Pareek, A., S.K. Sopory, H.J. Bohnert, and Govindjee (eds.) 2010. Abiotic stress adaptation in plants: Physiological, Molecular and Genomic Foundation.*,* Dordrecht, The Netherlands: Springer.

Prakash, C.S. and U. Varadarajan. 1992. Genetic transformation of sweetpotato by particle bombardment. Plant Cell Reports 11:53-57.

Rees, D., R. Kapinga, E. Rwiza, R. Mohammed, Q. Van Oirschot, E. Carey, and A. Westby. 1998. The potential for extending the shelf-life of sweetpotato in East Africa through cultivar selection. Tropical Journal of Agriculture 75:208-211.

Rukarwa, R.J., A.B. Mashingaidze, S. Kyamanywa, and S.B. Mukasa. 2010. Detection and elimination of sweetpotato viruses. African Crop Science Journal 18:223-233.

Saleh, H. and O. Zahor. 2007. Farmers' perception and varieties acceptability of orange-fleshed sweetpotato in Zanzibar. *In:* Kapinga, R., R. Kingamkono, M. Msabaha, J. Ndunguru, B. Lemaga, and G. Tusiime. (eds.) *Proceedings of the Thirteenth Triennial Symposium of the International Society of Tropical Root Crops.* AICC, Arusha: International Society of Tropical Root Crops (ISTRC).

Schafleitner, R., L.R. Tincopa, O. Palomino, G. Rossel, R.F. Robles, R. Alagon, C. Rivera, C. Quispe, L. Rojas, and J.A. Pacheco. 2010. A sweetpotato gene index established by de

novo assembly of pyrosequencing and Sanger sequences and mining for gene-based microsatellite markers. BMC Genomics 11:604.

Shin, J.M., B.K. Kim, S.G. Seo, S.B. Jeon, J.S. Kim, B. Jun, S.Y. Kang, J.S. Lee, M.N. Chung, and S.H. Kim. 2011. Mutation breeding of sweetpotato by gamma-ray radiation. African Journal of Agricultural Research 6:1447-1454.

Sihachakr, D., R. Haïcour, J.M. Cavalcante Alves, I. Umboh, D. Nzoghé, A. Servaes, and G. Ducreux. 1997. Plant regeneration in sweetpotato (*Ipomoea batatas* L., Convolvulaceae). Euphytica 96:143-152.

Srisuwan, S., D. Sihachakr, and S. Siljak-Yakovlev. 2006. The origin and evolution of sweetpotato (*Ipomoea batatas* Lam.) and its wild relatives through the cytogenetic approaches. Plant Science 171:424-433.

Stathers, T.E., D. Rees, D. Jeffries, S. Kabi, N. Smith, L. Mbilinyi, H. Kiozya, S. Jeremiah, M. Nyango, and C. Moss. 1999. Investigating the potential of cultivar differences in susceptibility to sweetpotato weevil as a means of control. *Crop Post-harvest Programme.* UK: DFID.

Stathers, T.E., D. Rees, S. Kabi, L. Mbilinyi, N. Smith, H. Kiozya, S. Jeremiah, A. Nyango, and D. Jeffries. 2003. Sweetpotato infestation by *Cylas* spp. in East Africa: I. Cultivar differences in field infestation and the role of plant factors. International Journal of Pest Management 49:131-140.

Tai, G.C.C. 1974. A method for quantitative genetic analysis of early clonal generation seedlings for asexual crops with special application to a breeding population of the potato (*Solanum tuberosum* L.). TAG Theoretical and Applied Genetics 45:150-156.

Tairo, F., A. Kullaya, and J.P.T. Valkonen. 2004. Incidence of viruses infecting sweetpotato in Tanzania. Plant Disease 88:916-920.

Tairo, F., S.B. Mukasa, R.A.C. Jones, A. Kullaya, P.R. Rubaihayo, and J.P.T. Valkonen. 2005. Unravelling the genetic diversity of the three main viruses involved in sweetpotato virus disease (SPVD), and its practical implications. Molecular Plant Pathology 6:199-211.

Thottappilly, G. and G. Loebenstein. 2009. Concluding Remarks. *In:* Loebenstein, G. and G. Thottappilly. (eds.) The Sweetpotato*.* Springer Netherlands.

Thresh, J.M. 2003. Control of plant virus diseases in sub-Saharan Africa: The possibility and feasibility of an integrated approach. African Crop Science Journal 11:199-223.

Ting, Y.U.C. and A.E. Kehr. 1953. Meiotic studies in the sweetpotato. Journal of Heredity 44:207.

Tomita, R.N., G. Suzuki, K. Yoshida, Y. Yano, T. Tsuchiya, K. Kakeda, Y. Mukai, and Y. Kowyama. 2004. Molecular characterization of a 313-kb genomic region containing the self-incompatibility locus of *Ipomoea trifida*, a diploid relative of sweetpotato. Breeding science 54:165-175.

Troung, V.D., R.Y. Avula, K. Pecota, and C.G. Yencho. 2011. Sweetpotatoes. *In:* Sinha, N.K. (ed.) Handbook of vegetables and vegetable processing. New Jersey: Wiley-Blackwell.

Tsakama, M., A.M. Mwangwela, T.A. Manani, and N.M. Mahungu. 2010. Physiochemical and pasting properties of starch extracted from eleven sweetpotato varieties. African Journal of Food Science and Technology 1:90-98.

Tseng, Y.T., H.F. Lo, and S.Y. Hwang. 2002. Genotyping and assessment of genetic relationships in elite polycross breeding cultivars of sweetpotato in Taiwan based on SAMPL polymorphisms. Botanical Bulletin of Academia Sinica 43:99-105.

Ulukan, H. 2009. The evolution of cultivated plant species: Classical plant breeding versus genetic engineering. Plant System Evolution 280:133-142.

Untiveros, M., S. Fuentes, and J. Kreuze. 2008. Molecular variability of sweetpotato feathery mottle virus and other potyviruses infecting sweetpotato in Peru. Archives of Virology 153:473-483.

Vaeasey, E.A., A. Borges, M.S. Rosa, J.R. Queiroz-Silva, E.A. Bressan, and N. Peroni. 2008. Genetic diversity in Brazilian sweetpotato (*Ipomoea batatas* (L.) Lam., Solanales, Convolvulaceae) landaraces assessed within microsatellite markers. Genetic and Molecular Biology 31:725-733.

Valverde, R.A., C.A. Clark, and J.P.T. Valkonen. 2007. Viruses and virus disease complexes of sweetpotato. Plant Viruses 1:116-126.

Van Den Bosch, F., M. Jeger, and C. Gilligan. 2007. Disease control and its selection for damaging plant virus strains in vegetatively propagated staple food crops; a theoretical assessment. Proceedings of the Royal Society B: Biological Sciences 274:11-18.

Vuylsteke, M. and F. Van Eeuwijk. 2008. The use of general and specific combining abilities in a context of gene expression relevant to plant breeding. Euphytica 161:115-122.

Waddington, S., X. Li, J. Dixon, G. Hyman, and M. De Vicente. 2010. Getting the focus right: production constraints for six major food crops in Asian and African farming systems. Food Security 2:27-48.

Wambugu, F.M. 2003. Development and transfer of genetically modified virus-resistant sweetpotato for subsistence farmers in Kenya. Nutrition Reviews 61:S110-S113.

Wang, Y., F. Wang, H. Zhai, and Q. Liu. 2007. Production of a useful mutant by chronic irradiation in sweetpotato. Science 35:24-34.

Woolfe, J.A. 1992. Sweetpotato: An untapped food resource, Cambridge, England, Cambridge University Press.

Yang, X. 2010. Rapid production of virus-free plantlets by shoot tip culture *in vitro* of purple sweetpotato (*Ipomoea batatas* (L.) Lam). Pakistan Journal of Botany 42:2069-2075.

Yi, G., Y.-M. Shin, G. Choe, B. Shin, Y. Kim, and K.-M. Kim. 2007. Production of herbicide-resistant sweetpotato plants transformed with the bar gene. Biotechnology Letters 29:669-675.

Zhang, D., J. Cervantes, Z. Huamán, E. Carey, and M. Ghislain. 2000. Assessing genetic diversity of sweetpotato (*Ipomoea batatas* (L.) Lam.) cultivars from tropical America using AFLP. Genetic Resources and Crop Evolution 47:659-665.

Chapter two

2.   Assessment of sweetpotato farming systems, production constraints and breeding priorities in eastern Tanzania

Abstract

Sweetpotato is an important food security crop in Tanzania. The crop is grown under diverse farming systems with very low yields. The objective of this study was to assess the present sweetpotato farming systems, farmers' preferences, production constraints and breeding priorities in eastern Tanzania. Participatory rural appraisal was conducted at Gairo, Kilosa and Kilombero districts of Morogoro region and Mkuranga district of the Coast region of Tanzania. Primary and secondary data were collected using semi-structured questionnaire, focus group discussions and field observations. The study showed that more than 94% of the respondents depended on farming for their livelihoods. Main sweetpotato production constraints were Sweetpotato virus disease (SPVD) and pests, drought, unavailability of markets and lack of transport, low prices, inadequate extension services and postharvest losses. Preferred sweetpotato attributes included high yield, high dry matter content, tolerance to diseases and early maturity. Farmers expressed their persuasive needs towards improved extension service delivery, SPVD tolerant cultivars and reliable and coordinated market systems of sweetpotato.

Key words: Farmers' preferences; persuasive needs; production constraints; sweetpotato; Tanzania

2.1. Introduction

Sweetpotato is grown for food and feed in many developing countries (Low et al., 2009). It is an important food security crop, often crucial during famine periods due to its excellent drought tolerance and rapid production of storage roots (Mukhopadhyay et al., 2011). It is an important crop grown by subsistence farmers for food security in Tanzania (Kulembeka et al., 2005; Masumba et al., 2005). It contributes significantly to livelihoods of many households. There is no recent data that comprehensively reported the sweetpotato production constraints in Tanzania. In the country sweetpotato virus disease (SPVD) is the most devastating biotic constraint in farmers' fields (Tairo et al. 2004). The disease is caused by dual infection and synergistic interaction of Sweetpotato chlorotic stunt virus and Sweetpotato feathery mottle virus (Gibson et al., 2004). Yield losses due to SPVD can reach up to 98% (Gibson et al., 1998).

Farmers are the ultimate beneficiaries of newly developed cultivars and production technologies. Therefore, development of improved sweetpotato cultivars, production technologies and alleviating socio-economic constraints would improve sweetpotato productivity. Moreover, in-depth knowledge of farmers' preferences, production challenges and priorities in technology development is vital. Participatory rural appraisal (PRA) have been widely used to collect information on farmers' needs and challenges to venture in breeding new sweetpotato cultivars (Kiiza et al., 2012).

Participatory rural appraisal is flexible and time saving approach used to collect and analyze information involving farmers and researchers (Bhandari, 2003). The approach enables communities to share and enhance their experiences, plan and act together with external agents to enrich their livelihoods (Bar-On and Prinsen, 1999). It empowers local people to assume an active role in analyzing their own living conditions, problems and potential in order to change their situation. Gibson et al. (2011), Mwanga et al. (2011) and Kiiza et al. (2012) suggested the need to consider farmers and consumers in sweetpotato variety development and selection for enhanced adoption. Therefore, the objective of this study was to assess the present farming systems, farmers' preferences, production constraints and breeding priorities of sweetpotato in eastern Tanzania.

2.2. Materials and methods

2.2.1. Description of the study areas

The study was conducted during 2013/2014 cropping season in Mkuranga in Coast region, Gairo, Kilombero and Kilosa in Morogoro region in eastern Tanzania. The districts grow sweetpotato at varying degrees. The rainfall pattern received in the zone varies, while Mkuranga and Kilombero receive rains during October to December and March to May/June, Gairo and Kilosa have one rain season starting in November/December to April/May. With exception of Gairo and Kilosa districts which are dry and cool, the zone experiences high temperatures and humidity except for the month of June. Geographical Positioning System (GPS) was used to determine the locations of the surveyed areas (Table 2.1).

Table 2.1. Regions and corresponding districts and villages of eastern Tanzania sampled for the study.

Region	District	Village	Elevation (m)	Geographic coordinates
Morogoro	Gairo	Ibuti	1317	S06^{0}08.181', E036^{0}53.997'
		Ihenje	1163	S06^{0}09.625', E036^{0}56.304'
	Kilosa	Kiyegeya	1037	S06^{0}11.224', E037^{0}03.730'
		Msolwa ujamaa	320	S07^{0}44.263', E036^{0}55.615'
	Kilombero	Sanje	313	S07^{0}46.230', E036^{0}54.810'
		Ichonde	316	S07^{0}52.835', E036^{0}52.628'
Coast	Mkuranga	Magoza	116	S06^{0}07.684', E039^{0}06.810'
		Kise	134	S07^{0}09.584', E039^{0}67.060'
		Matanzi	78	S07^{0}19.167', E039^{0}02.640'

2.2.1.1. Sampling procedures

Purposive sampling was employed to identify regions, districts, villages, and farmers for the survey. Coast and Morogoro regions were selected due to their potential for sweetpotato production. Gairo, Kilosa, Kilombero and Mkuranga districts were chosen based on prior information on the importance of sweetpotato in these areas. Nine villages were selected based on their accessibility. The target group was sweetpotato farmers. Farmers were randomly selected by village and hamlet leaders with the help of agricultural extension officers. In each

village, 13 to 18 sweetpotato farmers and 13 to 20 individuals were selected for household interviews and focus group discussion, respectively.

Focus groups comprised of sweetpotato farmers and other key informants with broad knowledge on diverse social issues in the village. Key informants comprised of retired village leaders and other civil servants. For both individual interviews and focus group discussions, it was necessary to ensure both males and females were represented through purposively sampling.

2.2.1.2.   Data collection

Primary data were collected using semi-structured questionnaire, focus group discussions and field visits. Focus groups were used to collect general information on food and cash crops grown, sweetpotato cultivars and their characteristics, cropping systems, production calendar, production constraints, preferred traits and gender relations in sweetpotato production.

Semi-structured questionnaire was used to collect household's information regarding sweetpotato production, preferred attributes, cropping systems, constraints, yields and breeding priorities. Other data collected were gender relationships in sweetpotato production, seasonal calendar to identify planting and harvesting periods in a year. Data on yield given by farmers were converted into tons per hectare. Field observations were conducted to comprehend the cropping systems and disease and pest incidences and severity. Secondary data was collected from previous reports at district agricultural departments.

2.2.1.3.   Data analysis

Collected data were captured and analyzed using Statistical Package for Social Sciences computer package (SPSS, 2011) and Microsoft Excel (Windows Office 2010; Microsoft Inc., Redmond, WA). Frequencies and descriptive statistics were computed for each district. Cross tabulations were used in the analysis and the number or percentages of respondents per district were summarized and presented in tables.

2.3. Results

2.3.1. Households and farming characteristics

A total of 138 small-scale farmers were interviewed during household survey (Table 2.2). Sixty five percent of farmers were males and 35% were females. The mean family size was 6.1 with 54% of interviewed households having family size between 6-10 members. Mkuranga district had

the highest number of interviewed households with family size >10 members (Table 2.2). Household size has implication on family labour available for production. Majority (57%) of households' heads interviewed aged between 26-50 years; the most productive group of the population. Sixty three percent of the population attended primary education, being capable to read and write; those who attended post-secondary education were mainly primary school teachers and village leaders.

Table 2.2. Description of household characteristics in surveyed districts of eastern Tanzania during 2013/2014.

Variable	Districts				Total
	Gairo	Kilosa	Kilombero	Mkuranga	
Sex					
Male	23 (69.7)	9 (60.0)	28 (60.9)	30 (68.2)	90 (65.2)
Female	10 (30.3)	6 (40.0)	18 (39.1)	14 (31.8)	48 (34.8)
Age (years)					
<25	10 (30.3)	3 (20.0)	13 (28.3)	10 (22.7)	36 (26.1)
26-50	18 (54.5)	10 (66.7)	25 (54.3)	25 (56.8)	78 (56.5)
>50	5 (15.2)	2 (13.3)	8 (17.4)	9 (20.5)	24 (17.4)
Family size					
<6	9 (27.3)	5 (33.3)	21 (45.6)	22 (50.0)	57 (41.3)
6-10	23 (69.7)	10 (66.7)	23 (50.0)	18 (40.9)	74 (53.6)
>10	1 (3.0)	0	2 (4.4)	4 (9.1)	7 (5.1)
Education level					
Illiterate	2 (6.1)	1 (6.7)	2 (4.4)	3 (6.8)	8 (5.8)
Primary education	20 (60.6)	7 (46.7)	30 (65.2)	30 (68.2)	87 (63.0)
Vocational training	4 (12.1)	2 (13.3)	4 (8.7)	4 (9.1)	14 (10.2)
secondary education	4 (12.1)	3 (20.0)	6 (13)	5 (11.4)	18 (13.0)
Post-secondary	3 (9.1)	2 (13.3)	4 (8.7)	2 (4.5)	11 (8.0)
Source of incomes					
Farms	32 (97.0)	14 (93.0)	43 (94.0)	41 (93.0)	130 (94.2)
Others	1 (3.0)	1 (7.0)	3 (6.0)	3 (7.0)	8 (5.8)

The number in brackets represents relative percentages of respondents

More than 94% of respondents depended on farming for their livelihoods. Secondary income sectors included mini-shops, gardening, labour hiring and charcoal business (Table 2.2). During

offseason farmers grew vegetables and engaged in micro-trading such as making and selling '*Mandazi',* and local brews. Majority of households kept a limited number of animals such as pigs and chicken.

2.3.2. Crops grown and farming systems

Major crops grown in the four districts are presented in Table 2.3. Sweetpotato and maize were the most important crops. Rice was only grown at Kilombero and Mkuranga. These crops were primarily grown for household's consumption and little for sale to earn cash for other family obligations such as clothing and medical costs. Sugarcane and cashew nut were main cash crops in Kilombero and Mkuranga, respectively.

Table 2.3. Crops grown by farmers (%) in surveyed districts of eastern Tanzania

| Crop | Districts | | | | |
	Gairo	Kilosa	Kilombero	Mkuranga	Mean
Banana	0.0	0.0	2.0	1. 8	0.9
Dry beans	15.1	14.5	0.0	0.0	7.4
Cashewnuts	0.0	0.0	0.0	6.9	1.7
Cassava	0.0	4.8	5.3	17.9	7.0
Cowpea	1.8	0.0	0.7	3.6	1.5
Tangerine	0.0	0.0	0.0	1.5	0.4
Maize	29.8	24.2	20.9	16.8	22.9
Mangoes	0.0	0.0	0.0	1.3	0.3
Orange	0.0	0.0	0.0	4.5	1.1
Coconuts	0.0	0.0	0.0	3.1	0.8
Passion fruit	0.0	0.0	0.0	0.5	0.1
Pigeon pea	7.5	24.2	0.0	4.3	9.0
Pineapple	0.0	0.0	0.0	2.3	0.6
Rice	0.0	0.0	24.5	12.1	9.1
Simsim	0.0	0.0	0.0	2.8	0.7
Sugarcane	0.0	0.0	15.9	0.0	4.0
Sunflower	15.3	4.8	0.0	0.0	5.0
Sweetpotato	28.8	24.2	27.6	20.3	25.2
Tomato	0.9	1.6	0.6	0.0	0.8
Other vegetables	0.9	1.6	2.5	0.5	1.4

2.3.3. Sweetpotato production

Land allocated for sweetpotato production varied among households with majority allocating between 1-2 hectares. However, productivity of sweetpotato under farmers' fields was very minimal with mean yield of 2.22 t ha^{-1}.

Time for sweetpotato planting varied among districts. Most farmers (63%) planted sweetpotato during January/March. At Gairo and Kilosa, sweetpotato was planted during January/March. There were multiple planting seasons at Kilombero and Mkuranga where farmers planted sweetpotato during January-March, April-June and October-December. January-March and October-December plantings depended on onset of long and short rains, respectively. April-June planting followed rice harvesting. About 82% of the farmers harvested sweetpotato from June-September.

Sweetpotato cropping systems varied greatly across districts. Sweetpotato was grown either as monoculture or intercropped. It was intercropped with either maize, cowpea, pigeon pea, cassava or cashew nut (Table 2.4). Rotation with maize and rice was also practiced. Rotation with rice was practiced at Kilombero and Mkuranga in which rice was planted during main rain season and sweetpotato planted after rice harvesting. Due to scarcity of land, rotation with maize was done on yearly basis. Moreover, fallowing was practiced for soil fertility restoration and disease and pest control.

Table 2.4. Farmers (%) practicing different sweetpotato farming systems in surveyed districts of eastern Tanzania

Cropping system	Districts				
	Gairo	Kilosa	Kilombero	Mkuranga	Mean
Rotation with maize	81.8	60.0	19.6	75.0	59.1
Rotation with rice	0.0	0.0	74.1	9.0	20.8
Rotation with maize and cowpeas	9.1	40.0	0.0	2.3	12.9
Intercropping with cassava	0.0	0.0	0.0	2.3	0.6
Intercropping with pigeon peas	9.1	0.0	6.3	9.1	6.1
After fallowing	0.0	0.0	0.0	2.3	0.6

It was established that, farmers did not use fertilizers in sweetpotato production. Farmers solely depended on natural soil fertility. Lack of awareness was the predominant reason; further high prices limited use of fertilizer not only in sweetpotato production but also in other crops (Table 2.5).

Table 2.5. Reasons of not using fertilizers in sweetpotato production and corresponding proportion of respondents (%) across surveyed districts of eastern Tanzania

Reasons	Gairo	Kilosa	Kilombero	Mkuranga	Mean
			Districts		
Expensive	3	6.6	4.3	2.3	4.05
Lack of knowledge	75.8	66.7	84.8	93.2	80.13
Soils naturally fertile	-	-	4.3	4.5	2.20
Fertilizers destroy soil	-	-	2.2	-	0.55
Fertilizers burn the crop	3	-		-	0.75
Others	18.2	26.7	4.4	-	12.32

Sweetpotato is principally vegetatively propagated. Results revealed that, 66% of farmers used vines from their fields, 29% from neighbours while only 2% sourced planting materials from research institutes (Table 2.6).

Table 2.6. Sources of sweetpotato planting materials reported by farmers (%) across surveyed districts of eastern Tanzania

Sources	Gairo	Kilosa	Kilombero	Mkuranga	Mean
			Districts		
Own fields	72.7	80	63	47.7	65.9
Neighbours	24.3	20	28.3	42.3	28.7
Research institutes	0	0	4.4	4.4	2.2
Own fields and neighbors	3	0	4.3	5.6	3.2

Farmers in Mkuranga district received planting materials from Sugarcane Research Institute (SRI) based at Kibaha. Non-governmental organizations such as Tanzania Agricultural Productivity Programme (TAPP) and Developing Alternatives Initiative-Improving Multi-sectoral AIDS

Responses to Incorporate Economic Strengthening for Households Affected by AIDS (DAI-IMARISHA) distributed vines for demonstration on processing technologies and promotion of orange-fleshed sweetpotato (OFSP). These NGOs outsourced planting materials from SRI and multiplied under controlled environments before distributing to farmers.

2.3.4. Commonly grown and farmers' preferred sweetpotato varieties

Sweetpotato varieties grown in the four districts are presented in Table 2.7. Variety Gairo was most popular in Kilombero and Mkuranga; and varieties Shangazi and Morogoro were common in Gairo and Kilosa, respectively. Farmers grew local varieties bearing different names. The name of variety was given either by place of origin or the person who pioneered it. Interestingly, OFSP were also grown. At Gairo, Kilosa and Mkuranga the OFSP were popularized by SRI through on-farm evaluation. About 9% of farmers were interested to grow OFSP varieties (Tables 2.7 and 2.15). Despite lacking most of preferred attributes, some varieties such as Bora Kupata, Lingukulu and Sindano are grown in pursuit of food security.

Table 2. 7. Commonly grown sweetpotato varieties across surveyed districts of eastern Tanzania

| Variety | Percent respondents | | | | Mean |
	Gairo	Kilombero	Kilosa	Mkuranga	
Gairo	-	71.7	6.7	84.1	40.6
Simama	12.1	6.5	-	-	4.7
Shangazi	63.6	-	33.3	9.1	26.5
Morogoro	21.2	-	60.0	-	20.3
Shinyanga	-	6.5	-	-	1.6
Carrot	-	-	-	2.3	0.6
Msukuma	-	4.3	-	-	1.1
Orange fleshed	-	8.7	-	-	2.2
Canada	-	-	-	4.5	1.1
Maghimbi	3.0	2.2	-	-	1.3

Farmers described preferred traits for a given variety (Table 2.8). The most preferred traits were high yield (33%), resistance to diseases mainly SPVD (15%), high dry matter content (14%), early maturity (10%), drought tolerance (10%), marketability (9.8%), sweet taste (7%) and elliptic root shape (1%). Elliptic root shape was preferred for easy packaging for transportation.

Table 2.8. Farmers' preferred sweetpotato traits and corresponding respondents (%) across four selected districts of eastern Tanzania

Preferred traits	Districts				Mean
	Gairo	Kilosa	Kilombero	Mkuranga	
Early maturity	12.1	6.7	8.7	11.4	9.7
High yield	33.3	40	32.6	25	32.7
High dry matter	12.1	13.3	16.9	13.6	14
Sweet taste	6.1	6.7	2.2	13.6	7.2
Drought tolerance	12.1	6.7	6.5	15.9	10.3
Disease tolerance	18.2	13.3	15.2	13.6	15.1
Elliptic shape			2.2	2.2	1.1
Marketability	6.1	13.3	13	6.8	9.8

Some sweetpotato varieties were abandoned by farmers. Farmers rejected some varieties and yet opted to grow others. Low yield, susceptibility to diseases and pests and poor marketability were the most important rejection criteria (Table 2.9). However, a variety abandoned in one area was found to be grown in other areas suggesting varied preferences.

Farmers received new sweetpotato varieties from research institutes. About 73, 39, 13 and 37% of respondents from Kilosa, Gairo, Kilombero and Mkuranga, respectively, received new or candidate sweetpotato varieties from SRI. Varieties received for the past five years were NASPOT1, Kabode, Ukerewe, Simama, Mataya, Kiyegeya, Kakamega, Polista, Maghimbi, 03-03, 0656 and 06/676. While Cultivars NASPOT1, Kakamega and Kabode were released for Lake Zone; cultivars Mataya and Kiyegeya were released for eastern and central zones, respectively. Other varieties were yet to be registered by the Ministry of Agriculture.

Table 2.9. Abandoned sweetpotato varieties, reasons for abandonment and respective proportion of respondent farmers (%) during the last ten years in four districts of eastern Tanzania.

Obsolete variety	Districts				Mean	Reasons for abandonment	Districts				Mean
	Gairo	Kilosa	Kilombero	Mkuranga			Gairo	Kilosa	Kilombero	Mkuranga	
Gairo	0	0	0	2.3	0.6	Susceptible to diseases and pests	24.2	13.3	15.2	11.3	16.0
Simama	3	0	0	0	0.8	Poor marketability	18.2	33.3	21.7	9.1	20.5
Shangazi	0	0	0	2.3	0.6	Poor taste	6.1	6.7	19.6	9.1	10.3
Morogoro	3	0	0	2.3	1.3	Watery/soft when cooked	0	6.7	4.3	0	2.8
Carrot	36.4	20	10.9	22.7	22.5	Low yields	42.4	33.3	34.8	47.7	39.6
Msukuma	0	0	2.2	0	0.6	Small root size	0	0	2.2	2.3	1.1
Canada	3	0	0	29.5	8.1	Late maturity	3	6.7	0	20.5	7.6
Sindano	6.1	46.7	0	2.3	13.8	Drought sensitive	6.1	0	2.2	0	2.1
Others	48.5	33.3	86.9	38.6	51.8						

2.3.5. Contribution of sweetpotato production to households' livelihoods

Sweetpotato played multiple roles for food and cash (Table 2.10). The crop contributed significantly to generating household income. At harvest, farmers sold part of the produce to meet family and other community obligations; remaining portion was for household consumption. Harvesting was done either in staggered manner or at once. For household consumption, staggered harvesting was commonly practiced.

Table 2.10. Uses of sweetpotato and corresponding proportion of respondent farmers (%) in surveyed districts of eastern Tanzania

Uses	Districts				Mean
	Gairo	Kilosa	Kilombero	Mkuranga	
Food	49	60	26	50	46.3
Market	15	14	24	16	17.3
Food and market	36	26	50	34	36.5

2.3.6. Gender relationships in sweetpotato production

The study envisaged to establish gender relations in sweetpotato production chain. It was revealed that men played a significant role in sweetpotato production contrary to the idea that sweetpotato was a women's crop. There was equal participation of men and women from land preparation to harvesting. However, men were decisions makers on selling and handling the money earned (Table 2.11). More than 93% of the resources were owned by men and 85% of family care activities were women's roles.

Table 2.11. Gender relations in sweetpotato production and marketing and corresponding proportion of respondent (%) in surveyed districts in eastern Tanzania

| Production activity | Districts | | | | | | | | Mean | |
	Gairo		Kilosa		Kilombero		Mkuranga		Men	Female
Land preparation	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
Planting	33.3	66.7	33.3	66.3	66.7	33.3	50.0	50.0	45.8	54.2
Weeding	50.0	50.0	33.3	66.3	50.0	50.0	40.0	60.0	43.3	56.6
Harvesting	50.0	50.0	50.0	50.0	33.3	66.7	60.0	40.0	48.3	51.7
Selling	66.7	33.3	50.0	50.0	50.0	50.0	75.0	25.0	60.4	39.6
Keeping the money	50.0	50.0	50.0	50.0	100.0	0.0	33.3	66.7	58.3	41.7
Decision making on use of cash generate from sweetpotato	66.7	33.3	50.0	50.0	66.7	33.3	75.0	25.0	64.6	35.4
Resource ownership	100.0	0.0	100.0	0.0	100.0	0.0	75.0	25.0	93.8	6.2
Family care	33.3	66.7	0.0	100.0	0.0	100.0	25.0	75.0	14.6	85.4

2.3.7. Sweetpotato production constraints

The most important constraints identified were pests and diseases, unreliable markets, drought and low prices (Table 2.12). Others were lack of transport, lack of credit facilities and extension services. Sweetpotato virus disease was the common problem in surveyed areas. Farmers did not name SPVD, but clearly described typical symptoms of the disease such as stunted growth and leaf chlorosis. While 47% of farmers prevented spreading and controlled SPVD by uprooting infected plants, 53% did not consider any strategy. Likewise, sweetpotato weevil was the main pest affecting sweetpotato in most fields. Unreliable markets with low prices were regarded as major constraints of sweetpotato production limiting farmers to pull out of poverty. Farmers sold the produce in the fields, local markets and along public roads. The price for produce was very low and unprofitable to farmers. Only 2% of the respondents described that their sales fetched high market price.

Table 2.12. Major constraints to sweetpotato production and corresponding proportion of respondents (%) in surveyed districts of eastern Tanzania

Constraints	District				Mean
	Gairo	Kilosa	Kilombero	Mkuranga	
Pest and diseases	30.4	26.6	32.6	36.4	31.5
Lack of reliable markets	21.2	13.3	19.6	9.1	15.8
Drought	21.2	20	10.9	9.1	15.3
Lack of extension services	3	6.7	-	13.6	5.8
Low market prices	18.2	6.7	4.3	2.3	7.9
Low yielding varieties	3	-	-	2.3	1.3
Lack of credit facilities	-	20	8.7	15.9	6.5
Poor transport systems	3	6.7	15.2	6.8	7.8
Post-harvest losses	-	-	6.5	4.5	2.8
Theft	-	-	2.2	-	0.4

Majority of farmers were discontented and ranked sweetpotato price to be low (Table 2.13). The low prices were due to the fact that middlemen determined the price of the produce (Table 2.14). Farmers were forced to sell at low prices due to perishability of the crop. Early and late harvested sweetpotato fetched high prices compared to produce sold during peak harvesting periods.

Farmers at Mkuranga, Kilombero and Gairo established informal micro-cooperatives to search for attractive prices. Some farmers reported that they were trained on post-harvest processing technologies but were incapable of purchasing processing equipment due to lack of capital.

Table 2.13. Price ranking of sweetpotato (%) in surveyed districts of eastern Tanzania

Price	Districts				Mean
	Gairo	Kilosa	Kilombero	Mkuranga	
Very low	0	0	2.2	6.8	2.3
Low	87.9	73.3	63	70.5	73.6
Average	12.1	26.7	32.6	18.2	22.4
High	0	0	2.2	4.5	1.7

Very low ≤ 4000/Tanzanian Shillings (Tshs), Low = 4000-5000/Tshs, average = 5000-6000/Tshs and High ≥7000/Tshs. Prices based on 20kgs. (1US$ = 1650/ Tshs in 2013/2014)

Table 2.14. Price regulating agents for sweetpotato (%) in surveyed districts of eastern Tanzania

Price regulating agents	Districts				Mean
	Gairo	Kilosa	Kilombero	Mkuranga	
Farmers	9.1	20	19.6	18.2	16.7
Middlemen	81.8	73.3	63	77.2	73.8
Farmers and middlemen	9.1	6.7	17.4	2.3	8.9
Cooperatives	0	0	0	2.3	0.6

2.3.8. Field observation

The interviewers and farmers made field visits to assess cropping systems and incidences and severity of SPVD. The visited fields were severely affected by SPVD and drought. Famers were desperate and expressed the devastating effect of SPVD. Further, it was reported that co-occurrences of SPVD and prolonged drought greatly retarded plant growth and yields.

2.3.9. Future needs for improved sweetpotato production

Farmers expressed their most immediate needs for enhancing sweetpotato production. Extension services, SPVD resistant varieties and coordinated markets ranked the top (Table 2.15). Establishment of price governing boards, availability of healthy planting materials and cooperatives were also pointed to be important. Also, farmers expressed their interests on OFSP cultivars. Farmers emphasized their need for extension officers to empower them on various agronomic practices and post-harvest processing techniques.

Table 2.15. Persuasive needs for improved sweetpotato production and corresponding proportion of respondents (%) in surveyed districts of eastern Tanzania

Needs	Districts					Rank
	Gairo	Kilosa	Kilombero	Mkuranga	Mean	
Extension services	18.2	30.6	32.6	27.3	27.2	1
Coordinated markets	6.2	20	19.6	20.5	16.6	3
Price regulating board	21.1	6.7	10.9	11.4	12.5	4
OFSP	6.2	16	6.5	6.8	8.9	6
Disease tolerant cultivars	27.1	20	23.9	13.6	21.1	2
Timely supply of high quality planting materials	18.2	6.7	6.5	18.2	12.4	5
Establishment of cooperatives	3	0	0	2.2	1.3	7

2.4. Discussion

Ninety four percent of farmers depended on farming for their livelihoods. The result concurs with data presented by the national statistics that more than 80% of Tanzanian population depended on agriculture (Maltsoglou and Khwaja, 2010). Also, farmers have multiple crop enterprises; practiced mixed cropping for diversification. Apart from agricultural activities, farmers engaged in non-agricultural enterprises for additional incomes. Similar finding was reported by Fawole (2007) in Nigeria, where sweetpotato was intercropped with other crops for food security and households' incomes.

The study revealed that farmers were knowledgeable about sweetpotato varieties and their attributes. Sweetpotato varieties with diverse attributes were found to be grown. Most of the varieties were landraces with white or cream flesh. Similar to this study, Chiona (2009) reported different sweetpotato varieties grown by farmers in Zambia. Orange fleshed cultivars were recently introduced and grown by few farmers. Most farmers were aware on the nutritional value of OFSP. Kulembeka et al. (2005) and Laurie and Magoro (2008) reported acceptance of OFSP cultivars in Tanzania and South Africa, respectively. Similarly, Mwanga and Ssemakula (2011) reported an increased area and demand for OFSP varieties in Uganda.

Farmers grew sweetpotato varieties possessing diverse attributes. Farmers preferred varieties with high yield and dry matter content, resistance to diseases and pests, early maturing, sweet taste, elliptic root shape and drought tolerance. High yield, early maturity, sweetness and disease tolerance were the most important selection attributes by farmers in Tanzania (Kapinga et al., 2003). Low fibre, insect tolerance and high root firmness were also considered important. Similar findings were reported by Gibson et al. (2011). Farmers in South Africa were reported to prefer sweetpotato varieties with sweet taste, dry texture and good yield (Domola, 2003). Zawedde et al. (2014) reported that higher yield, taste, and maturity period were primary criteria for adopting new cultivars in Uganda.

The present study observed ahigh level of participation of men in sweetpotato production, though women were the major players in the sector. Stathers et al. (2013), grouped gender roles and responsibilities in sweetpotato production chain into three categories, namely; sweetpotato as female's crop with few or no men growing it, sweetpotato as male's crop with few or no women growing it and sweetpotato grown by both men and women on individually or family owned plots. Increased sweetpotato market demand has brought changes in the traditional roles and responsibilities related to sweetpotato production. Similar to present study, Lederman (1989) reported that land preparation, planting, weeding and harvesting were mainly women's responsibilities in New Guinea. Moreover, Olagunju et al (2013) reported more participation of males in sweetpotato production activities than females in Nigeria. Also, Low (2004) reported that increased role of sweetpotato as cash crop in South Nyanza in Kenya has attracted men involvement in sweetpotato production. Therefore, increased market demand for sweetpotato has greatly attracted men participation in sweetpotato production.

Despite remarkable role of sweetpotato, its productivity is very low compared to yield potential of 15-23 tha^{-1} (Sebastiani et al., 2007). Low productivity was due to several biotic, abiotic and socio-economic constraints. Prevalence of SPVD, unavailability of healthy planting materials, drought,

inadequate extension services, markets and low prices contributed to low crop productivity. Similar findings were reported in Kenya by Kivuva et al. (2014).

The main sources of planting materials were largely from farmers' fields or neighbors. Farmers preserved their planting materials in home gardens and valley bottoms; farmers have used local and low yielding sweetpotato landraces for decades. Ndolo et al. (2001) and Tairo et al. (2004) reported similar practices in Kenya and Tanzania, respectively.

Generally, diseases, pests and use of old vines constrained sweetpotato production. Farmers identified SPVD as the most important constraint. Limited access to and unavailability of healthy planting materials contributed to persistence of SPVD. This result concurs with findings reported by Fugile (2007) who reported that unavailability of healthy planting materials and high yielding cultivars was amongst the hindrances in improving sweetpotato production. As a clonally propagated crop, utilization of vines from stock with latent infection speeds the buildup, multiplication and spread of SPVD. Farmers controlled the disease either by selecting symptomless planting materials or rouging infected plants. Similar practices were reported by Ndunguru and Kapinga (2007). Also, Gutiérrez et al. (2003) suggested production of healthy planting materials to control SPVD.

Sweetpotato weevils and other insects such as Elegant grasshoppers (*Zonocerus elegans*) were found to severely damage sweetpotato storage roots and leaves. Farmers controlled sweetpotato weevils by crop rotation and hilling up. Stathers et al. (2003) reported similar practices to control and reduce weevils' damage. Drought was reported to constrain sweetpotato production. Despite being drought tolerant, prolonged dry spells during and after crop establishment severely affect crop growth and development and ultimately yields. Drought tolerance is one of the selection criteria for adoption of new varieties by farmers (Masumba et al., 2004). Sweetpotato is predominantly sold fresh after harvest. Poor, uncoordinated markets dominated by middlemen who set and control product prices diminish farmers' economic returns. Low (1998) reported unorganized markets with low prices being the major limiting factor in sweetpotato marketing. Lack of capital and credit facilities have caused farmers to remain underdeveloped for decades. Despite some farmers being trained on post-harvest processing technologies, lack of capital to purchase processing equipment has caused the knowledge gained redundant. Fawole (2007) reported that lack of capital and credit facilities caused low sweetpotato yield in Nigeria. Moreover, lack of transport, transportation facilities and dilapidated roads were other bottlenecks to sweetpotato business. Unavailability and inadequate extension services contributed to low sweetpotato production. Most of extension workers are overworked with agricultural and non-

agricultural activities such as health campaigns and elections; depending on what was pressing at a particular time. Further, most extension workers have limited knowledge on sweetpotato agronomy. Although a post-harvest loss was only mentioned by farmers from Mkuranga district, it was a critical problem in all sweetpotato growing areas. Since the crop is perishable and there were no developed storage and processing facilities, harvest losses are to be expected. Fugile (2007) reported strong need for improvement of postharvest utilization and marketing infrastructures.

In an endeavor to improve sweetpotato production and productivity, improved extension services, supply of disease and insect resistant varieties and well-coordinated markets are critical. Timely supply of healthy planting materials would improve productivity, income and nutritional status of farmers. Establishment of price regulating boards and cooperatives were the wishes of farmers.

2.5. Conclusions

Sweetpotato is a food security crop for subsistence communities. However, its productivity is low. Diseases and pests, drought, unavailability of markets, low sweetpotato prices, inadequate extension services and post-harvest losses were the main production constraints. Sweetpotato attributes preferred by farmers were high yield, high dry matter content, tolerance to SPVD and early maturity. Farmers expressed their persuasive needs towards improved extension service delivery, SPVD tolerant cultivars and reliable and coordinated markets.

References

Bar-On, A. A and G. Prinsen. 1999. Planning, communities and empowerment An introduction to participatory rural appraisal. International Social Work 42:277-294.

Bhandari, B.B. 2003. Participatory rural appraisal (PRA). Virgina: Institute for Global Environmental Strategies. Module 4: Patumwan, Bangkok, Thailand.

Chambers, R. 1990. Rapid and participatory rural appraisal. Appropriate Technology (UK) 16:14-16.

Chiona M. 2009. Towards enhancement of β-carotene content of high drymass sweetpotato genotypes in Zambia. PhD Thesis, University of KwaZulu-Natal, Pietermaritzburg.

Domola, M.J. 2003. Survey and characterisation of sweetpotato viruses in South Africa. MSc. Thesis. University of Pretoria, South Africa.

Fawole, O.P. 2007. Constraints to production, processing and marketing of sweetpotato in selected communities in Offa Local Government Area, Kwara State. Nigeria. Journal of Human Ecology 22:23-25.

Fugile, K.O. 2007. Priorities for sweetpotato research in developing countries: Results of a survey. HortiScience 42:1200-1206.

Gibson, R., I. Mpembe, and R. Mwanga. 2011. Benefits of participatory plant breeding (PPB) as exemplified by the first-ever officially released PPB-bred sweetpotato cultivar. The Journal of Agricultural Science 149:625-632.

Gibson R.W., V. Aritua, E. Byamukama, I. Mpembe, and J. Kayongo. 2004. Control strategies for sweetpotato virus disease in Africa. Virus Research 100:115-122.

Gibson R.W., I. Mpembe, T. Alicai, E.E. Carey, R.O.M. Mwanga, S.E. Seal, and H.J. Vetten. 1998. Symptoms, aetiology and serological analysis of sweetpotato virus disease in Uganda. Plant Pathology 47:95-102.

Gutiérrez, D.L., S. Fuentes, and L.F. Salazar. 2003. Sweetpotato virus disease (SPVD): Distribution, incidence and effect on sweetpotato yield in Peru. Plant Disease 87:297-302.

Kapinga, R., S. Jeremiah, E. Rwiza, and D. Rees. 2003. Farmer criteria for selection of sweetpotato varieties. In: Rees, D. (ed). Sweetpotato post-harvest assessment: Experiences from East Africa. NRI, CPHP, DFID, CIP and Ministry of Agriculture Tanzania, Chatman, UK.

Kiiza, B., L.G. Kisembo, and R.O.M. Mwanga. 2012. Participatory plant breeding and selection impact on adoption of improved sweetpotato varieties in Uganda. Journal of Agricultural Science and Technology 2:673-681.

Kivuva, B.M., F.J. Musembi, S.M. Githiri, C.G. Yencho, and j. Sibiya. 2014. Assessment of production constraints and farmers' preferences for sweetpotato genotypes. Journal of Plant Breeding and Genetics 2:15-29.

Kulembeka, H., C. Rugutu, E. Kanju, B. Chirimi, E. Rwiza, and R. Amour. 2005. The agronomic performance and acceptability of orange fleshed sweetpotato varieties in the Lake Zone of Tanzania. African Crop Science Journal 12:229-240.

Laurie, S. and M. Magoro. 2008. Evaluation and release of new sweetpotato varieties through farmer participatory selection. African Journal of Agricultural Research 3:672-676.

Lederman, R. 1989. Contested order: Gender and society in the southern New Guinea Highlands. American Ethnologist 16:230-247.

Low, J. 2004. The changing role of sweetpotato in South Nyanza, Kenya. Adapting Social Science to the Changing Focus of International Agricultural Research: Proceedings of a Rockefeller Foundation--ILCA Social Science Research Fellows Workshop 14-18 November 1994. ILCA, Addis Ababa, Ethiopia. Pp. 95-118.

Low, J., J. Lynam, B. Lemaga, C. Crissman, I. Barker, G. Thiele, S. Namanda, C. Wheatley, and M. Andrade. 2009. Sweetpotato in Sub-Saharan Africa. In: Loebenstein, G. and G. Thottappilly. (eds). The sweetpotato. Springer Netherlands. Pp. 359-390.

Low, J.W. 1998. Determinants of sweetpotato commercialization in south Nyanza, Kenya. Root crops and poverty alleviation. Paper presented at The Sixth Triennial Symposium of the International Society for Tropical Root Crops; Africa Branch Capital City, Lilongwe, Malawi. 22-28 October 1995.

Maltsoglou, I. and Y. Khwaja. 2010. Bioenergy and food security: The BEFS analysis for Tanzania. Environmental and natural resources management working paper 35, United Nations Food and Agricultural Organization. FAO, Rome.

Masumba, E., R. Kapinga, S.M. Tollano, M. Yongolo, and D.C. Kitundu. 2005. Adaptability and acceptability of new orange-fleshed sweetpotato varieties in selected areas of eastern and central zones of Tanzania. In: R. Kapinga, R. Kingamkono, M. Msabaha, J. Ndunguru, B. Lemagaand G. Tusiime (eds). Proceedings of the Thirteenth Triennial Symposium of the International Society for Tropical Root Crops, 10-14 November. AICC, Arusha, pp 737-745.

Masumba, E., H. Kulembeka, S. Tollano, and M. Yongolo. 2004. Participatory evaluation of improved sweetpotato varieties in Eastern Tanzania. African Crop Science Journal 12:259-265.

Mukhopadhyay, S., A. Chattopadhyay, I. Chakraborty, and I. Bhattacharya. 2011. Crops that feed the world 5. Sweetpotato. Sweetpotatoes for income and food security. Food Security 3:283-305.

Mwanga, R.O., C. Niringiye, A. Alajo, B. Kigozi, J. Namukula, I. Mpembe, S. Tumwegamire, R.W. Gibson, And G.C. Yencho. 2011. 'NASPOT 11', a sweetpotato cultivar bred by a participatory plant breeding approach in Uganda. HortiScience 46:317-321.

Mwanga, R.O. and G. Ssemakula. 2011. Orange-fleshed sweetpotatoes for food, health and wealth in Uganda. International Journal of Agricultural Sustainability 9:42-49.

Ndolo, P.J., T. Mcharo, E.E. Carey, S.T. Gichuki, C. Ndinya, and J. Maling'a. 2001. Participatory on-farm selection of sweetpotato varieties in Western Kenya. African Crop Science Journal 9:41-48.

Ndunguru, J. and R. Kapinga. 2007. Viruses and virus-like diseases affecting sweetpotato subsistence farming in southern Tanzania. African Journal of Agricultural Research 2:232-239.

Olagunju, F., S. Fakayode, R. Babatunde, and F. Ogunwole-Olapade. 2013. Gender analysis of sweetpotato production in Osun State, Nigeria. Asian Journal of Agricultural Extension, Economics and Sociology 2:1-13.

Sebastiani, S.K., A. Mgonja, F. Urio, and T. Ndondi. 2007. Agronomic and economic benefits of sweetpotato (*Ipomoea batatas*) response to application of nitrogen and phosphorus fertilizer in the northern highlands of Tanzania. The Eighth African Crop Science Society Conference. El-minia, Egypt, pp. 1207-1210.

SPSS. 2011. IBM SPSS statistics for Windows, version 20.0. New York: IBM Corp.

Stathers, T., S. David, J.W. Low, G. Mulongo, and A. Mbabu. 2013. Gender and diversity aspects. Everything you ever wanted to know about sweetpotato: Reaching agents of change training manual. International Potato Center, Nairobbi, Kenya. Pp.272-286.

Stathers, T.E., D. Rees, S. Kabi, L. Mbilinyi, N. Smith, H. Kiozya, S. Jeremiah, A. Nyango, and D. Jeffries. 2003. Sweetpotato infestation by *Cylas* spp. in East Africa: I. Cultivar differences in field infestation and the role of plant factors. International Journal of Pest Management 49:131-140.

Tairo, F., A. Kullaya, and J.P.T. Valkonen. 2004. Incidence of viruses infecting sweetpotato in Tanzania. Plant Disease 88:916-920.

Zawedde, B.M., C. Harris, A. Alajo, J. Hancock, and R. Grumet R. 2014. Factors influencing diversity of farmers' varieties of sweetpotato in Uganda: Implications for conservation. Economic Botany 68:337-349.

Chapter three

3. Screening of Tanzanian sweetpotato germplasm for yield and related traits and resistance to sweetpotato virus disease

Abstract

Sweetpotato (*Ipomoea batatas* [L.] Lam) is a versatile crop globally serving as food, feed and raw material for industries. Designed selection for higher yields and related traits is crucial to identify complementary sweetpotato clones for breeding. The objective of this study was to determine phenotypic variation among diverse sweetpotato collections with regard to yield, dry matter content and sweetpotato virus disease resistance and to identify suitable clones for breeding. A total of 144 sweetpotato genotypes were evaluated at two sites in Tanzania using a 12x12 simple lattice design. Data collected included 10 quantitative and 17 qualitative agro-morphological traits and virus reaction. Results indicated differences among genotypes for most traits studied. The mean dry matter content was 36% with clones Zapallo and Ukerewe exhibiting the lowest and highest values of 29 and 45%, respectively. The mean storage root yield of clones was 5.1 t/ha with genotype Jewel expressing the highest yield of 11.3 t/ha. Genotypes Resisto and Mataya were early flowering at 40 and 50 days, respectively while Ex-Mwanza and Kandoro did not flower at all. Fifty eight percent of the genotypes showed resistant reaction to SPVD while 31% and 11% were moderately susceptible and susceptible to the disease, respectively. A positive correlation was reported for number of roots and fresh root yield. Seven clones including Simama, Ukerewe, Mataya, Resisto, 03-03, Ex-Msimbi-1 and Gairo were selected for high storage root yield and related traits or SPVD resistance. The selected genotypes are recommended as potential parents for sweetpotato breeding.

Keywords: Farmers' preferences; persuasive needs; production constraints; sweetpotato; Tanzania

3.1. Introduction

Sweetpotato (*Ipomoea batatas* [L.] Lam, 2n=6x=90) is a versatile crop globally serving as food, feed and industrial raw material. It is an excellent companion crop with strong ability to adjust in many cropping systems. Both phenotypic and genotypic variations exist among sweetpotato genotypes. Sweetpotato diversity analyses have given a better understanding of the extent of variation available between and within germplasm collections for breeding and conservation (Tumwegamire et al., 2011). Thus germplasm identification and characterization are essential steps for successful conservation, management and utilization of genetic resources (Arizio et al., 2009). Further, genetic diversity is a precondition for plant breeding which requires diverse genetic pool to develop new cultivars that meet the changing needs regarding adaptation to growing conditions, resistance to biotic and abiotic stresses, yield potential or specific quality requirements of consumers (Ulukan, 2009). Therefore the most efficient and effective ways in breeding programmes is to use promising parents selected from a well-characterized germplasm of wide and diverse genetic pool.

Traditionally, sweetpotato genetic characterization has been based on morphological and agronomic traits as they are easy to evaluate and the methods are relatively cheap (Elameen et al., 2011). However, the expression of these traits is subjected to genetic constitution, environmental factors and their interactions.

Sweetpotato diversity studies using morphological descriptors have been extensively used in describing sweetpotato germplasm. Sweetpotato displays a high degree of phenotypic variations and thus morphological descriptors have been widely used in genotype identification (Huaman, 1999; Tsegaye et al., 2007). Veasey et al. (2007) used morphological and agronomic traits to describe sweetpotato landraces from Vale do Riberia in Brazil. Jha (2011) and Beah et al. (2014) using agro-phenotypic characters reported wide genetic diversity among sweetpotato genotypes in India and Sierra Leone, respectively. Phenotypic characterization is relatively cheap in terms of time and resources and represents the real architecture or ideotype of the plants and provides baseline information for breeding and strategic conservation. Also, Jha (2011) and Beah et al. (2014) used agro-phenotypic characters and reported wide genetic diversity among sweetpotato genotypes in India and Sierra Leone, respectively. Therefore, designed selection for higher yields and related traits is crucial to identify complementary sweetpotato clones for breeding.

In Tanzania, sweetpotato is an important food security crop supporting millions of people. It ranks fifth in terms of food production after maize, cassava, rice and sorghum. It is the second most important root crop after cassava. According to Kapinga et al. (1995) and Sebastian et al. (2007),

sweetpotato yields in the country ranges from 3–6 tha^{-1}, lower than the potential yields of 15- 27 tha^{-1} . The average area harvested for the last ten years was 536451 hectares with mean yield of 3.8 tha^{-1} (FAOSTAT, 2015). The national sweetpotato yields are low due to several biotic, abiotic and socio-economic constraints. Sweetpotato virus diseases and sweetpotato weevils are the most devastating biotic constraints. Sweetpotato virus disease (SPVD) caused by the dual infection and synergistic interaction of sweetpotato chlorotic stunt virus and sweetpotato feathery mottle virus is distributed worldwide (Gibson et al., 1998, Mukasa et al., 2006). It is the most devastating disease causing reduction in plant growth and storage root yields (Gibson et al., 2004, Gibson, 2005, Kapinga et al., 2009). Also SPVD limits the length of time the roots can be kept in the ground and shorten the storage duration of the harvested crop (Engoru et al., 2005, Tsakama et al., 2010). The damage caused by SPVD ranges from 50-98% (Gibson et al., 1998, Njeru et al., 2004, Tairo et al., 2004). Although research has led to many recommendations for practices to increase production of sweetpotato at farm level, the rate of adoption of improved practices is low (Kapinga et al., 2003). Amongst farmers' the selection criteria for sweetpotato varieties are high yields, early maturity, tolerance to diseases and pests, dry matter content and sweetness (Kapinga et al., 2003; Masumba et al., 2005; Masumba et al., 2007). There are limited studies on the description of local and improved sweetpotato varieties with regard to yield, dry matter content and other related traits in Tanzania. Tairo et al. (2008) and Elameen et al. (2011) described Tanzanian sweetpotato germplasm collection using morphologic and agronomic descriptors. However, thorough description of currently grown sweetpotato varieties with regard to farmers' preferences is vital. Consequently, germplasm was collected in the eastern zone (Dar es Salaam, Morogoro, Coast and Tanga regions) and Kagera from Lake Zone. Germplasm from Kagera were collected and used in screening due to high SPVD pressure in that region, hence could be used as a source of resistance in breeding programme. Therefore, the objective of this study was to determine phenotypic variation among sweetpotato accessions with regard to yield, dry matter content and resistance to sweetpotato virus disease (SPVD) and to identify suitable clones for breeding.

3.2. Materials and Methods

3.2.1. Germplasm collection, multiplication and preliminary evaluation

A total of two hundred and thirty nine sweetpotato genotypes grown in Tanzania were collected in 2012. The regions and the number of germplasm collected were: Dar es Salaam (6°49'24" S,

39°16'10" E) (14), Coast (7°15'0" S, 38°49'59" E) (71), Kagera (4°39'36" S, 30°40'08" E) (32), Morogoro (6°49'15" S, 37°39'40" E) (74), Tanga (5°0'0" S, 38°15'0" E) (47) and Zanzibar Island (6°09'50" S, 39°11'52" E) (1). The collections were planted at Sugarcane Research Institute (SRI) – Kibaha for multiplication. The germplasm consisted of landraces, elite and breeding clones and exotic sweetpotato genotypes. Only 144 genotypes were included for phenotypic diversity studies after two growing seasons of preliminary evaluations that allowed selection of redundant clones. The pre-selection criteria were evident morphological duplicates and production of sufficient and healthier planting vines.

3.2.2. Characterization of study sites

The genotypes were evaluated during 2013 at two sites: SRI – Kibaha (S06°46'834'', E038°58.435'') and Kilombero Agricultural and Training Research Institute (KATRIN) – Ifakara (S08°03'693'', E036°40'005'') representing the Coast and Morogoro regions, respectively. The selected sites are hotspots for SPVD. The physico-chemical soil properties of the two sites are presented in Table 3.1.

Table 3.1. Geographical locations and their soil characteristics of the study sites

Study sites	Geographic location			Soil characteristics				
	Latitude	Longitude	Altitude (masl)	pH	TN (%)	OC (%)	K (meq 100/g)	Av. P. (meq 100/g)
SRI-Kibaha	S06°46'834''	E038°58.435'	172	7.1	0.08	0.5	0.13	3.67
KATRIN-Ifakara	S08°03'693''	E036°40'005''	286	6.1	0.13	2.12	1.23	4.56

(meq 100/g = Milliequivalent per 100g of soil, Av. P. = Available phosphorus, K = potassium, masl = metres above sea level, OC = Organic carbon, TN = total nitrogen.

The soils are clay and clay loam with neutral and slightly acidic soil reactions for SRI-Kibaha and KATRIN-Ifakara, respectively. While SRI-Kibaha had very low organic carbon and total nitrogen, KATRIN-Ifakara had medium organic carbon and low total nitrogen. Both sites had low levels of available phosphorus.

3.2.3. Experimental design and field trial establishment

The 144 sweetpotato genotypes were evaluated in a 12 x 12 simple lattice design (Gomez and Gomez, 1984). At SRI-Kibaha the trial was established during 22nd March and at KATRIN-Ifakara on 19th April, 2013. Each plot consisted of two rows of 6 m long with a total of 40 plants. The intra-row and inter-row spacing were 0.3 m and 1 m, respectively. Four to six node vine cuttings were planted on ridges. Agronomic practices such as weeding were done per recommendation in the study areas.

3.2.4. Data collection

Sweetpotato virus disease reactions data was collected at 60, 90 and 120 days after planting using a 1 to 5 scale; where 1 = no visible symptoms, 2 = mild symptoms (a few local lesions on a few leaves), 3 = moderate symptoms (mosaic symptoms on leaves), 4 = severe symptoms (mosaic symptoms with plant stunting) and 5 = very severe symptoms of purpling/yellowing or mosaic on leaves, severe leaf distortion, reduced leaf size and severe stunting (Mwanga et al., 2013). Genotypes Shangazi and Simama were used as susceptible and resistant checks, respectively. Graft inoculation was conducted only to genotypes which appeared to be resistant under field conditions. This was done in an insect proof screen house at SRI-Kibaha. Five plants were selected from each genotype and each plant was grafted onto *Ipomoea setosa*, an SPVD indicator plant. Plants were grown and maintained in one litre capacity plastic pots. Five weeks after planting the sweetpotato scions were grafted to *I. setosa* the root stock. After grafting, observation for the symptoms of SPVD was conducted and recorded using the above described scale.

Genotypes were characterized using selected agro-morphological traits (Table 3.2) following the phenotypic descriptors of Huamán (1999). Above ground and storage root traits were evaluated three months after planting and at harvest, respectively. Four plants per genotype were randomly selected and tagged to collect data on quantitative agro-morphological traits. Time to fifty percent flowering was recorded from the 30th day after planting and thereafter on weekly basis until 100 days after planting.

The field trials were harvested at 120 days after planting. At harvesting, all root characteristics were collected from four tagged plants. Storage roots were grouped into marketable and un-marketable types and their fresh weight (kg) was recorded. The number of roots was expressed on per plant basis. The root and vine yield were collected on plot basis and later converted to

tones per hectare (t/ha). From each plot, a sample of three storage roots was collected for determination of dry matter content.

The dry matter content was determined using methods described by Carey and Reynoso (1999) and Tairo et al. (2008) with some modifications. A sample of 200 g was chopped from undamaged roots for each entry in each replication. The samples were air-dried and then oven dried at 70^0C until constant weight. The dried samples were weighed using an electronic balance and the resulting figures were used to calculate dry matter content as percentage of the fresh weight.

3.2.5. Data analysis

The data for root and vine yield; number of storage roots, dry matter content and SPVD across the two sites were subjected to analysis of variance using Statistical Analysis System version 9.2 (SAS, 2008). A separate analysis was done for each site; however, due to homogeneity in error variances, a combined analysis of variance for both sites was conducted (Gomez and Gomez, 1984).

Data collected were subjected to hierarchical cluster analysis using un-weighted pair group method with arithmetic means (UPGMA). Using 24 agro-morphological characters, a dendrogram grouping the test genotypes based on similarity index was generated. All introductions were excluded in in cluster analysis. Pearson and Spearman correlation coefficients were used to determine the associations between quantitative and qualitative traits, respectively.

Table 3.2. Agro-morphological traits used in characterisation of sweetpotato germplasm in the study.

Trait	Description of data	Unit
Leaf	General outline of leaf: Rounded (1), reniform (2), cordate (3), triangular (4), hastate (5), lobed (6) or divided (7)	Code number
	Type of leaf lobes: No lobe (1), slight (2), very slight (3), moderate (4), deep (5) or very deep (6)	Code number
	Number of leaf lobes	Number
	Shape of central lobe: Absent (1), toothed (2), triangular (3), semicircular (4), semielliptic (5), elliptic (6), lanceolate (7), oblanceolate (8) or linear (9)	Code number
	Pigmentation	
	Abaxial vein pigmentation: yellow (1), green (2), purple spot at base of main rib (3), purple spots on several veins (4), main rib partially purple (5), main rib mostly or totally purple (6), all veins partially purple (7), all veins mostly or totally purple (8) or lower surface and veins totally purple (9)	Code number
	Petiole pigmentation: green (1), green with purple near stem (2), green with purple near leaf (3), green with purple at both ends (4), green with purple spots throughout petiole (5), green with purple stripes (6), purple with green near leaf (7), some petioles purples, others green (8) or totally or mostly purple (9)	Code number
Vine	Length of main vine	cm
	Growth habit: erect (3), semi-compact (5), spreading (7), extremely spreading (9)	Code number
	Vine tip pubescence: none (0), sparse (3), moderate (5), heavy (7), very heavy (9)	Code number
	Size of vine internode:	
	Length	cm
	Diametre	mm
Storage root	Storage formation: Closed cluster (1), open cluster (2), dispersed (3) or very dispersed (4).	Code number
	Storage root shape: Round (1), round elliptic (2), elliptic (3), ovate (4), obovate (5), oblong (6), long oblong (7), long elliptic (8) or long irregular (9).	Code number
	Storage root skin colour: Whitish (1), cream (2), yellow (3), orange (4), brown (5), pink (6), red (7), purple (8).	Code number
	Storage root flesh colour: White (1), cream (2), yellow (3), orange (4), purple (5).	Code number
Yield and dry matter content	Number of storage roots	Number
	Weight of storage roots	Kg/ha
	Weight of vines	Kg/ha
	Dry matter content	%
SPVD	Symptoms in response to SPVD infection on a scale of 1 to 5 (see above)	Code number

Sources: Huamán (1999) and Mwanga et al. (2013)

3.3. Results

3.3.1. Analysis of variance of dry matter content, number of roots, and fresh root and vine yields of sweetpotato genotypes

Analysis of variance showed highly significant (p<0.001) differences among genotypes for dry matter content, number of roots, storage root and vine yields and response to SPVD across sites (Table 3.3). There was a significant (p<0.001) effect of site by entry interaction for these traits suggesting differential response of genotypes across sites. The mean performance of each genotype per site is presented in Table 4.4.

3.3.2. Performance of genotypes for various traits

3.3.2.1. Reaction to sweetpotato virus disease

Analysis of variance showed highly significant (p ≤ 0.001) difference in the response of genotypes to SPVD. Symptoms severity ranged from 1 to 5 with the mean of 2.02. Fifty eight percent of the genotypes had resistant reaction to SPVD with scores of 1 and 2, 31% had moderate reaction and 11% were susceptible (Table 3.4). Genotypes with code number 42 and 106 were the most susceptible and genotypes Kabode and 91 were the most resistant. There were significant differences (p ≤ 0.05) in responses to SPVD across sites (Table 3.3). Genotypes such as Kibakuli, Mataya and Mkombozi were symptomless in the field; however, after graft-inoculation, *I. setosa* manifested typical symptoms for SPVD in the screen house.

Table 3.3. Analysis of variance of dry matter content, number of roots, and root and vine yields of 144 sweetpotato genotypes evaluated across two sites in Tanzania

Sources of variation	DF	Mean squares				
		DMC (%)	NR/plant	Yield (t/ha)	Vine (t/ha)	SPVD
Site	1	26.48***	4.00**	1353.40***	81.89***	2.00*
Rep(site)	2	0.13	0.34^{ns}	3.63^{ns}	0.09^{ns}	0.84^{ns}
Block(Rep)	44	2.89^{*}	0.76^{ns}	5.31***	3.09^{ns}	0.34^{ns}
Entry	143	25.38***	4.59***	22.65***	12.30***	3.18***
Site*entry	143	2.44^{**}	0.96***	10.38***	8.48***	0.31^{ns}
Error	265	1.74	0.53	2.75	2.91	0.39

ns, *, **, *** no significant at P<0.05, significant at p<0.05, p<0.01 and significant at p<0.001; respectively; DF = degrees of freedom, DMC = dry matter content, NR/ha = number of roots, SPVD = Sweetpotato virus disease

3.3.2.2.   Time to 50% flowering

The tested sweetpotato genotypes showed great differences on of duration and ability of flowering (Table 4). Time to 50% flowering ranged from 40-100 days. For instance, the time to 50% flowering for genotypes Resisto and Mataya were 40 and 45 days, respectively. The genotypes were early and profuse flowering. From this study, the genotypes could be grouped into early, intermediate and late flowering varieties with others not flowering at all. Hence, 2, 48, 47 and 47 genotypes were early, intermediate, late and non-flowering, in that order. For instance, genotypes EX-Mwanza and Mchikichini did not produce flower at both test sites.

Table 3.4. Means for dry matter content, number of roots, fresh root yield, fresh vine yield and SPVD reaction of 144 sweetpotato genotypes evaluated at two sites in eastern Tanzania

SR. No	Genotype/code	DMC (%)		Number of roots/plant		Fresh root yield (t/ha)		Fresh vine yield (t/ha)		SPVD		Time to 50% flowering
		SRI–Kibaha	KATRIN–Ifakara	SRI–Kibaha	KATRIN–Ifakara	SRI–Kibaha	KATRIN–Ifakara	SRI–Kibaha	KATRIN–Ifakara	SRI–Kibaha	KATRIN–Ifakara	
1	28	37.50	35.00	5	4	5.8	6.8	3.63	1.58	1.0	1.5	68
2	109	40.00	38.75	5	3	6.4	5.5	3.08	2.46	2.5	4.0	86
3	123	41.25	40.00	6	6	5.3	9.2	5.42	3.42	1.5	2.0	73
4	23	36.25	35.00	5	5	3.6	8.5	2.99	2.93	2.0	3.0	72
5	122	36.25	36.25	3	3	3.4	9.0	5.31	1.99	1.0	1.0	61
6	124	37.50	38.75	6	7	6.8	12.1	4.32	3.48	2.5	2.5	Na
7	57	36.25	37.50	4	3	1.9	6.8	2.52	2.19	1.5	2.0	Na
8	60	32.50	31.50	8	6	5.5	12.8	7.32	6.55	1.0	1.0	78
9	Kandoro	35.00	33.75	3	4	7.8	11.8	4.96	2.13	1.0	1.0	81
10	SP2008/70	37.50	35.00	6	4	6.8	8.9	5.39	8.22	1.0	1.0	85
11	Jitihada	36.25	36.25	5	5	8.4	12.7	7.17	3.89	4.5	2.5	Na
12	117	32.50	33.75	4	6	3.2	9.2	1.76	3.29	2.5	2.5	75
13	7	40.00	38.75	4	5	6.3	8.0	3.8	5.5	1.0	1.0	Na
14	66	33.75	35.00	6	5	5.6	7.6	0.46	0.66	1.0	1.0	75
15	101B	36.25	35.00	6	4	3.6	4.6	4.41	2.23	1.5	2.0	68
16	SPSP2008/01	32.50	33.75	4	6	6.5	17.6	5.52	3.77	2.5	2.5	65
17	77	33.75	32.50	4	5	3.0	7.2	2.49	4.46	1.0	1.0	72
18	Ex-Ungindoni	36.25	35.00	4	4	3.1	5.0	3.76	0.84	1.5	2.0	Na
19	15	37.50	35.00	7	5	3.3	14.1	2.59	5.94	3.5	4.0	Na
20	Ex-Sungwi	33.75	35.00	3	4	8.1	17.0	8.47	6.17	1.0	1.0	78
21	Ex-Madina	32.50	30.00	5	7	5.2	14.2	7.73	5.56	1.0	1.0	Na
22	NASPOT 1	32.50	31.25	5	6	5.5	9.6	3.28	7.08	1.5	1.0	80
23	16	36.25	36.25	5	5	2.9	1.7	3.02	2.03	1.0	1.0	71
24	17	32.50	32.50	4	4	11.9	9.6	7.24	2.56	2.0	2.0	68
25	Shangazi	37.50	37.50	5	3	4.9	5.9	3.59	3.48	5.0	4.0	Na
26	59	36.25	36.25	3	4	4.6	8.3	3.72	4.06	3.0	2.5	78
27	30	36.25	35.00	6	5	6.7	6.2	3.69	0.65	1.0	1.0	85
28	Carrot njano	31.25	31.25	5	6	6.0	8.1	3.84	1.79	1.5	2.5	na
29	Binti jongo	33.75	33.75	4	5	7.8	12.8	11.5	2.87	1.5	1.0	na
30	95	33.75	33.75	5	4	3.5	5.5	3.37	1.45	2.5	2.5	na
31	Ex-Mwanza	38.75	38.75	4	4	3.5	3.2	1.97	2.97	1.0	1.0	na
32	Mkombozi	33.75	31.25	6	6	9.2	15.2	4.81	4.32	3.0	3.5	68
33	Ex-Yohana	35.00	33.75	5	6	5.8	10.5	6.05	5.11	1.0	1.5	na
34	Ex-Mengwa – 3	41.25	41.25	3	4	5.9	3.0	4.23	5.02	2.5	2.5	67
35	Jewel	31.25	28.75	4	5	6.0	10.7	3.13	3.49	1.0	1.0	80
36	Ex-Kazimzumbwe – 2	35.00	33.75	4	4	2.6	2.4	2.36	2.3	2.5	2.5	55

37	O3-03	35.00	35.00	4	3	4.8	5.8	3.32	1.42	1.5	2.0	60
38	68	34.00	31.25	5	3	9.3	11.2	3.76	1.62	1.0	1.0	80
39	101A	37.50	40.00	3	3	3.2	6.3	6.11	1.56	3.0	3.0	71
40	74	37.50	38.75	4	4	4.9	5.4	3.19	1.58	2.5	3.0	74
41	63	35.00	32.50	4	4	9.1	5.9	5.15	2.16	2.0	2.0	75
42	1	36.25	35.00	4	3	4.0	9.5	5.12	4.41	5.0	4.0	78
43	19	36.25	37.50	4	4	5.5	7.8	3.57	1.44	2.5	2.5	73
44	Ex-Maneromango-2	36.25	36.25	2	3	5.8	8.3	7.07	3.69	2.5	3.0	76
45	26	33.75	33.75	7	8	9.3	10.3	3.4	23.94	2.5	2.0	80
46	Simama	36.25	36.25	5	6	7.6	10.8	5.68	2.05	1.5	1.5	71
47	Kiegea	35.00	33.75	5	4	8.4	7.5	2.54	1.64	2.0	3.0	59
48	Matako mapana	37.50	37.50	6	6	9.1	11.8	3.1	0.63	2.5	3.0	80
49	73	37.50	37.50	4	5	3.2	4.6	3.53	1.59	3.0	2.5	80
50	2	36.25	35.00	5	4	5.7	9.8	3.21	3.43	1.0	1.0	na
51	Ex-Ramadhani	37.50	37.50	4	3	2.6	3.5	2.46	1.79	2.5	1.5	na
52	Emil Julius-2	33.75	35.00	4	4	4.3	8.6	6.13	4.69	1.0	1.0	81
53	Liponjwa	35.00	33.75	5	4	3.7	6.7	2.87	2.17	3.0	2.5	na
54	106	37.50	36.25	3	4	3.3	8.0	2.86	1.52	3.5	3.5	78
55	18	35.00	33.50	6	7	3.3	5.6	8	6.01	2.0	2.0	78
56	92	32.50	31.25	6	5	4.4	5.9	3.31	2.61	1.5	2.5	74
57	25	34.00	33.75	5	4	8.4	9.1	3.02	2.3	1.0	2.5	76
58	13	37.50	35.00	4	5	8.4	8.7	5.55	4.2	3.5	4.5	78
59	82	36.25	36.25	4	6	2.6	4.8	1.96	2.86	1.5	2.0	78
60	79	37.50	40.00	4	5	6.6	8.8	3.74	2.92	2.5	2.5	80
61	Ex-Kibuta – 2	35.50	35.00	3	3	2.4	12.5	6.2	2.74	1.0	1.0	na
62	Ex-Berene	36.25	36.25	6	5	3.4	15.1	8.65	10.86	1.0	1.0	85
63	Mnyalu	31.25	30.00	5	5	1.7	2.5	2.27	4.33	1.0	2.0	53
64	121	40.00	41.25	4	4	4.4	8.7	2.51	4.03	2.5	2.5	na
65	Carrot east	32.50	31.25	5	5	3.7	12.7	3.74	5.99	3.0	2.5	na
66	Mkwakwa	38.75	38.75	6	6	3.4	7.8	6.32	7.42	3.0	2.5	68
67	Gairo	35.00	37.50	6	7	6.5	9.9	5.59	2.32	3.0	2.5	78
68	Ex-Msimbu – 2	36.25	37.50	5	7	3.4	2.8	0.34	1.2	2.5	3.0	69
69	45	33.75	35.00	6	7	4.4	9.4	4.96	1.03	3.5	3.5	na
70	27	37.50	36.25	4	6	3.6	8.8	2.63	5.84	1.5	2.5	80
71	Ex-Kibugumo	37.50	35.00	3	4	4.9	13.4	4.12	3.89	1.5	2.0	80
72	Ex-Miale – 2	36.25	35.00	4	3	7.5	15.5	6.09	3.59	3.0	2.5	63
73	50	40.00	36.25	6	6	5.3	6.3	3.59	3	2.5	2.5	60
74	11	35.00	36.25	4	4	4.1	5.0	2.9	4.07	1.0	1.0	63
75	Kikabeji	36.25	35.00	3	4	6.0	7.8	8.48	2.83	1.0	1.0	na
76	Kigambile nyoko	37.50	40.00	4	5	1.5	2.4	5.42	1.93	2.5	3.0	75
77	SPBOP2006/943	35.00	35.00	5	4	7.1	10.5	6.41	2.45	1.5	1.0	na
78	78	37.50	37.50	6	6	5.1	6.4	2.95	1.94	2.5	2.5	na
79	127	33.75	35.00	3	3	5.2	2.3	2.89	1.16	1.5	1.5	na
80	Carrot Dar	32.50	32.50	6	5	6.9	9.2	5.22	1.92	2.0	1.0	Na

81	130	35.00	36.25	5	6	7.8	14.9	2.19	2.68	2.5	2.5	80
82	65	40.00	41.25	6	4	3.4	2.9	1.89	4.17	1.5	1.5	73
83	85	36.25	39.07	3	4	5.1	12.1	1.69	3.23	1.0	2.0	78
84	Mataya	35.00	32.50	5	5	7.8	10.0	2.07	2.27	3.0	3.5	45
85	NASPOT 6	32.50	33.75	4	6	2.4	12.4	8.43	6.65	1.0	1.5	na
86	Carrot C	31.25	32.50	3	4	5.1	12.7	4.88	5.15	2.5	2.5	na
87	Ejumla	31.25	32.50	5	5	4.2	12.4	3.53	2.84	2.0	1.5	80
88	Kabuchenji	38.75	38.75	6	6	5.1	5.6	7.22	3.09	1.5	1.0	75
89	Mayai	35.00	35.00	8	7	2.5	8.1	7.06	3.46	1.5	1.5	75
90	Tembele la kisukuma	33.75	32.50	4	5	0.3	3.6	1.09	3.5	1.0	2.0	na
91	SPKCC2008/01	37.50	35.00	6	7	10.6	19.4	3.22	1.43	1.5	1.5	75
92	Resisto	30.00	31.25	3	4	4.2	4.7	2.47	0.88	4.0	3.5	45
93	116	32.50	35.00	6	3	2.7	6.1	4.97	1.63	1.0	1.0	80
94	128	37.50	35.00	5	4	8.2	10.8	4.69	3.46	1.0	2.0	80
95	SPBOP2008/920	37.50	38.75	4	4	2.3	6.5	7.07	3.31	1.0	1.5	80
96	SP9062/0P	33.75	35.00	5	5	5.6	8.2	5.76	1.45	1.5	1.5	na
97	12	38.75	38.75	6	5	3.3	6.0	3.27	6.19	1.5	1.5	na
98	Ex-Kiboda-4	36.25	36.25	3	3	2.8	7.4	8.05	10.5	3.0	2.0	85
99	O69	33.75	35.00	4	5	6.0	1.8	1.81	5.45	1.0	1.0	55
100	Sekondari	33.75	31.25	4	4	2.2	2.2	2.6	2.41	1.0	1.0	75
101	Ex-Kiboda-2	36.25	36.25	5	5	0.9	1.7	1.77	3.35	1.0	2.0	60
102	81	37.50	36.25	4	4	2.6	2.9	1.48	0.78	3.0	2.0	80
103	Kagole	35.00	35.00	3	6	5.3	9.5	8.3	2.45	1.0	1.0	na
104	Zambezi	32.50	35.00	4	5	8.5	10.6	3.4	2.28	2.0	2.0	65
105	Kakamega	33.75	32.50	4	3	3.3	8.7	5.42	-0.36	1.0	1.0	95
106	9	36.25	33.75	3	4	6.8	9.1	4.75	1.51	4.5	4.5	na
107	94	35.00	32.50	5	4	3.1	8.6	3.34	3.09	1.5	2.0	na
108	Ex-Msimbu-1	42.50	40.00	4	4	2.4	18.1	7.87	1.58	1.5	3.5	75
109	Polista	36.25	33.75	6	7	4.5	14.9	7.22	4.02	1.5	1.5	90
110	14	41.25	41.25	4	4	3.8	14.3	5.73	7.83	3.0	4.0	80
111	3	38.75	38.75	5	4	8.3	14.2	3.88	4.17	3.0	2.0	na
112	55	37.5	37.50	3	3	8.7	15.4	5.96	5.98	1.0	1.0	70
113	44	36.25	36.25	5	5	6.4	11.5	3.25	2.66	1.0	1.0	65
114	75	35.00	30.00	4	5	6.0	6.5	2.53	4.53	1.0	2.0	80
115	86	37.5	37.50	6	6	3.5	5.3	2.19	2.37	4.5	4.0	na
116	32	37.50	36.25	3	2	7.4	7.5	2.92	2.6	1.0	1.0	na
117	Ex-Msimbu-3	35.00	33.75	4	4	7.3	6.7	1.8	1.46	2.5	2.5	80
118	Ex-Kiboda-1	40.00	40.00	5	5	5.2	6.5	1.54	1.45	3.0	2.5	na
119	Canada nyekundu	31.25	33.75	4	4	7.6	6.1	2.04	2.44	2.5	2.5	80
120	Berene	33.75	31.25	5	5	6.0	8.7	2.97	1.81	1.5	1.5	na
121	99	38.75	37.50	8	10	5.4	6.0	1.89	3.99	1.5	2.0	80
122	Ex-Kibuta-3	35.00	32.50	5	7	6.7	11.8	6.65	7.83	2.5	2.5	80
123	Ukerewe	46.25	43.75	6	6	12.4	8.2	3.43	1.73	1.0	2.0	75
124	43	32.50	30.00	6	7	8.4	10.6	5.27	5.01	1.5	1.5	80
125	Mchikichini	32.50	32.50	6	4	5.9	5.9	2.35	1.91	2.5	2.5	na

SR No	Name											
126	Ex-Halima-3	35.00	32.50	4	4	8.6	10.7	2.82	2.18	1.0	1.0	65
127	91	36.25	37.50	3	2	3.4	7.1	5.33	3.45	1.0	1.0	71
128	20	35.00	37.50	4	4	4.9	7.6	6.31	1.28	1.0	1.0	71
129	Mwanatata	40.00	37.50	4	5	6.9	6.8	3.07	2.48	3.0	2.5	na
130	Zapallo	30.00	27.50	5	5	3.9	5.7	5.69	2.94	4.0	3.5	na
131	Ex-Bwana	37.50	40.00	6	6	6.2	8.0	2.36	5.52	1.5	2.5	80
132	Mjomba mkwe	33.75	31.25	3	5	3.2	7.8	2.57	1.97	1.5	1.5	na
133	Ex-Halima-2	36.25	37.50	5	6	7.2	14.3	5.43	7.68	1.0	1.0	80
134	8	40.00	40.00	4	6	5.8	8.1	6.38	3.41	3.5	4.0	65
135	5	33.75	33.75	5	6	5.7	5.5	5.81	4.21	4.5	4.0	73
136	Ex-Kazimzumbwe-1	37.50	35.00	6	7	10.4	5.7	2.45	2.13	4.0	4.0	73
137	96	35.00	37.50	4	5	5.2	8.0	2.88	3.28	3.0	3.5	na
138	Ex-Msimbu-4	33.75	33.75	5	6	2.9	6.3	2.93	2.57	1.0	1.0	na
139	119	37.50	36.25	5	5	5.5	6.5	1.94	1.42	1.0	1.0	na
140	47	36.25	36.25	5	4	7.0	8.5	4.41	3.13	1.0	1.0	80
141	Kibakuli	32.50	32.50	6	6	9.5	12.6	2.83	2.56	3.5	4.0	65
142	98	33.75	33.75	4	4	6.1	6.9	2.66	9.03	3.0	2.5	na
143	Mbutu	35.00	35.00	4	4	3.2	4.1	4.86	2.68	2.0	3.0	80
144	Kabode	35.00	32.50	5	4	6.5	2.9	1.92	1.45	1.0	1.0	na
	Mean	35.72	35.30	4.45	4.60	5.3	8.4	3.44	64.19	1.96	2.08	
	CV (%)	3.73	3.76	15.65	15.67	28.6	20.9	67.19	15.93	37.08	23.53	
	R Square	0.90	0.92	0.87	0.89	0.84	0.92	0.77	0.96	0.82	0.90	
	EMS	1.78	1.76	0.48	0.53	2.4	3.1	5.33	0.45	0.52	0.24	
	LSD	2.64	2.63	1.38	1.43	7.1	8.1	4.57	1.98	1.44	0.97	

CV = Coefficient of variation, DMC = Dry matter content, EMS = Error mean square, LSD = List significant difference, na= not available (no flowering the entire study period), SPVD = Sweetpotato virus disease, SR No = Serial number

3.3.2.3. Number of roots per plant

There was significant difference in the number and yield of fresh roots among genotypes within and across sites (Table 3.3). The number of roots ranged from 2-9 with average of 4 roots/plant (Table 3.4). Genotype with code 26 had the highest mean number of roots per plant. On the other hand, genotypes with codes 26, Mayai and 99 had the lowest mean number of roots per plant (Table 3.4).

3.3.2.4. Fresh root yield

Genotypes performed differently in terms of fresh root yield within and across sites (Table 3.3). Storage root yield ranged from 0.3-15 t/ha with average yield of 6.9 t/ha for Tembele la kisukuma and SPKCC2008/01, respectively (Table 3.4). Genotypes SPKCC2008/01 and Ex-kiboda-2 had the highest and lowest yields, respectively. Genotypes Mataya, Simama and Ex-Msimbu-1 with yield of 8.8, 9.2 and 10.2 t/ha, respectively were selected for crossing. Despite high yield, genotype Jewel was not selected due to poor flowering (Table 3.4).

3.3.2.5. Vine yield

There were significant differences in vine yield within and across sites (Table 3.3). Vine yield ranged from 0.56-13.67 t/ha with mean of 3.81 t/ha (Table 4). Genotypes 26, Ex-Berene and 81 had the highest vine yield of 13.67, 9.75 and 9.27t/ha, respectively (Table 3.4). However, the vine yields were relatively low.

3.3.2.6. Dry matter content

There was highly significant differences ($p < 0.001$) in storage root dry matter content among genotypes and across sites (Table 3.3). Dry matter content ranged from 28.8-45% with mean value of 35.5% (Table 3.4). Genotypes Zapallo and Ukerewe had the lowest and highest DMC, respectively. Based on DMC, genotypes Ukerewe, Ex-Msimbu-1 and Simama with DMC values of 45, 41.3 and 36.3%, respectively were selected for breeding.

3.3.3. Cluster analysis

The un-weighted pair group method with arithmetic means (UPGMA) grouped the 144 genotypes into five main clusters. Each of the clusters had two sub-clusters (Table 3.5). Clustering of these genotypes displayed similarity coefficients that ranging from 0.65 to 1.0 (data not shown). Due to the large number of genotypes included in the analyses the dendrogram was not shown but data presented in Table 3.5 showing the five clusters and genotypes.

The first cluster had common primary and secondary vine colour, mature leaf colour and petiole pigmentation. Sub-clustering was due to differences in petiole length among the genotypes. The second cluster had common vine primary colour and diametre, mature leaf and skin colour and leaf outline and size. Sub-clustering was due to root formation. The third cluster, despite having the same primary vine and leaf colour, had the same leaf outline and size, storage root skin colour and reaction to SPVD. The fourth cluster had common leaf size and the fifth one had common leaf outline, lobe number, leaf size and root shape.

Table 3.5. Summary of cluster analyses when evaluating 144 sweetpotato genotypes across two sites in Tanzania

Clusters	Number of genotypes	Sub-clusters	Codes of genotypes
I	50	A	1, 41,107, 52, 118, 40, 28, 65, 26, 108, 30, 59, 102, 76, 69, 115, 137, 20, 112, 21, 78, 138, 83, 140, 116, 114, 88, 46, 56, 124, 128, 131, 8
		B	86, 11, 16, 80, 32, 91, 129, 19, 141, 72, 136, 73, 44, 98
II	15	A	37, 50, 70, 117, 93, 133, 139
		B	60, 122, 134, 61, 77, 95, 96
III	14	A	4, 123, 71, 120, 68
		B	10, 79, 63, 103, 109, 23, 97, 62
IV	31	A	5, 113, 55, 34, 82, 111, 24, 43, 127, 75, 89
		B	7, 9, 51, 13, 36, 67, 99, 14, 38, 27, 100, 121, 48, 66, 47, 84, 126, 53
V	34	A	2, 110, 6, 12, 17, 143, 42, 49, 54, 58, 57, 81, 15, 90, 39, 64, 45
		B	3, 94, 106, 29, 119, 18, 25, 142, 125, 135, 74, 132, 33, 101, 31

See Table 4 for codes and names of genotypes

For all clusters, there was great variability in most of the agronomic traits namely; number of roots, DMC and root and vine yield. Genotypes varied based on both qualitative and quantitative traits across the two sites, however; greater variations were largely due to quantitative traits than qualitative traits. Further, the variations could be due to genotypes, environment and their interactions.

3.3.4. Correlation between traits

The correlation coefficients between quantitative and qualitative phenotypic traits studied are presented in Tables 3.6 and 3.7. Highly significant and positive correlations (p=0.01) were reported between growth habit and dry matter content (r=0.26), vine diametre and petiole length (r=0.26), petiole length and vine yield (r=0.27), number of roots and fresh root and vine yield (r=0.30) and fresh root yield and vine yield (r=0.40) (Table 6). Also, a significant and positive correlations (r=0.19; p=0.05) were reported between growth habit and vine yield and leaf size with dry matter content (r=0.18) (Table 3.6). Non-significant, negative correlations were reported between vine diametre and number of roots with dry matter content (Table 3.6).

Among qualitative traits (Table 3.7), highly significant and positive correlations (p=0.01) were reported between vine primary colour with mature, immature leaf colour and petiole pigmentation, petiole pigmentation and root skin colour; immature leaf colour with petiole pigmentation and root skin colour, and petiole pigmentation and root skin colour. Significant and positive correlations (p=0.05) were reported between mature leaf colour with immature leaf colour and petiole pigmentation. On the other hand, highly significant and negative correlations were reported between growth habit and petiole pigmentation with root flesh colour. Also, negative correlations were reported for immature leaf colour with roof flesh colour. There was no correlation between mature leaf colour and root flesh colour.

Table 3.6. Pearson correlation coefficients among quantitative traits when evaluating 144 sweetpotato genotypes across two sites in Tanzania

	Growth habit	Vine diametre	Leaf size	Petiole length	Number of roots	Fresh root yield	Vine yield	Dry matter content
Growth habit	1	-0.160^{ns}	0.150^{ns}	0.113^{ns}	-0.040^{ns}	0.067^{ns}	0.187^{*}	0.255^{**}
Vine diametre		1	0.105^{ns}	0.262^{**}	0.061^{ns}	0.042^{ns}	0.095^{ns}	-0.050^{ns}
Leaf size			1	0.135^{ns}	-0.092^{ns}	-0.226^{**}	0.090^{ns}	0.176^{*}
Petiole length				1	0.069^{ns}	0.142^{ns}	$.268^{**}$	0.134^{ns}
Number of roots					1	0.537^{**}	0.304^{**}	-0.080^{ns}
Fresh root yield						1	0.402^{**}	0.030^{ns}
Vine yield							1	0.127^{ns}
Dry matter content								1

ns = non-significant correlation, *, and ** denote significant correlations at the 0.05 and 0.01 probability levels, respectively.

Table 3.7. Spearman correlation coefficients among qualitative traits when evaluating 144 sweetpotato genotypes across two sites in Tanzania

	Primary colour	Mature leaf colour	Immature leaf colour	Petiole pigmentation	Root skin colour	Root flesh colour
Primary colour	1	0.280**	0.36**	0.879**	0.505**	-0.226**
Mature leaf colour		1	0.203*	0.207*	0.157ns	0
Immature leaf colour			1	0.253**	0.410**	-0.174*
Petiole pigmentation				1	0.476**	-0.291**
Root skin colour					1	-0.111
Root flesh colour						1

ns = non-significant correlation, * and ** denote significant correlations at the 0.05 and 0.01 probability levels, respectively.

3.4. Discussion

3.4.1. Reaction to SPVD

Under natural field infections, the genotypes showed variable reactions to SPVD. Generally, the genotypes were grouped into three groups due to their reaction to SPVD, namely; resistant, moderately resistant and susceptible (Table 3.4). Fifty eight percent of genotypes showed low levels of SPVD infections. Since the study sites were hotspots for SPVD, field SPVD inoculum pressure was capable of causing moderate to severe infection in plants (Mwanga et al., 2013). The low incidences of SPVD may refer either to cultivar resistance or tolerance to the disease or disease transmitting insects (Gasura and Mukasa, 2010; Mwanga et al., 2013). Similar to this study, Ndunguru and Kapinga (2007) and Ndunguru et al. (2009) reported highly signifant differences in severity of SPVD symptoms among sweetpotato cultivars. Further, they reported significant difference in severity of SPVD symptoms among locations studied in Southern Tanzania and in Northwestern of Tanzania and Central Uganda.

Some genotypes recovered from SPVD infection over time under field conditions. Recovery could be a natural mechanism for some form of resistance (Gasura and Mukasa, 2010). Mwanga et al. (2002) reported recovery in some genotypes with severe SPVD symptoms. It is suspected that the recovery from SPVD infection could have greatly contributed to the persistence of most of landraces in farmers' fields (Aritua et al., 1998).

Although, most of the genotypes had relatively moderate dry matter content no definite trend could be established at this stage on the relationship between dry matter content and reaction to SPVD for the genotypes studied. However, 61% of genotypes that were resistant had dry matter content between 35-41% which is higher compared to some susceptible varieties such as Zapallo and Resisto with dry matter content of 28.75 and 30%, respectively (Table 3.4). Based on resistance to SPVD (score between 1-2), genotypes Simama, Ukerewe, Gairo and 03-03 were selected for breeding. Despite being susceptible or moderately susceptible to SPVD, genotypes Resisto and Mataya, and Ex-Msimbu-1 were selected for breeding due to high beta carotene content and high vine yield, respectively (Table 3.4).

3.4.2. Performance of genotypes for different traits

3.4.2.1. Time to 50% flowering

Poor flowering ability is one of the main challenges in sweetpotato breeding programmes. A wide range of variations were reported in time to 50% flowering among the genotypes (Table 3.4). The starting time of flowering and time to 50% flowering markedly varied among genotypes. Based on differences in time to 50% flowering, the tested sweetpotato genotypes can be grouped into early, intermediate and late flowering types. Resisto and Mataya flowered early compared to other genotypes with 40 and 45 days, respectively. Genotypes such as Mataya, 03-03 and 069 had profuse flowering ability except very limited crossing window period. Consequently, production of few flowers and narrow 'flowering window' limits the number of crosses that can be made. Further, differences in time to flowering in addition to self- and cross-incompatibility, poses a great challenge in genetic improvement of the crop.

A number of factors such as genotype, day length, and plant nutrition and water availability greatly influence flowering ability in sweetpotato. Veasey et al. (2007) reported a wide range in flower initiation in different local varieties which ultimately determine the time to 50% flowering. Similar to this study, the same author reported the presence of non-flowering accessions. Lardizabal and Thompson (1990) reported production of limited number of flowers despite flower induction. Also, the author found that seed setting is variety dependent.

3.4.2.2. Number of roots per plant

Sweetpotato is mainly grown for its roots. The number of storage roots produced differed significantly among varieties and across the two sites (Table 3.3). Similar result was reported by Tairo et al. (2008) who found significant variations among sweetpotato genotypes for number of roots and root weight. The differences in number of roots and ultimately yield were probably attributed to differences in cultivars, maturity and response to environmental conditions (Oggema et al., 2007). Bhattacharya et al. (1985) reported a number of roots at high carbondioxide concentration.

3.4.2.3. Fresh root yield

The significant differences in root yield were reported between genotypes and across sites (Tables 3.3 and 3.4). Since management practices were the same, the differences in root yields among genotypes within and across sites could have been attributed to genotypic variations, differences in maturity and their interactions with the environments. The storage root yield depends on the number of roots per plant and the rate and efficiency at which the photosythate

translocate to storage roots (Bhagsari and Ashley, 1990; Kapinga et al., 2003). Bhagsari and Ashley (1990) reported a significant difference in yield among sweetpotato genotypes in the United States. Similar findings have been reported by An et al. (2003) and Abdissa et al. (2012). However, none of the genotypes in this study attained the expected yield potential of 15-23 t/ha set by Department of Research and Development, Ministry of Agriculture, Tanzania (Sebastiani et al., 2007). This could have been attributed to early stoppage of rains which to some extent affected root bulking; however, too much rain may also compromise yield. Hartemink et al. (2000) reported lower sweetpotato yields in New Papua Guinea due to soils, weather and cultivar differences. According to Lebot (2010) the yield of sweetpotato is determined by the length of the growing period. Additionally, Mwanga and Zamora (1988) and Oggema et al. (2007) reported that varietal differences, growing conditions and management practices may significantly cause yield differences in sweetpotato genotypes. Further, Harrison and Jackson (2011) reported that, sweetpotato yields vary depending on varieties, length of growing season, cultural management and environmental conditions. In the case of this study, the yield differences reported could be due to genotypic variations, differences in maturity and their interactions with the environments because the management practices were the same.

3.4.2.4.   Vine yield

The genotypes performed differently in vine production (Table 3.3). Sweetpotato is primarily cultivated for its fresh storage roots. However, in some sweetpotato cultivars their young and tender vines and leaves vines are used as vegetables. Also, their aboveground biomass is used as forage (An et al., 2003). This is an important attribute in both rural and urban areas for livestock feed. However, high tonnage of vine may compromise storage root yields (Abdissa et al., 2012). Apart from animal feed, in rural areas sweetpotato vines are either used as organic manure or burnt and used to improve soil fertility (Abdissa et al., 2012). The genotypic differences in vine production within and across sites could be due to cultivar differences, environment and their interaction.

3.4.2.5.   Dry matter content

Generally, most of the accessions had high dry matter content (Table 3.4). Dry matter content is an important and most preferred market attribute and is one of the criteria famers use in selecting sweetpotato cultivars (Tairo et al., 2008). Dry matter content for different varieties falls within the range of 17-49% (Tairo et al., 2008; Karuri et al., 2009). Dry matter content is associated with farmers' and consumers' preferences and processing quality. Farmers prefer sweetpotato cultivars which are tasty with high dry matter content. Further, it affects eating quality, shelf-life

and industrial processing (Lebot, 2010). Tairo et al. (2008) reported differences in dry matter content among sweetpotato germplasm collected from different agro-ecological zones of Tanzania. Similarly, An et al. (2003) reported differences in storage root dry matter content among sweetpotato varieties. Generally high dry matter content is a common phenomenon to east African sweetpotato genotypes (Gichuki et al., 2003). In a participatory rural appraisal conducted in Mkuranga, Kilosa, Kilombero and Gairo districts of Tanzanian in 2014 (Ngailo et al., 2015; in press), it was learned that, low dry matter content is amongst the attribute that has led to abandonment of many varieties by famers.

Dry matter content varies with varieties, environments, cultural practices and seasons (Tsakama et al., 2010). Mwanga and Zamora (1989) reported a significant decrease in dry matter content due to shading. The application of farm yard manure and green leaf manure in sweetpotato production yielded storage root with high dry matter content compared to application of inorganic fertilizer (Nedunchezhiyan et al., 2010). Gomes and Carr (2003) reported that, the competition of assimilates between two principal sinks, namely, vines and storage roots affects the dry matter content in sweetpotato. Also, dry matter content is likely to be compromised by number of storage roots (Lowe and Wilson, 1974). A large number of storage roots might reduce dry matter content as the plant may not be able to supply enough photosynthetic assimilates to all storage roots (Gasura et al., 2010).

3.4.3. Cluster analysis

The cluster analysis of the genotypes using 24 characters revealed a great phenotypic diversity (Table 3.5). The variability could have been attributed to genetic differences, environment and their interactions. The genotypes exhibited variability in growth habit, vine characteristics, skin and flesh colour and reaction to SPVD. This result is comparable to that reported by Gwandu et al (2012) in Tanzanian elite sweetpotato genotypes who reported two clusters with sub-clusters. Also, Karuri et al. (2010) reported high genetic diversity among Kenyan sweetpotato germplasm using morphological and SSR markers. It is suspected that natural mutations, high ploidy level asexual reproduction, self-incompatibility and cross-pollination of sweetpotato could have contributed to great variability among genotypes (Villordon and LaBonte, 1995; Veasey et al., 2007).

3.4.4. Correlation between traits

Correlation analysis among different traits revealed diverse relationships (Tables 3.6 and 3.7). However, most of the traits revealed positive and high significant relationships. For instance, a highly significant correlation was reported between number of roots and fresh root and, vine yield (r=0.30) and fresh root yield and vine yield (r=0.40). Kiarie (1988), Afuape et al. (2011) and Solankey et al. (2014) reported a highly significant and positive correlation between number of roots and root yield. Comparable finding was reported by Tsegaye et al. (2006) and Yada et al. (2011). Similar to this study, Abdissa et al. (2012) reported a positive correlation between root yield and vine yield as the increase in vine or plant top led to greater amount of photosynthate translocation to the storage roots causing their increase in size and ultimately root yield. Consistent with this study, a positive and significant correlation between vine weight and number of roots was reported by Jha (2011). On the other hand an inverse relationship between SPVD infection and dry matter content has been reported. Karuri et al. (2009) reported low dry matter content for genotypes which were resistant to SPVD. Lebot et al. (2011) reported high correlation coefficient between vine pigmentation and petiole pigmentation and non-significant correlation between aerial and underground traits. Moreover, a positive correlation of r = 0.647 between primary vine colour and petiole pigmentation compared to r = 0.879 in this study has been reported by Norman et al. (2014). While there was no correlation between mature leaf colour and root flesh colour in this study, a negative correlation (r=0.0117) between the two traits was reported by Koussao et al. (2014) in Burkina Faso. Provided that the correlations between traits are well established, it is possible for the known variable to predict the potential of corresponding trait (Augustina et al., 2013). On the other hand, the lack of correlation between mature leaf colour and root flesh colour may be of special interest for further investigation.

3.5. Conclusions

The present study selected the following genotypes; Simama, Ukerewe, Mataya, Resisto, 03-03, Ex-Msimbi-1 and Gairo. They were selected based on resistance to SPVD (Simama and Ukerewe), high storage root yields (Simama and Mataya), better dry matter content (Ukerewe, Simama and Ex-Msimbu-1), vine yield (Ex-Msimbu-1), suitable flesh colour (Resisto, 03-03 and Mataya) and elliptical root shape which is preferred by farmers for easy packaging. In addition, a clone SPKBH008 was selected owing to its early and long lasting profuse flowering ability. The selected eight genotypes are recommended as promising parents for sweetpotato breeding.

References

Abdissa, T., N. Dechassa, and Y. Alemayehu. 2012. Sweetpotato growth parameters as affected by farmyard manure and phosphorus application at Adami Tulu, central rift valley of Ethiopia. Agricultural Science Research Journal 2:1-12.

Afuape, S., P. Okocha, and D. Njoku. 2011. Multivariate assessment of the agromorphological variability and yield components among sweetpotato (*Ipomoea batatas* (L.) Lam) landraces. African Journal of Plant Science 5:123-132.

An, L.V., B.E. Frankow-Lindberg, and J.E. Lindberg. 2003. Effect of harvesting interval and defoliation on yield and chemical composition of leaves, stems and tubers of sweetpotato (*Ipomoea batatas* (L.) (Lam.) plant parts. Field Crops Research. 82:49-58.

Aritua, V., T. Alicai, E. Adipala, E.E. Carey, and R.W. Gibson. 1998. Aspects of resistance to sweetpotato virus disease in sweetpotato. Annal Applied Biology 132:387-398.

Arizio, C.M., N. Hompanera, E.Y. Suarez, and M.M. Manifesto. 2009. Genotypic identification and diversity evaluation of a sweetpotato (*Ipomoea batatas* (L). Lam) collection using microsatellites. Plant Genetic Resource Characterization and Utililization 7:135-138.

Augustina, U.A., O.P. Iwunor, and O.R. Ijeoma. 2013. Heritability and character correlation among some rice genotypes for yield and yield components. Journal of Plant Breeding and Genetics 1:73-84.

Beah, A., J. Samba, M. Tucker, M. Benya, and S. Fomba. 2014. Agro-phenotypic characterization of sweetpotato (*Ipomoea batatas L.*) genotypes using factor and cluster analyses. Agricultural Science Research Journal 4:30-38.

Bhagsari, A.S. and D.A. Ashley. 1990. Relationship of photosynthesis and harvest index to sweetpotato yield. Journal of American Society of Horticultural Science 115:288-293.

Bhattacharya, N.C., P.K. Biswas, S. Battacharya, N. Sionit, and B.R. Strain. 1985. Growth and yield response of sweetpotato to atmospheric CO_2 enrichment. Crop Science 25:975-981.

Carey, E.E. and D. Reynoso 1999. Procedure for evaluation of pathogen-tested sweetpotato clones. In*:* Huamán, Z. editor, Sweetpotato germplasm management. Training manual 3. Evaluation and breeding*.* International potato Centre (CIP), Lima

Elameen, A., A. Larsen, S. Klemsdal, S. Fjellheim, L. Sundheim, S. Msolla, E. Masumba, and O. Rognli. 2011. Phenotypic diversity of plant morphological and root descriptor traits within

a sweetpotato germplasm collection from Tanzania. Genetic Resources and Crop Evolution 58:397-407.

Engoru, P., J. Mugisha, and B. Bashaasha. 2005. Tuber utilization options among sweetpotato producers in eastern Uganda. African Crop Science Journal 7:715-719.

FAOSTAT. 2015. Food and Agricultural Organization, Agricultural data. Crops and products domain available at http.faostat.fao.org/ [Online]. Rome: FAO. [Accessed 12th October 2015].

Gasura, E., A.B. Mashingaidze, and S.B. Mukasa. 2010. Genetic variability for tuber yield, quality, and virus disease complex traits in Uganda sweetpotato germplasm. African Crop Science Journal 16:147-160.

Gasura, E. and S.B. Mukasa. 2010. Prevalence and implication of sweetpotato recovery from sweetpotato virus disease in Uganda. African Crop Science Journal 18:195-205.Gibson, R.W. 2005. Working with farmers to control sweetpotato virus disease in East Africa: Crop protection programme. UK: Natural resource institute.

Gibson R.W., V. Aritua, E. Byamukama, I. Mpembe, and J. Kayongo. 2004. Control strategies for sweetpotato virus disease in Africa. Virus Research 100:115-122.

Gibson R.W., I. Mpembe, T. Alicai, E.E. Carey, R.O.M. Mwanga, S.E. Seal, and H.J. Vetten. 1998. Symptoms, aetiology and serological analysis of sweetpotato virus disease in Uganda. Plant Pathology 47:95-102.

Gichuki, S.T., M. Berenyi, D. Zhang, M. Hermann, J. Schmidt, J. Glössl, and K. Burg. 2003. Genetic diversity in sweetpotato *[Ipomoea batatas* (L.) Lam.] in relationship to geographic sources as assessed with RAPD markers. Genetic Resources and Crop Evolution 50:429-437.

Gomes, F. and M. Carr. 2003. Effects of water availability and vine harvesting frequency on the productivity of sweetpotato in southern Mozambique. II. Crop water use. Experimental Agriculture 39:39-54.

Gomez, K.A. and A.A. Gomez 1984. Statistical procedures for agricultural research. John Wiley and Sons.

Gwandu, C., F. Tairo, E. Mneney, and A. Kullaya. 2012. Characterization of Tanzanian elite sweetpotato genotypes for sweetpotato virus disease (SPVD) resistance and high dry

matter content using simple sequence repeat (SSR) markers. African Journal of Biotechnology 11:9582-9590.

Harrison, H.F., Jr. and D.M. Jackson. 2011. Response of two sweetpotato cultivars to weed interference. Crop Protection 30:1291-1296.

Hartemink, A.E., S. Poloma, M. Maino, K.S. Powell, J. Egenae, and J.N.O. Sullivan. 2000. Yield decline of sweetpotato in the humid lowlands of Papua New Guinea. Agricultural Ecosystem and Environment 79:259-269.

Huaman, Z. 1999. Botany, origin, evolution and biodiversity of the sweetpotato. Sweetpotato Germplasm Management Training Manual. International Potato Center, Lima Peru:1-11.

Jha, G. 2011. Emerging research technology against climate change through selecting ideal genotypes from open pollinated seedling population of sweetpotato (*Ipomoea batatas* (L.) Lam.). International Quartery Journal of Environmental Science 1:179-185.

Jones, A. 1980. Sweetpotato. American Society of Agronomy 46:645-655.

Jones, A., P.D. Dukes, and J.M. Schalk (eds.) 1986. Sweetpotato breeding, Westport, CT, USA: AVI Publishing Co.

Kapinga, R.E., J. Ndunguru, G. Mulokozi, and S. Tumwegamire. 2009. Impact of common sweetpotato viruses on total carotenoids and root yields of an orange-fleshed sweetpotato in Tanzania. Scientia Horticulturae 122:1-5.

Kapinga, R.E., S. C. Jeremiah, E.J. Rwiza, and D. Rees. 2003. Farmer criteria for selection of sweetpotato varieties. In Rees, D. (editor) Sweetpotato postharvest assessment: Experiences from East Africa. Sweetpotato postharvest assessment: Experiences from East Africa. Chapman, UK.

Kapinga, R., D. Zhang, B. Lemaga, M. Andrade, R.O.M. Mwanga, S. Laurie, P. Ndoho, and E. Kanju. 2003. Sweetpotato improvement in sub-Saharan Africa and future challenges. In: Kapinga, R., R. Kingamkono, M. Msabaha, J. Ndunguru, B. Lemaga and G. Tusiime editors, The Thirteenth Triennial Symposium of the International Society for Tropical Root Crops. International Society for Tropical Root Crops (ISTRC), AICC, Arusha; p. 82-94.

Karuri, H.W., E.M. Ateka, R. Amata, A.B. Nyende, and A.W.T. Muigai. 2009. Characterization of Kenyan sweetpotato genotypes for SPVD resistance and high dry matter content using simple sequence repeat markers. African Journal of Biotechnology 8:2169-2175.

Kiarie, A.W. 1988. Yield stability studies in some sweetpotato (*Ipomea batatas* (L) Lam) cultivars in Kenya. MSc. Plant breeding, University of Naitobi, Nairobi.

Korada, R.R., S.K. Naskar, A.R. Prasad, A.L. Prasuna, and K.N. Jyothi. 2010. Differential volatile emision from sweetpotato plant: mechanism of resistance in sweetpotato for weevil *Cylas foricarius* (Fab). Current Science 99:1597-1601.

Koussao, S., V. Gracen, I. Asante, E.Y. Danquah, J.T. Ouedraogo, T.J. Baptiste, B. Jerome, and T.M. Vianney. 2014. Diversity analysis of sweetpotato (*Ipomoea batatas* [L.] Lam) germplasm from Burkina Faso using morphological and simple sequence repeats markers. African Journal of Biotechnology 13:729-742.

Lardizabal, R.D. and P.G. Thompson. 1990. Growth Regulators Combined with Grafting Increase Flower Number and Seed Production in Sweetpotato. HortScience 25:79-81.

Lebot, V. 2010. Sweetpotato. In*:* Bradshaw, J.E. editor, Root and tuber crops: Handbook of plant breeding*.* Springer, London.

Lebot, V., A. Ndiaye, and R. Malapa. 2011. Phenotypic characterization of sweetpotato, *Ipomoea batatas* (L.) Lam. genotypes in relation to prediction of chemical quality constituents by NIRS equations. Plant Breeding 130:457-463.

Lowe, S. and L. Wilson. 1974. Comparative analysis of tuber development in six sweetpotato (*Ipomoea batatas* (L.) Lam) Cultivars 1. Tuber initiation, tuber growth and partition of assimilate. Annual Botany 38:307-317.

Masumba, E., R. Kapinga, S.M. Tollan, M. Yongolo, and D.C. Kitundu. 2007. Adaptability and acceptability of new orange-fleshed sweetpotato varieties in selected areas of eastern and central zones of Tanzania. *In:* Kapinga, R., R. Kingamkono, M. Msabaha, J. Ndunguru, B. Lemaga, and G. Tusiime. (eds). *The Thirteenth Triennial Symposium of International Society of Tropical Root Crops* 10-14 November 2003 AICC, Arusha. Tanzania: International Society of Tropical Root Crops (ISTRC), 737-745.

Masumba, E., H. Kulembeka S. Tollano, and M. Yongolo. 2005. Participatory evaluation of improved sweetpotato varieties in Eastern Tanzania. African Crop Science Journal 12:259-265.

Mohammadi, S. and B. Prasanna. 2003. Analysis of genetic diversity in crop plants-salient statistical tools and considerations. Crop Science 43:1235-1248.

Mukasa, S.B., P.R. Rubaihayo, and J.P.T. Valkonen. 2006. Interactions between a crinivirus, an ipomovirus and a potyvirus in co-infected sweetpotato plants. Plant Pathology 55:458-467.

Mullen, M.A. 1984. Influence of sweetpotato weevil infestation on the yields of twelve sweetpotato lines. Journal of Agricultural Entomology 1:227-230.

Munyiza, H., P. Stevenson, R. Mwanga, H. Talwana, J. Murumu, and B. Odongo. 2007. The relationship between stem base and root damage by *Cylass* spp. on sweetpotato. African Crop Science Journal 8:955-957.

Mwanga, R., G. Yencho, and J.W. Moyer. 2002. Diallel analysis of sweetpotatoes for resistance to sweetpotato virus disease. Euphytica 128:237-248.

Mwanga, R.O. and O.B. Zamora. 1988. Response of sweetpotato (*Ipomoea batatas* (L.) lam) to varying levels of shade: I. Yield and yield components. Philippine Journal of Crop Science 13:133-139.

Mwanga, R.O. and O.B. Zamora. 1989. Agronomic responses of sweetpotato (*Ipomoea batatas* (L.) Lam) to varying levels of shade. Philippine Journal of Crop Science 14:83-90.

Mwanga, R.O.M., C.G.C. Yencho, R.W. Gibson, and J.W. Moyer. 2013. Methodology for inoculating sweetpotato virus disease: Discovery of tip dieback, and plant recovery and reversion in different clones. Plant Disease 97:30-36.

Nedunchezhiyan, M., G. Byju, and S.N. Dash. 2010. Effects of organic production of orange fleshed sweetpotato (*Ipomoea batatas* L.) on root yield, quality and soil biological health. International Research Journal of Plant Science 1:136-143.

Njeru, R.W., M.W.K. Mburu, E. Cheramgoi, R.W. Gibson, Z.M. Kiburi, E. Obudho, and D. Yobera. 2004. Studies on the physiological effects of viruses on sweetpotato yield in Kenya. Annals of Applied Biology 145:71-76.

Norman, P.E., A.A. Beah, J.A. Samba, M.J. Tucker, M.T. Benya, and S.N. Fomba. 2014. Agro-phenotypic characterization of sweetpotato (*Ipomoea batatas* L.) genotypes using factor and cluster analyses. Agricultural Science Research Journal 4:30-38.

Oggema, J.N., M.G. Kinyua, J.P. Ouma, and J.O. Owuoche. 2007. Agronomic performance of locally adapted sweetpotato (*Ipomoea batatas* (L) Lam) cultivatars derived from tissue culture regenerated plants. African Journal of Biotechnology 6:1418-1425.

Rauf, S., J.A. Teixera Da Silva, A.A. Khan, and A. Naveed. 2010. Consequences of plant breeding on genetic diversity. International Journal of Plant Breeding 4:1-21.

SAS. 2008. SAS software, version 9.2. SAS Institute Cary, NC, USA.

Sebastiani, S.K., A. Mgonja, F. Urio, and T. Ndondi 2007. Agronomic and economic benefits of sweetpotato *(Ipomoea batatas)* response to application of nitrogen and phosphorus fertilizer in the northern highlands of Tanzania. *The Eighth African Crop Science Society Conference. African Crop Science Society*, El-minia, Egypt, pp.1207-1210.

Sokal, R. and F. Rohlf. 1969. Kruskal-Wallis test. Biometry. San Francisco (CA): WH Freeman and Co: pp.388-389.

Solankey, S.S., P.K. Singh, and R.K. Singh. 2014. Genetic diversity and interrelationship of qualitative and quantitative traits in sweetpotato. International Journal of Vegetable Science DOI: 10.1080/19315260.2013.867295

Stathers, T.E., D. Rees, D. Jeffries, S. Kabi, N. Smith, L. Mbilinyi, H. Kiozya, S. Jeremiah, M. Nyango, and C. Moss. 1999. Investigating the potential of cultivar differences in susceptibility to sweetpotato weevil as a means of control, Crop Post-harvest Programme, DFID. UK.

Stathers, T.E., D. Rees, S. Kabi, L. Mbilinyi, N. Smith, H. Kiozya, S. Jeremiah, A. Nyango, and D. Jeffries. 2003. Sweetpotato infestation by *Cylas* spp. in East Africa: I. Cultivar differences in field infestation and the role of plant factors. International Journal of Pest Management 49:131-140.

Tairo, F., E. Mneney, and A. Kullaya. 2008. Morphological and agronomical characterization of sweetpotato [*Ipomoea batatas* (L.) Lam.] germplasm collection from Tanzania. African Journal of Plant Science 2:077-085.

Tairo, F., A. Kullaya, and J.P.T. Valkonen. 2004. Incidence of viruses infecting sweetpotato in Tanzania. Plant Disease 88:916-920.

Tsakama, M., A.M. Mwangwela, T.A. Manani, and N.M. Mahungu. 2010. Physiochemical and pasting properties of starch extracted from eleven sweetpotato varieties. African Journal of Food Science and Technology 1:90-98.

Tsegaye, E., N. Dechassa, and E.V.D. Sastry. 2007. Genetic variability for yield and other agronomic traits in sweetpotato. Journal Agronomy 6:94-99.

Tsegaye, E., E.V.D. Sastry, and N. Dechassa. 2006. Correlation and path analysis in sweetpotato and their implications for clonal selection. Journal fo Agronomy 5:391-395.

Tumwegamire, S., P. Labonte, D. Diaz, F. Kapinga, R. Mwanga, and R. Grüneberg. 2011. Genetic diversity in white-and orange-fleshed sweetpotato farmer varieties from East Africa evaluated by simple sequence repeat markers. Crop Science 51:1132-1142.

Ulukan, H. 2009. The evolution of cultivated plant species: Classical plant breeding versus genetic engineering. Plant System Evolution 280:133-142.

Veasey, E.A., J.R.D.Q. Silva, M.S. Rosa, A. Borges, E.D.A. Bressan, and N. Peroni. 2007. Phenology and morphological diversity of sweetpotato (*Ipomoea batatas*) landraces of the Vale do Ribeira. Scientia Agricola 64:416-427.

Villordon, A.Q. and D.R. Labonte. 1995. Variation in randomly amplified DNA markers and storage root yield in Jewel' sweetpotato clones. Journal of American Society of Horticultural Science 120:734-740.

Zawedde, B.M., C. Harris, A. Alajo, J. Hancock, and R. Grumet. 2014. Factors influencing diversity of farmers' varieties of sweetpotato in Uganda: Implications for conservation. Economy Botany 68:337-349.

Chapter four

4. Genetic diversity assessment of Tanzanian sweetpotato genotypes using simple sequence repeat markers

Abstract

Genetic diversity assessment of 48 Tanzanian sweetpotato genotypes was conducted using nine polymorphic simple sequence repeat markers to determine genetic relationship and select unique parents which could be used for future breeding. Genetic diversity parameters, cluster analysis, and analysis of molecular variance were calculated to determine genetic diversity and relationships. Results showed that the SSR markers used had the mean PIC of 0.78, allelic richness per locus ranged from 4-17 with a mean of 10.0 and the number of effective alleles varied from 2.2-6.1 with a mean value 3.5. The un-weighted pair group method with arithmetic mean allocated the germplasm collection into three major genetic clusters. The greatest genetic distance was identified between the genotypes sourced from Kagera, Temeke, Mkuranga and Kisarawe areas of Tanzania. The study identified genetically unrelated and complementary sweetpotato genotypes such as Ex-Ramadhani, Kibakuli, Mkombozi, Mjomba, Ex-Halima-3 and Kabuchenji which are recommended for future breeding programmes.

Keywords: Genetic diversity, genotyping, SSR markers, Sweetpotato, Tanzania

4.1. Introduction

Sweetpotato is an important root crop serving as food, feed and raw material globally. Its role as cash crop is significantly increasing due to crop's high yield potential and ability to grow in wide range of environments (Chiona, 2009; Wang et al., 2011). Most agricultural practices have greatly improved crops through selection and breeding (Messeguer, 2003). Targeted selection for specific traits such as high yields has narrowed genetic diversity among modern cultivars compared to farmers' varieties (Ulukan, 2009).

Genetic diversity analyses give better understanding on the extent of variation available between and within germplasm collections (Tumwegamire et al., 2011). Genetic diversity is a precondition for successful plant breeding (Ulukan, 2009). Several approaches have been used in crop genetic diversity analysis including morphological, agronomical, biochemical and DNA-based markers (Mohammadi and Prasanna, 2003). The choice of approach depends on objectives, required information and resources. Molecular markers have become important tools in genetic diversity analysis of sweetpotato for enhancing efficient sweetpotato breeding (Buteler et al., 2002; Hu et al., 2004; Wang et al., 2011; Zhao et al., 2013). Molecular techniques used in sweetpotato genetic diversity studies include randomly amplified polymorphic DNAs (Gichuki et al., 2005), amplified fragment length polymorphisms (Elameen et al., 2008) and simple sequence repeat (SSR) markers (Karuri et al., 2009). The SSR markers have been widely used in genetic diversity analysis of sweetpotato. Previous studies by Yada et al. (2010) and Rodriguez-Bonilla et al. (2014) showed that SSR markers revealed the highest level of polymorphism due to co-dominance nature and high numbers of alleles per locus. These markers are powerful and have the ability to discriminate genotypes including those related by pedigree.

In Tanzania, sweetpotato is an important food crop supporting millions of people. It is the second most important root crop after cassava. Sweetpotato yields in Tanzania ranges from 3-6 tha^{-1}, lower than yield potential of 15-27 tha^{-1} (Kapinga et al. 1995; Sebastian et al. 2007). Average area harvested for the last ten years was 500 000 hectares with mean yield of 3.83 tha^{-1} (FAOSTAT, 2015). Sweetpotato productivity could be enhanced through effective selection of locally adapted and farmers' preferred genotypes and targeted breeding. This requires genetic diversity analysis using effective molecular tools such as SSR markers.

There are limited sweetpotato genetic diversity studies conducted in Tanzania. Tairo et al. (2008) and Elameen et al. (2011) used agro-morphological parameters to study the diversity present within Tanzanian sweetpotato germplasm. Elameen et al. (2008) and Gwandu et al. (2012) used

amplified fragment length polymorphism and SSR markers, respectively to analyze the genetic diversity of sweetpotato germplasm. Gwandu et al. (2012) specifically analyzed the genetic diversity among elite sweetpotato genotypes for resistance to sweetpotato virus disease (SPVD) and dry matter content. The author reported relatively high level of genetic variation within the studied germplasm. However, most farmers grow landraces and have limited access to elite sweetpotato varieties. Systematic genetic grouping of sweetpotato genotypes well-adapted to diverse geographical locations may offer a unique genetic resource base. Use of polymorphic SSR markers could efficiently assist genetic grouping of sweetpotato germplasm and consequently reduce the timeline for developing sweetpotato cultivars in the country. Therefore, the objective of this study was to determine the genetic relationship within Tanzania sweetpotato germplasm and select unique parents for breeding using SSR markers.

4.2. Materials and methods

4.2.1. Plant materials, DNA extraction, SSR amplification and polymerase chain reaction

A total of 48 agronomically useful and morphologically distinct sweetpotato genotypes (Table 4.1) were selected from the 144 germplasm collected from lake and eastern zones of Tanzania. The selection of genotypes was based on agro-morphological attributes and their reaction to Sweetpotato virus disease (SPVD).

DNA samples of the sweetpotato genotype were collected on FTA cards. The sap was extracted from fresh tender leaves of five plants per genotype grown at Sugarcane Research Institute (SRI) – Kibaha in 2013/2014. Genotyping was conducted at Incotec laboratory, South Africa. All samples were used in bulked amplification, using DNA from five individual leaf samples. A single punch of each card per submission was taken and homogenized in the Finnzymes dilution buffer (Kit). Two micro liter of each bulked sample was used in the polymerase chain reaction (PCR).

The PCR products were fluorescently labeled and separated by capillary electrophoresis on an ABI 3013 automatic sequencer (Applied Biosystems, Johannesburg, South Africa); analysis was performed using GeneMapper 4.1. A total of nine polymorphic SSR markers were used for this study (Table 4.2). Markers were selected based on their polymorphic information content (PIC) values which ranged from 0.52 to 0.81 and their history from previous related studies (Table 4. 2).

Table 4.1. Description of sweetpotato genotypes used in the study

Sr. No.	Genotypes	Zone	District	DMC (%)	Yield (t/ha)	Root flesh colour	Reaction to SPVD
1	Ex-Kazimzumbwe-4	Eastern	Kisarawe	33.75	2.5	2	2
2	Ex-Halima-1	Eastern	Mkuranga	36.25	8.9	2	1
3	Ex-Miale-1	Eastern	Mkuranga	35.00	8.5	2	2
4	Ex-Kibuta-1	Eastern	Kisarawe	35.5	6.0	1	2
5	Ex-Maneromango-1	Eastern	Kisarawe	36.25	6	1	2
6	Ex-Kazimzumbwe-3	Eastern	Kisarawe	34.40	6.5	2	2
7	Shangazi	Eastern	Kilosa	37.50	4.0	4	4
8	Ex-Kibuta-2	Eastern	Kisarawe	35.00	5.0	2	1
9	Ex-Kazimzumbwe-2	Eastern	Kisarawe	33.75	4.0	3	2
10	Mwanatata	Lake	Kagera	37.50	4.5	3	2
11	Ex-Halima-2	Eastern	Mkuranga	36.25	7.0	1	1
12	Ex-Maneromango-2	Eastern	Kisarawe	36.25	5.5	1	2
13	Ex-Miale-2	Eastern	Kilombero	36.25	8.9	1	2
14	Gairo	Eastern	Kilombero	36.25	4.6	3	3
15	Mbutu	Eastern	Bagamoyo	35.00	3.5	1	3
16	Ex-Madina	Eastern	Kisarawe	31.25	7.6	3	1
17	Ex-Msimbu-2	Eastern	Kisarawe	36.90	2.5	1	2
18	Ex-Msimbu-4	Eastern	Kisarawe	33.75	4.0	4	1
19	Berene	Lake	Kagera	32.50	6.0	1	1
20	Ex-Ungindoni	Eastern	Temeke	35.60	4.0	2	1
21	Ex-Msimbu-3	Eastern	Kisarawe	34.40	5.0	3	2
22	Mkombozi	Lake	Kagera	32.50	9.0	4	3
23	Ex-Kibugumo	Eastern	Temeke	36.25	6.0	3	1
25	Kabuchenji	Lake	Kagera	38.75	7.0	2	1
26	Ex-Halima-3	Eastern	Mkuranga	33.75	6.5	1	1
27	Ex-Mengwa-3	Eastern	Kisarawe	41.25	3.0	1	2
28	Mjomba mkwe	Eastern	Kisarawe	32.50	4.0	4	1
29	Ex-Kiboda-2	Eastern	Temeke	36.25	1	2	2
30	Liponjwa	Eastern	Mkuranga	34.40	3	1	2
31	Ex-Sungwi	Eastern	Kisarawe	34.40	8.7	3	1
32	Kikabeji	Lake	Kagera	35.60	7.5	2	1
33	Sekondari	Lake	Kagera	32.50	3.0	2	1
34	Matako mapana	Eastern	Bagamoyo	37.50	6.5	1	2
35	Ex-Ramadhani	Eastern	Kisarawe	37.50	2.0	1	1
36	Mchikichini	Eastern	Temeke	32.50	6.0	3	2
37	Mkwakwa	Eastern	Kisarawe	38.75	5.5	2	2
38	Kigambile nyoko	Lake z	Kagera	38.75	3.0	4	2
39	Ex-Kiboda-4	Eastern	Temeke	36.25	3.0	3	2
40	Ex-Berene	Lake	Kagera	36.25	6.5	3	1
41	Ex-Msimbu-1	Eastern	Kisarawe	41.25	7.0	1	3
42	Ex-Kiboda-1	Eastern	Temeke	40.00	3.5	2	2
43	Kandoro	Eastern	Kisarawe	34.40	5.5	1	2
44	Ex-Yohana	Eastern	Kisarawe	34.40	6.0	1	1
45	Ex-Mwanza	Lake	Kagera	38.75	5.5	3	1
46	Ex-Bwana	Eastern	Kisarawe	38.75	6.5	3	1
47	Ex-Kazimzumbwe-1	Eastern	Kisarawe	36.25	4.5	2	3
48	Binti Jongo	Eastern	Mkuranga	33.75	6.5	2	1

Root flesh colour: 1 = White, 2 = cream, 3 = yellow and 4 = orange, SPVD: 1 = no visible symptoms, 2 = mild symptoms (a few local lesions on a few leaves), 3 = moderate symptoms (mosaic symptoms on leaves), 4 = severe symptoms (mosaic symptoms with plant stunting) and 5 = very severe symptoms of purpling/yellowing or mosaic on leaves, severe leaf distortion, reduced leaf size and severe stunting.

Table 4.2. Details of SSR markers used to genotype 48 sweetpotato genotypes collected from Tanzania

Name	Dye	Primer 5'-3'	Primer reverse 5'-3'
IB-R03	PET	GTAGAGTTGAAGAGCGAGCA	CCATAGACCCATTGATGAAG
1B-S07	FAM	GCTTGCTTGTGGTTCGAT	CAAGTGAAGTGATGGCGTTT
IB-R12	NED	GATCGAGGAGAAGCTCCACA	GCCGGCAAATTAAGTCCATC
IB-R16	VIC	GACTTCCTTGGTGTAGTTGC	AGGGTTAAGCGGGAGACT
1B-R19	PET	GGCTAGTGGAGAAGGTCAA	AGAAGTAGAACTCCGTCACC
IB-CIP13	NED	CGTGCTTGAGGTCTGAGTAGAA	TTCCCTAGAAGCTGCGTGAT
SSR 07	PET	TTTTCAACGACAAGCCTCTTGC	TCAAAGGTCCGCATGGAAATC
SSR 09		AAGTTAATCTAAGGTGGCGGGG	CGTCGATTCCAGTCTAATCCAATCC
690524	VIC	AAGGAAGGGCTAGTGGAGAAGGTC	CAAGGCAACAAATACACACACG

Sources: Karuri et al., 2009; Gwandu et al., 2012.

4.2.2. Data analysis

4.2.2.1. Genetic diversity analysis

Genotypic data were subjected to analyses with various measures of genetic diversity within and among genotypes using FSTAT version 2.9.3 and GenAlex software version 6.5 (Goudet, 2001; Peakall and Smouse, 2012). Genetic diversity parameters such as total number of alleles per locus, number of effective alleles per locus, Shannon's Information Index, gene diversity were determined using the protocol of Nei and Li (1979). Other genetic parameters such as differentiation, gene flow and polymorphic information content (PIC) were estimated using GenAlex software. Based on Euclidian distances, analysis of molecular variance (AMOVA) was conducted using GenAlex software to partition total genetic variations into, within and among districts and agro-ecologies of germplasm collection so as to quantify the diversity level and genetic relationship among genotypes.

4.2.2.2.   Cluster analysis

The SSR marker alleles were converted to binary data scored as either presence or absence of the band for all the 48 sweetpotato clones and treated as dominant marker. To evaluate the results of SSR markers, each amplified fragment was considered as one locus. The genetic dissimilarity matrix of the 48 sweetpotato clones was calculated using the Jaccard's coefficient (Jaccard, 1908).

Cluster analysis was done based on neighbor-joining algorithm using the un-weighted pair group method using arithmetic average (UPGMA) in DARwin 5.0 software (Perrier and Jacquemoud-Collet, 2006). A dendrogram was then generated on the dissimilarity matrix. To investigate the genetic relationships among accessions, genetic distances between all pairs of individual accessions were estimated to draw a dendrogram.

4.3. Results

4.3.1. Characteristics of the SSR markers

The polymorphic information content (PIC) values reflecting the genetic diversity of the nine SSR markers used ranged from 0.61 for the marker SSR07 to 0.88 for the IB-R16 with a mean of 0.78 (Table 4.3). All the primers considered in this study were highly polymorphic. The high mean PIC implies that the SSR markers used for analysis were very informative with high discriminating ability; hence the markers can suitably be used in genetic diversity and relationship analysis.

4.3.1.1.   Genetic diversity and relationship among sweetpotato genotypes

A summary statistics for various genetic diversity parameters are presented in Table 4.3. The total number of alleles amplified per locus ranged from 4 to 17 with a mean of 9.78. Eighty eight putative alleles were detected among the 48 genotypes studied. The lowest and highest number of alleles per locus were detected from the markers SSR07 (4) and IB-R12 (17), respectively. The effective number of alleles per locus ranged from 2.2-5.1 with mean value of 3.5. The markers SSR07 and IB-R16 had the lowest and highest number of effective alleles of 2.2 and 6.1, respectively. The high allelic richness indicates high level of genetic diversity among Tanzanian sweetpotato genotypes useful for further systematic breeding.

The Shannon's diversity value ranged from 0.78 to 1.69 with a mean of 1.22. The loci SSR07 and IB-R12 had the lowest and highest diversity values, respectively (Table 4.3). This suggests that the germplasm used in the present study was highly variable.

The gene diversity ranged from 0.51 to 0.84 with a mean of 0.69 (Table 4.3). Markers SSR07 and IB-R12 had the lowest and highest gene diversity, respectively among the nine markers.

The genetic differentiation ranged from 0.1 to 0.41 with a mean of 0.21 (Table 4.3). The markers IB-R12 and IB-CIP13 had the lowest and highest genetic diversity, respectively. Therefore, the germplasm demonstrated sufficiently large genetic differentiation.

Table 4.3. Summary of characteristics and genetic parameters of nine SSR markers used in assessing genetic diversity of 48 sweetpotato collections from Tanzania

Marker	Size range of alleles	Genetic parameters						
		N	Ne	I	He	F_{ST}	Nm	PIC
IB-R03	150-220	15	4.87	1.61	0.82	0.11	1.96	0.86
IB-S07	130-175	14	4.16	1.37	0.78	0.18	1.18	0.87
IB-R12	80-140	17	5.05	1.69	0.84	0.10	2.18	0.85
IB-R16	135-200	15	5.11	1.64	0.83	0.11	1.99	0.88
IB-R19	155-205	5	2.47	0.95	0.60	0.21	0.94	0.68
IB-CIP13	130-190	5	2.27	0.83	0.57	0.41	0.36	0.74
SSR07	90-115	4	2.16	0.78	0.51	0.29	0.61	0.61
SSR09	155-180	7	2.61	1.03	0.61	0.27	0.68	0.78
690524	158-190	6	2.88	1.08	0.64	0.22	0.89	0.75
Overall mean		10	3.51	1.22	0.69	0.21	1.20	0.78
SE		5.31	0.26	0.08	0.03	0.03	0.22	0.10

N = number of alleles, Ne = number of effective alleles, I = Shannon's information index, He = gene diversity, F_{ST} = genetic differentiation, Nm = gene flow, PIC = polymorphic information content, SE = standard error.

The gene flow for the studied germplasm collection ranged from 0.36 to 2.18 with an overall mean of 1.20 (Table 4.3). Short distances between agro-ecologies or limited introductions of new gene-pools could have greatly contributed to easier gene flow between locations.

4.3.1.2.   Analysis of molecular variance (AMOVA)

There was a highly significant difference (P ≤ 0.001) in molecular variance among genotypes within district and agro-ecologies of collection (Tables 4.4). Most of the genetic variability was due to differences among individuals within districts and agro-ecologies contributing to 87 and 84% of the variations, respectively. Only 9 and 4% was due to variations within genotypes within districts and agro-ecologies, respectively.

Table 4.4. Analysis of molecular variance for (AMOVA) of the SSR markers among and within the 48 sweetpotato genotypes studied

Source of variation	df	SS	MS	Estimated variation	Percentage variation	F-Statistics
Districts						
Among populations	4	49.13	12.28	0.32	9	0.001
Among individuals	43	282.55	6.57	3.21	87	0.001
Within individuals	48	7	0.15	0.15	4	0.001
Agro-ecologies						
Among populations	1	21.47	21.47	0.46	12	0.001
Among individuals	46	310.2	6.74	3.3	84	0.001
Within individuals	48	7	0.15	0.15	4	0.001

df = degrees of freedom; SS =sum of squares, MS = mean square

4.3.1.3.   Genetic distance and genetic identity

The average Nei's unbiased genetic distance (Nei, 1987) indicated among and within location of germplasm collections is presented in Table 4.5. The analysis showed the greatest distance for genotypes sampled between the areas of Kagera and Temeke (1.764) followed by Kagera and Mkuranga (1.562). The shortest genetic distance was between Kisarawe and Mkuranga (0.195). Similarly, genetic identity among genotypes and districts varied from 0.171 to 0.8 (Table 4.5). The highest genetic identity (0.823) was between Kisarawe and Mkuranga and lowest (0.171) was between Kagera and Temeke.

Table 4.5. Nei's unbiased genetic identity (top diagonal) and genetic distance (bottom diagonal) of 48 Tanzanian sweetpotato genotypes characterized using nine SSR makers

Locations	Zanzibar	Kagera	Kisarawe	Mkuranga	Temeke
			Genetic identity		
Zanzibar		0.504	0.800	0.586	0.472
Kagera	0.686		0.464	0.210	0.171
Kisarawe	0.223	0.768		0.823	0.649
Mkuranga	0.535	1.562	0.195		0.739
Temeke	0.751	1.764	0.432	0.303	
			Genetic distance		

4.3.2. Cluster analysis

The UPGMA cluster analysis based on genetic dissimilarity using the neighbor-joining method in DARwin 5.0 grouped the 48 genotypes into three major clusters (Figure 4.1). Clusters I and II each had 21 genotypes and III had 6 genotypes. Each cluster had sub-clusters. The SSR markers cluster analysis did not comply with the predefined genotype grouping based on their geographical origins. From cluster I, genotype Ex-Ramadhani originally collected from Kisarawe area was clearly identified. This genotype was characterized by cream fleshed storage roots with high dry matter content and resistant to SPVD. From cluster III genotype Kibakuli was selected. This genotype was collected from Zanzibar and displays orange fleshed roots with low dry matter content and susceptibility to SPVD. Further, genotype Mkombozi in cluster III was sourced from Kagera region in Lake Zone has orange flesh and relatively high root yields but low in dry matter content. Mkombozi could be integrated with genotype Mjomba mkwe collected from Kisarawe (cluster III) which displayed moderate yields and high dry matter content. The genotype Ex-Halima-3 collected from Mkuranga (cluster III) was cream fleshed, tolerant to SPVD, relatively high yielder but low in dry matter content but could be integrated to genotype Kabuchenji originated from Kagera area (cluster II) with yellow fleshed roots, moderately susceptible to SPVD, high yield and dry matter content.
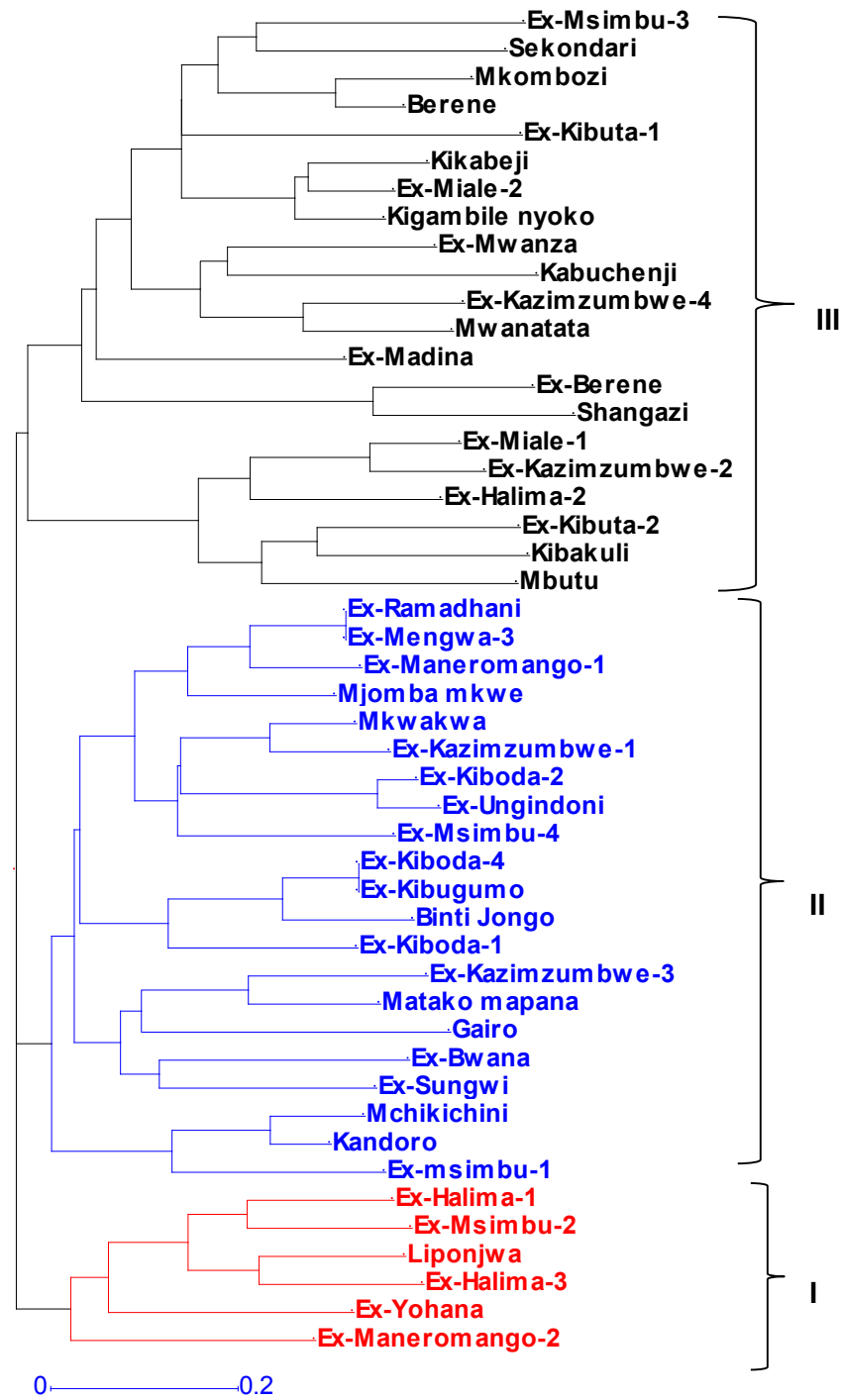
Figure 4.1. Dendrogram showing genetic relationship among 48 sweetpotato genotypes tested using nine SSR markers

4.4. Discussion

4.4.1. Characteristics of the SSR markers

All primers used in the present study were highly polymorphic. The high mean PIC implied that the SSR markers were very informative. According to Botstein et al. (1980) PIC guideline, all the nine SSR markers were highly informative; they had PIC greater than 0.5. The PIC values calculated in the present study was in agreement with that reported by Koussao et al. (2014) who studied the genetic diversity of Burkina Faso's sweetpotato germplasm using SSR markers and reported a mean PIC of 0.73. Similarly, Yada et al. (2010) and Gwandu et al. (2012) reported mean PIC values of 0.62 and 0.50 for Ugandan and Tanzanian sweetpotato germplasm, respectively. Vaeasey et al. (2008) reported a high mean PIC value of 0.96 using SSR markers for Brazilian sweetpotato genotypes. Also, Rodriguez-Bonilla et al. (2014) using 23 SSR markers to assess genetic diversity in Puerto Rico's sweetpotato germplasm reported a high mean PIC value of 0.79. The high levels of polymorphism reported could be due to large genome size, allopolyploid, outcrossing nature and heterozygosity of sweetpotato (Hwang et al., 2002). He et al. (1995) reported a high level of polymorphisms in sweetpotato which was fixed through vegetative reproduction and maintained through high level of gene flow due to self-incompatibility. Therefore, the SSR markers used in this study confirmed the existence of high genetic variability in sweetpotato germplasm.

4.4.1.1.   Genetic diversity and relationship among sweetpotato genotypes

The effective number of alleles per locus ranged from 2.2 - 5.1 with mean value of 3.5. This result is comparative to findings reported by Gwandu et al. (2012) who reported 11 - 22 alleles per locus when studying elite sweetpotato genotypes from Tanzania. Further, Rodriguez-Bonilla et al. (2014) reported number of alleles ranging from 4-25 per locus when charactering sweetpotato germplasm from Puerto Rico. The high number of alleles in sweetpotato could be due its hexaploidy (Karuri et al., 2010; Rodriguez-Bonilla et al., 2014). The high allelic richness indicates high level of genetic diversity among Tanzanian sweetpotato genotypes useful for further systematic breeding.

The Shannon's diversity value ranged from 0.78 to 1.69 with a mean of 1.22. The diversity values from this study are slightly lower compared to those reported by Arizio et al. (2009) with mean diversity value of 2.69 and slightly higher than those reported by da Silva et al. (2014) with a mean diversity index of 0.45, while studying the genetic diversity of Northern Brazil collection using

random amplified polymorphic DNA (RAPD). Therefore, the germplasm sampled in this study are genetically diverse. However, the result of this study is similar to the findings of Gwandu et al. (2012) who reported the genetic diversity from 0 to 0.98 with mean of 0.55. The high level of genetic diversity might have been contributed largely by cross pollination, hexaploidy and vegetative propagation of the crop (He et al., 1995; Hwang et al., 2002; Yada et al., 2010). Also, farmers are known to maintain a high level of genetic diversity of a species as well as several varieties for a particular species (Peroni and Hanazaki, 2002). As a result, the germplasm used in this study was highly variable.

The gene diversity ranged from 0.51 to 0.84 with a mean of 0.69. The mean gene diversity reported in this study was higher than 0.55 reported by Hwang et al. (2002). The high levels of genetic diversity could be justified by the outcrossing and self-incompatibility in sweetpotato. Also, vegetative propagation could have attributed to maintaining high levels of genetic diversity of this crop.

The genetic differentiation ranged from 0.1 to 0.41 with a mean of 0.21. According to standard guidelines for the interpretation of genetic differentiation (Wright, 1978), the range 0–0.005 indicates little, 0.05–0.15 moderate, 0.15–0.25 great, and above 0.25 very large genetic differentiations. Therefore, F_{ST} values in the present study ranged from moderate to very large genetic differentiation. These values indicate that there is likelihood of gene recombination or exchange between populations or genotypes. This could have been contributed by outcrossing nature of sweetpotato. Therefore, the germplasm demonstrated sufficiently large genetic differentiation.

The gene flow for the studied germplasm collection ranged from 0.36 to 2.18 with an overall mean of 1.20. Short distances between agro-ecologies or limited introductions of new gene-pools could have greatly contributed to easier gene flow between locations (Elameen et al., 2008). Further, gene flow between and across sweetpotato populations has not only been contributed by being an outcrossing species but also due to the presence of self-incompatibility and free exchange of planting materials (Martin, 1968; Hwang et al., 2002; Rodriguez-Bonilla et al., 2014). Pollination mechanisms play a primary role in determining the levels of gene flow in plants (Govindaraju, 1988). Arizio et al. (2009) reported that, while self- incompatibility and cross-pollination in sweetpotato encourage high gene flow between genotypes, vegetative propagation helps to maintain its genetic identity. Depending on the existing systems, gene flow can occur at remarkable distances and rates (Ellstrand, 2003). According to Slatkin (1989) and Morjan and Rieseberg (2004), gene flow <1 is considered to be low, while Nm=1 is considered to be

moderate. Moderate or relatively low levels of gene flow can significantly alleviate the loss of genetic diversity by preventing the effect of genetic drift (Aguilar et al., 2008). Hence, routine exchange of planting materials between farmers in different agro-ecologies and limited introductions of new gene pools may have contributed to gene flow among sweetpotato populations.

4.4.1.2. Analysis of molecular variance (AMOVA)

There was a highly significant difference (P ≤ 0.001) of molecular variance among genotypes within district and agro-ecologies of collection. Similar to this study, Gichuki et al. (2003) reported a significantly high contribution of among genotypes within regions variation to the total variation. According to Veasey et al. (2007) the higher variability reported could provide some insights to the evolutionary dynamics of sweetpotato. The AMOVA result suggests that a small collection within a given region will capture the genetic diversity existed in Tanzanian Sweetpotato.

4.4.1.3. Genetic distance and genetic identity

The present study found genetic distance estimates which is generally higher than previous reports. Gwandu et al. (2012) reported a genetic distance of 0.55 in elite sweetpotato genotypes from Tanzania. Similarly, a mean genetic distance of 0.57 was reported in Ugandan sweetpotato germplasm (Yada et al., 2010). Also, it is much higher than those reported by Gichuki et al. (2003) in which the highest genetic distance between South America and Africa was at 0.1809. The high genetic distances for the genotypes studied could be attributed to the uniqueness of east African sweetpotato germplasm which seems to be different from other regions (Gichuki et al., 2003). The authors suggested that, evolutionary and germplasm exchange processes could have attributed to the current sweetpotato diversity in the region. According to Nei (1972), genetic distance is linearly related to geographical distance. However, the genetic distance values for Tanzanian germplasm (1.562 and 1.764) requires further confirmation by using more primers.

4.4.2. Cluster analysis

The UPGMA cluster analysis based on genetic dissimilarity using the neighbor-joining method in DARwin 5.0 grouped the 48 genotypes into three major clusters. The genotypes were not necessarily grouped according to the origin of collection suggesting genetic differences of collections from the same region. Similar to this study, the lack of geographic associations with the source of collections among genotypes was also reported by Elameen et al. (2008), Yada et al. (2010b) and Gwandu et al. (2012) for germplasm from Tanzania and Kenya, respectively.

Gichuru et al. (2006) reported a lack of association between genotypes and their origin of collections in cluster analysis among East African sweetpotato landraces and suggested that it could be due to random genetic variation within the East Africa. The random genetic variation could be due to gene flow arising from short distances between agro-ecologies which has led to routine exchange of planting materials among and between farmers who have been growing sweetpotato for decades (Karuri et al., 2010; Gwandu et al., 2012). Contrary to the present study which classified the entries into three major genetic groups, Elameen et al. (2008) using AFLP markers reported two major clusters for 97 sweetpotato genotypes from Tanzania. Consistent to previous authors, using four SSR markers Gwandu et al. (2012) found two major clusters except nine genotypes not being grouped into any of the clusters in elite sweetpotato genotypes from Tanzania. Overall, this variation could be due to genotypic differences and number and types of markers used.

4.5. Conclusions

From the present study, it is concluded that the nine SSR markers were highly polymorphic and sufficiently distinguished the 48 sweetpotato genotypes investigated. The genotypes indicated existence of relatively high genetic variability which could be exploited for future crop improvement. The extremely high genetic distances for some of the populations between districts call for further investigation and confirmation. The study identified genetically unrelated and complementary sweetpotato genotypes such as Ex-Ramadhani, Kibakuli, Mkombozi, Mjomba mkwe, Ex-Halima-3 and Kabuchenji. These are valuable genetic resources and are recommended for breeding for high yield and other related traits and resistance to sweetpotato virus diseases in Tanzania or similar agro-ecologies. Finally, the information generated will contribute significantly to sweetpotato germplasm management and conservation in the country.

References

Aguilar R., M. Quesada, L. Ashworth, Y. Herrerias-Diego, and J. Lobo. 2008. Genetic consequences of habitat fragmentation in plant populations: susceptible signals in plant traits and methodological approaches. Molecular Ecology 17:5177-5188.

Arizio, C.M., N. Hompanera, E.Y. Suarez, and M.M. Manifesto. 2009. Genotypic identification and diversity evaluation of a sweetpotato (*Ipomoea batatas* (L). Lam) collection using microsatellites. Plant Genetic Resources Characterization and Utilization 7:135-138.

Botstein, D., R.L. White, M. Skolnick, and R.W. Davis. 1980. Construction of a genetic linkage map in man using restriction fragment length polymorphisms. American Journal Human Genetics 32:314-331.

Buteler, M.I., D.R. Labonte, R.L. Jarret, and R.E. Macchiavelli. 2002. Microsatellite-based paternity analysis in polyploid sweetpotato. Journal of American Society of Horticultural Science 127:392-396.

Chiona, M. 2009. Towards enhancement of β-carotene content of high drymass sweetpotato genotypes in Zambia. PhD Thesis, University of KwaZulu Natal, Pietermaritzburg.

Da Silva, A.V.C., L.N. Tabosa, M.U. Correcirc, and L.R. Pinheiro. 2014. Genetic diversity of sweetpotato collection from Northeastern Brazil. African Journal of Biotechnology 13:1109-1116.

Elameen, A., S. Fjellheim, A. Larsen, O. Rognli, L. Sundheim, S. Msolla, E. Masumba, K. Mtunda, and S. Klemsdal. 2008. Analysis of genetic diversity in a sweetpotato *(Ipomoea batatas* L.) germplasm collection from Tanzania as revealed by AFLP. Genetic Resources and Crop Evolution 55:397-408.

Elameen, A., A. Larsen, S. Klemsdal, S. Fjellheim, L. Sundheim, S. Msolla, E. Masumba, and O. Rognli. 2011. Phenotypic diversity of plant morphological and root descriptor traits within a sweetpotato germplasm collection from Tanzania. Genetic Resources and Crop Evolution 58:397-407.

Ellstrand, N.C. 2003. Current knowledge of gene flow in plants: implications for transgene flow. Philosophical Transactions of the Royal Society of London. Biological Science 358:1163-1170.

FAOSTAT. 2015. Food and Agricultural Organization, Agricultural data. Crops and products domain available at http.faostat.fao.org/ [Online]. Rome: FAO. [Accessed 18th January 2015].

Gichuki, S.T., M. Berenyi, D. Zhang, M. Hermann, J. Schmidt, J. Glössl, and K. Burg. 2003. Genetic diversity in sweetpotato *[Ipomoea batatas* (L.) Lam.] in relationship to geographic sources as assessed with RAPD markers. Genetic Resources and Crop Evolution 50:429-437.

Gichuki, S.T., D. La Bonte, K. Burg, R. Kapinga, and J.C. Simon. 2005. Assessment of genetic diversity, farmer participatory breeding, and sustainable conservation of Eastern African. sweetpotato germplasm (Grant No. 02-476). Annual Report April 2004-March 2005. Pp. 181.

Gichuru, V., V. Aritua, G.W. Lubega, R. Edema, E. Adipala, and P.R. Rubaihayo. 2006. A preliminary analysis of diversity among east African sweetpotato landraces using morphological and simple sequence repeats (SSR) markers . Acta Horticulturae 703:159-164.

Goudet, J. 2001. FSTAT, version 2.9. 3, A program to estimate and test gene diversities and fixation indices. Lausanne University, Lausanne, Switzerland.

Govindaraju, D.R. 1988. Relationship between dispersal ability and levels of gene flow in plants. Oikos 52:31-35.

Gwandu, C., F. Tairo, E. Mneney, and A. Kullaya. 2012. Characterization of Tanzanian elite sweetpotato genotypes for sweetpotato virus disease (SPVD) resistance and high dry matter content using simple sequence repeat (SSR) markers. African Journal of Biotechnology 11:9582-9590.

He, G., C. Prakash, and R. Jarret. 1995. Analysis of genetic diversity in a sweetpotato (*Ipomoea batatas*) germplasm collection using DNA amplification fingerprinting*. Genome* 38:938-945.

Hu, J., M. Nakatani, K. Mizuno, and T. Fujimura. 2004. Development and characterization of microsatellite markers in sweetpotato. Breeding Science 54:177-188.

Hwang, S.Y., Y.T. Tseng, and H.F. Lo. 2002. Application of simple sequence repeats in determining the genetic relationships of cultivars used in sweetpotato polycross breeding in Taiwan. Scientia Horticulturae 93:215-224.

Jacard, P. 1908. Nouvelles Recherches Sue la Distribution Florale. Bulletin de la Socíete Vaundoise de sciences Naturelles 44:223-270.

Kapinga, R.E., P.T. Ewell, S.C. Jeremiah, and R. Kileo. 1995. Sweetpotato in Tanzanian farming and food systems: Implications for research. Internation potato Center (CIP) Sub-Saharan Africa Regional Office, Nairobi and Ministry of Agriculture, Dar es Salaam, Tanzania, pp.57.

Karuri, H.W., E.M. Ateka, R. Amata, A.B. Nnyende, A.W.T. Muigai, E. Mwasame, and S.T. Gichuki. 2010. Evaluating diversity among Kenyan sweetpotato genotypes using morphological and SSR markers. International Journal of Agriculture and Biology 12:33-38.

Karuri, H.W., E.M. Ateka, R. Amata, A.B. Nyende, and A.W.T. Muigai. 2009. Characterization of Kenyan sweetpotato genotypes for SPVD resistance and high dry matter content using simple sequence repeat markers. African Journal of Biotechnology 8:2169-2175.

Koussao, S., V. Gracen, I. Asante, E.Y. Danquah, J.T. Ouedraogo, T.J. Baptiste, B. Jerome, and T.M. Vianney. 2014. Diversity analysis of sweetpotato (*Ipomoea batatas* [L.] Lam) germplasm from Burkina Faso using morphological and simple sequence repeats markers. African Journal of Biotechnology 13:729-742.

Martin, F.W. 1968. The system of self-incompatibility in Ipomoea. Journal of Heredity 59:263-267.

Messeguer, J. 2003. Gene flow assessment in transgenic plants. Plant Cell Tissue and Organ Culture 73:201-212.

Mohammadi, S. and B. Prasanna. 2003. Analysis of genetic diversity in crop plants-salient statistical tools and considerations. Crop Science 43:1235-1248.

Morjan, C.L. and L.H. Rieseberg. 2004. How species evolve collectively: implications of gene flow and selection for the spread of advantageous alleles. Molecular Ecology 13:1341-1356.

Nei, M. 1987. Molecular evelutionary genetics. Columbia University Press. New York.

Nei, M. and W.H. Li. 1979. Mathematical model for studying genetic variation in terms of restriction endonucleases. Proceedings of the National Academy of Sciences 76:5269-5273.

Nei, M. 1972. Genetic distance between populations. American Naturalist 106:283-292.

Peakall, R. and P.E. Smouse. 2012. GenAlEx 6.5: Genetic analysis in Excel. Population genetic software for teaching and research—an update. Bioinformatics 28:2537-2539.

Perrier, X. and J.P. Jacquemoud-Collet. 2006. DARwin software. Dissimilarity Analysis and Representation for Windows. Available from http://www.darwin.cirad.fr/darwin.html.

Peroni, N. and N. Hanazaki. 2002. Current and lost diversity of cultivated varieties, especially cassava, under swidden cultivation systems in the Brazilian Atlantic Forest. Agriculture, Ecosystems and Environment 92:171-183.

Rodriguez-Bonilla, L., H.E. Cuevas, M. Montero-Rojas, F. Bird-Pico, and D. Luciano-Rosario. 2014 Assessment of genetic diversity of sweetpotato in Puerto Rico. D0i:10.1371/journal.pone.0116184. 9:1-14.

Sebastiani, S.K., A. Mgonja, F. Urio, and T. Ndondi. 2007. Agronomic and economic benefits of sweetpotato *(Ipomoea batatas)* response to application of nitrogen and phosphorus fertilizer in the northern highlands of Tanzania. *The Eighth African Crop Science Society Conference. African Crop Science Society*, El-minia, Egypt, pp. 1207-1210.

Slatkin, M. 1989. Detecting small amounts of gene flow from phylogenies of alleles. Genetics 121:609-612.

Tairo, F., E. Mneney, and A. Kullaya. 2008. Morphological and agronomical characterization of sweetpotato [*Ipomoea batatas* (L.) Lam.] germplasm collection from Tanzania. African Journal of Plant Science 2:077-085.

Tumwegamire, S., R Kapinga, P.R. Rubaihayo, D.R. Labonte, W.J. Grüneberg, G. Burgos, T. Zum Felde, R. Carpio, E. Pawelzik, and R.O. Mwanga. 2011. Evaluation of dry matter, protein, starch, sucrose, β-carotene, iron, zinc, calcium, and magnesium in East Africansweetpotato [*Ipomoea batatas* (L.) Lam] germplasm. HortScience 46:348–357.

Ulukan, H. 2009. The evolution of cultivated plant species: Classical plant breeding versus genetic engineering. Plant System Evolution 280:133-142.

Vaeasey, E.A., A. Borges, M.S. Rosa, J.R. Queiroz-Silva, E.A. Bressan, and N. Peroni. 2008. Genetic diversity in Brazilian sweetpotato (*Ipomoea batatas* (L.) Lam., Solanales, Convolvulaceae) landraces assessed within microsatellite markers. Genetic and Molecular Biology 31:725-733.

Veasey, E.A., J.R. Silva, M.S. Rosa, A. Borges, E.D.A. Bressan, and N. Peroni. 2007. Phenology and morphological diversity of sweetpotato (*Ipomoea batatas*) landraces of the Vale do Ribeira. Scientia Agricola 64:416-427.

Wang, Z., J. Li, Z. Luo, L. Huang, X. Chen, B. Fang, Y. Li, J. Chen, and X. Zhang. 2011. Characterization and development of EST-derived SSR markers in cultivated sweetpotato (*Ipomoea batatas*). BMC Plant Biology 11:1-9.

Wright, S. 1978. Evolution and the genetics of populations: variability within and among natural populations. University of Chicago Press, Chicago.

Yada, B., P. Tukamuhabwa, B.L. Wanjala, D.J. Kim, R.A. Skilton, A. Alajo, and R.O.M. Mwanga. 2010. Characterization of Ugandan sweetpotato germplasm using fluorescent labeled simple sequence repeat markers. HortScience 45:225-230.

Zhao, N., X. Yu, Q. Jie, H. Li, H. Li, J. Hu, H. Zhai, S. He, and Q. Liu. 2013. A genetic linkage map based on AFLP and SSR markers and mapping of QTL for dry-matter content in sweetpotato. Molecular Breeding 32:807-820.

Chapter five

5. Combining ability of sweetpotato clones for storage root yield and related traits and resistance to sweetpotato virus disease

Abstract

This study was conducted to determine general combining ability (GCA) and specific combining ability (SCA) effects of selected sweetpotato clones for number of roots, root yield, DMC and resistance to SPVD for further selection and breeding. Eight clones selected for their yield, DMC or SPVD resistance were crossed in a half diallel mating design. The generated families were evaluated at Sugarcane Research Institute (SRI), Kilombero Agricultural Training and Research Institute (KATRIN) and Sokoine University of Agriculture (SUA) in Tanzania. Results showed significant (p<0.001) differences among families for all traits. The number of roots ranged from 2-7 with a mean of 3. Root yield ranged from 9.5-17.1 t/ha with a mean of 13.4 t/ha. DMC ranged from 31.3-39.4% with a mean of 36.2%. The reaction to SPVD ranged from 1-4 with a mean score of 3. The GCA effects of parents were significant (P≤0.001) for number of roots, yield, DMC and SPVD resistance. The SCA effects of crosses were significant (P≤0.05) for number of root per plant, root yield, DMC and SPVD resistance. GCA and SCA interacted significantly with sites indicating environmental influence on the gene action for traits studied. Parents Simama and Gairo had positive and significant GCA effects for number of roots per plant of 0.23 and 0.26, respectively. Parents 03-03 and Simama had significant GCA effects for root yield, while Ukerewe and Simama had significant GCA effect for DMC. Ex-Msimbu-1 and Gairo had significant (P≤0.01) GCA effect for SPVD resistance. Therefore, parents Gairo, 03-03, Ukerewe, Simama and Ex-Msimbu-1 could be used in recurrent selection for sweetpotato breeding for improved yield, DMC and SPVD resistance. Best combining families with positive and significant SCA effects were: Mataya x Gairo and Simama x Gairo for number of roots per plant, Mataya x Ex-Msimbu-1 and 03-03 x Ex-Msimbu-1 and Resisto x Gairo for root yield and, Resisto x SPKBH008, Mataya x Gairo, 03-03 x Ukerewe and SPKBH008 x Gairo for DMC, and Mataya x SPKBH008 and Mataya x Gairo had negative and significant SCA effect for resistance to SPVD. The selected parents and families were the best candidates to develop improved sweetpotato varieties with high root yields, DMC and SPVD resistance.

Keywords: combining ability, diallel analysis, gene action, sweetpotato

5.1. Introduction

Sweetpotato (*Ipomoea batatas* [L.] Lam., 2n =6x=90) is grown for food, feed and industrial raw material in many countries. Nonetheless, the current crop yields in sub-Saharan Africa (SSA) are low due to several factors including biotic, abiotic and socio-economic constraints. Both improved sweetpotato cultivars and landraces that are widely grown succumb to several viral diseases, including the most devastating, sweetpotato virus disease (SPVD) (Gibson et al., 1998). In Tanzania, SPVD is the major constraint to sweetpotato production causing significant yield losses. Continued use of pest and disease susceptible, low yielding and late maturing varieties, and lack of effective control measures for SPVD contributes to reduced yields and disease build up, development and persistence. Several approaches have been devised in combating development and spread of the SPVD including use of clean and disease free planting materials and breeding of resistant genotypes. Development of genotypes resistant to SPVD will improve food security and income to small-scale farmers.

Diallel mating designs have been widely used in genetic studies to investigate the inheritance of different important traits of various crops including sweetpotato (Griffing, 1956; Mwanga et al., 2002; Hallauer et al., 2010). The design entails crossing of a parent with other parents in all possible combinations (Hayman, 1954). The design is used to study polygenic systems that determine quantitative traits and provides information on predominant gene action (Viana et al., 1999; Ferreira et al., 2004). With diallel analysis, it is assumed that the genes in the parents are independently distributed (Sughroue and Hallauer, 1997). According to Johnson and King (1997), the design is useful in providing pedigreed breeding population for selection, progeny tests and to estimate genetic parametres. In a breeding programme, selection of parents showing good general combining ability (GCA) effects and their progenies with high specific combining ability (SCA) effects for desirable traits are essential (Bridgwater et al., 1992; Johnson and King, 1997; Buteler et al., 2002; Ferreira et al., 2004). It provides for realized and expected gains arising from both additive and non-additive genetic effects (Bridgwater et al., 1992).

Contrary to other crops, sweetpotato may be poorly suited for SCA-based improvement due to incompatibility barriers which limit successful hybridization of selected parents (Buteler et al., 2002). In the past, considerable research efforts were made in Uganda and Kenya towards breeding for resistance to sweetpotato virus diseases. In Tanzania, sweetpotato improvement has been limited to evaluation of local, improved or exotic genotypes. There is therefore a need to devise a well-designed sweetpotato breeding program in the country to improve yield and yield related traits and disease resistance. Clonal selection and information on GCA and SCA effects

for the desired traits among the sweetpotato genotypes is important to identify the best combiners for successful breeding. Therefore, the objective of the present study was to determine the GCA and SCA effects of selected sweetpotato clones for the number of storage roots, fresh storage root yield, dry matter content (DMC) and resistance to sweetpotato virus disease (SPVD) for further selection and breeding.

5.2. Materials and methods

5.2.1. Plant materials

Eight selected sweetpotato genotypes described in Table 5.1 were used to generate new genetic combinations. The parents were selected based on field evaluation aiming at flowering ability, yield potential, dry matter content of storage root or resistance to sweetpotato virus disease (SPVD) (Ngailo et al., 2015).

5.2.2. Diallel crosses and seedling plants

The eight sweetpotato parents (Table 5.1) were crossed using a half diallel mating design in 2013 at Sugarcane Research Institute (SRI) (S06$°$46'701" and E038$°$58'315"). Plants were established in well-prepared seedbeds. The crossing block was irrigated on a daily basis from mid-May to end of September. Vines were tended to grow on wooden trellises tied with a plastic rope. Weeding and other agronomic practices were carried out to optimize flowering, fertilization, seed setting and maturity. Flower buds that were near to open were tagged between 3:00-4:00 pm. The next day each flower was hand pollinated between 7:00 and 11:00 am. The pollinated flowers were labeled and tagged and the dried seed capsules from successful crosses were regularly harvested and kept in seed envelopes. A total of 28 new families [n(n-1)2] were generated (Griffing, 1956; Shattuck et al., 1993).

The botanical seeds collected from successful crosses (Figure 5.1A) were soaked in a concentrated sulphuric acid (98% H_2SO_4) for 20 minutes. The acid was discarded and seeds rinsed with running tape water for 10 minutes. The seeds were placed in petri dishes lined with moistened tissue paper and covered with cotton (Figure 5.1B). The petri dishes were kept at an ambient temperature. After two to three days, germinated seeds were transferred into 20 L capacity plastic pots to raise seedlings (Figure 5.1C).

Table 5.1. Names, origin and important traits of sweetpotato genotypes used in an 8x8 half diallel crosses

Name of parents	Origin	SPVD reaction	DMC (%)	Root flesh colour
Mataya	Tanzania	Susceptible	30.61	Orange
03-03	Tanzania	Resistant	37.45	Orange
Resisto	CIP – Nairobi	Susceptible	30.81	Deep orange
Ukerewe	Tanzania	Resistant	42.34	Cream
SPKBH008	Breeding clone	unknown	31.81	Deep orange
Simama	Tanzania (commercial)	Resistant	41.72	Cream
Ex-Msimbu-1	Tanzania (local)	Resistant	41.01	White
Gairo	Tanzania (commercial)	Moderately Resistant	38.85	White

DMC = Dry matter content; CIP=International Potato Center (Centro Internacional de la Papa)

When seedlings reached a plant height of 40-60 cm, they were transplanted to multiplication seedbeds from where the planting materials for evaluation trials were collected (Figure 5.1D). From each cross, 15-20 seedling plants were selected for clonal evaluation across three sites.

Figure 5.1: A= Botanical seeds, B = Germinating seeds in petri dish, C = Seedlings established in plastic pots, D=seedlings transplanted in seedbeds at SRI.

5.2.3. Field trial establishment and evaluation

Study sites and experimental design

Clonal stage I, 28 families and eight parents were evaluated across three sites. The study sites are hot spot areas for SPVD and experience high disease pressure during the growing season. The sites were Sugarcane Research Institute (SRI) - Kibaha (S06°46'701'', E038°58'315"), Kilombero Agricultural Training and Research Institute (KATRIN) – Ifakara (S08°03'693", E036°40'005") and Sokoine University of Agriculture (SUA) – Morogoro (S06°50'279", E037°38'636"). The trials were established in March, April and May, 2014 for SRI, KATRIN and SUA, respectively. The trials at SRI and KATRI were rainfed, while that at SUA was under drip irrigation. The families and eight parents were evaluated using a 6x6 lattice design with three replications. The experimental plot consisted of a single 6 m long row with inter- and intra-spacing of 1 m and 0.3 m, respectively. Spreader rows of the SPVD susceptible variety Kibakuli were planted between rows of test clones. All agronomic practices were done as per recommendation for the study sites.

5.2.4. Data collection

5.2.4.1.   SPVD assessment

The data for SPVD reactions wasrecorded at 2, 3 and 4 months after planting. The SPVD reactions were assessed using a scale of 1 to 5, where 1 = no visible symptoms, 2 = mild symptoms (a few local lesions on a few leaves), 3 = moderate symptoms (mosaic symptoms on leaves), 4 = severe symptoms (mosaic with plant stunting) and 5 = very severe symptoms of purpling/yellowing or mosaic on leaves, severe leaf distortion, reduced leaf size and severe stunting (Figure 5.2) (Mukasa et al., 2004; Njeru et al., 2004; Mwanga et al., 2013). Graft inoculation with *Ipomoea setosa* (an indicator plant) was done in an insect proof screen house particularly for those in the scale of 1-3 to further confirm if they were disease free.

Figure 5.2: Some of sweetpotato clones showing the SPVD symptoms, A, B and C for SRI, KATRIN and SUA, respectively.

5.2.4.2.   Yield and related traits

Other data collected were number of roots per plant and fresh root yield per plant (kg per plant and later converted to t/ha). The test clones were generally variable and only plants with marketable roots were described in terms of root form, root shape, skin and flesh colour. This was done using a sweetpotato descriptor (Huaman, 1999). Further, CIP guide on sweetpotato flesh colour was used to describe the flesh colour. The trials were harvested 120 days after planting.

Figure 5.3: Different storage root shapes, skin and flesh colour for some of the new sweetpotato clones. A = elliptic shape, B = ovate shape, C and D = orange and yellow flesh colour, respectively.

Samples to determine root dry matter content were collected from marketable roots on plant basis. The dry matter content was determined using the methods described by Carey and Reynoso (1999), Fonseca et al. (1999) and Tairo et al. (2008) with some modifications. A sample of 200 g was chopped from undamaged roots for each plant in each replication. The samples were air-dried and then oven dried at 70°C for 72 hours until constant weight. The dried samples were weighed using an electronic balance and the resulting figures were used to calculate dry matter content as percentage of the fresh weight. The families mean dry matter content was finally used for analysis.

5.2.5. Data analysis

5.2.5.1.   Analysis of variance

The data for root yield, number of storage roots and dry matter content of the three sites were subjected to the standard analysis of variance using the GLM procedure of the SAS 9.2 statistical programme (SAS, 2008). The data were analyzed separately. After homogeneity of variance tests, a combined analysis of variance was conducted.

5.2.5.2. Estimation of general and specific combining ability effects

Analysis of variance was performed using the DIALLEL-SAS05 program (Zhang et al., 2005) to identify the significant level of general combining ability (GCA) of parents and specific combining ability (SCA) of crosses. The diallel analysis was performed using Griffing's (1956) method II random model with the genetic statistical model of:

$$Yij = \mu + g_i + g_j + s_{ij} + \frac{1}{b}\sum_k b_k + \frac{1}{b}\sum_k (bv)_{ijk} + \frac{1}{bc}\sum_k \sum_l \varepsilon_{ijkl}, \; \begin{vmatrix} i, j = 1,..., p, \\ k = 1,..., b \\ l = 1,..., c \end{vmatrix}$$

μ is the population mean,

g_i, g_j is the general combining ability effect for the ith and j^{th} parents

s_{ij} is the specific combining ability effect of the cross between the ith and jth parents such that

$s_{ij} = s_{ji}$

e_{ijkl} is the experimental error effect unique to the $ijkl^{th}$ observation (Griffing, 1956)

The narrow sense heritability was calculated according to the formula proposed by van Buijtenen (1976) and Kang (1994);

$$h^2c = \frac{\sigma^2_{GCA}}{\sigma^2_{GCA} + \sigma^2_{SCA} + \sigma^2_e / r} \; ; \; \text{Where; h}^2\text{c= cross narrow sense heritability,}$$

σ^2_{GCA}, genetic variance for general combining ability,

σ^2_{SCA} genetic variance component for specific combining ability,

σ^2_e/r = error variance divided by the number of replications.

Heterosis estimates for number of roots per plant, root yield, dry matter content and resistance to SPVD for each cross was estimated using mid-parent (MP) and better-parent (BP) means or scores for the trait concerned according to the following equations:

$$MPH = 100 \times \left(\frac{F1 - MP}{MP} \right) \text{ and } BPH = 100 \times \left(\frac{F1 - BP}{BP} \right)$$

Where;

F1 = mean performance of F1, MP = mean of the two parents making the cross and BP = mean of the better parent for that particular cross (Falconer and Mackay, 1996).

5.3. Results

5.3.1. Analysis of variance

Analysis of variance showed highly significant ($p<0.001$) differences among F1 families for number of roots per plant, storage root yield, dry matter content, and response to SPVD across sites (Table 5.2). There were significant ($p<0.001$) effects of site, entry and site by entry interaction for all traits suggesting differential performances of families across sites.

Table 5.2. Analysis of variance of four traits of 28 F1 sweetpotato families and their parents evaluated across three sites in Tanzania

Source of variation	DF	Mean square			
		Nrpp	Yield (t/ha)	DMC (%)	SPVD
Site	2	15.89***	44.16***	194.42***	6.78***
Rep (site)	6	6.08***	6.92^{ns}	4.99^{ns}	0.36^{ns}
Block (site*rep)	45	1.40^{ns}	4.86*	4.14^{ns}	0.61^{ns}
Genotypes	35	2.99***	57.85***	34.46***	1.91***
Site*genotypes	70	2.87***	21.81***	9.91***	1.04**
Error	165	1.16	3.28	3.54	0.60
Total	323				

DF = degree of freedom, DMC (%) = dry matter content (%), Nrpp = number of roots per plant, *. **, *** = Significant at 0.05, 0.01 and 0.001, respectively, ^{ns} = non-significant at $P≤0.05$, SPVD = Sweetpotato virus disease.

Site effects had significant contribution to the total variability than family and family by sites effects explained by the highest sum of squares for dry matter content and root yield and number storage

root yield. Conversely, entry effect contributed largely to total variability to resistance for SPVD compared to other components.

5.3.2. Mean response of yield and related traits

The mean performance of each genotype per site is presented in Table 5.3. There was highly significant difference (p<0.001) in the number storage roots among families within and across sites (Table 5.2). The number of storage roots ranged from 2-10, 2-5 and 2-6 for SRI, KATRIN and SUA, respectively, with the overall mean of 3 (Table 5.3). Eight families had mean number of storage roots of 2 at SRI. The families Mataya x Gairo and Simama x Gairo had the highest number of 6 and 10 roots per plant, respectively. On the other hand, 54% of the families had 2 storage roots per plant and family Resisto x Gairo had the highest number of roots of 5 at KATRIN (Table 5.3). Further, cross 03-03 x Resisto had the highest mean number of storage roots of 6 at SUA. More than 50% of the crosses had mean root number of 3 at SUA. On the other hand, the number of roots for parents ranged from 2-3.

There were highly significant differences (p<0.001) in storage root yield among families and across sites (Table 5.2). Overall, storage root yield ranged from 9.3-17.2 t/ha with the mean of 12.9 t/ha (Table 5.3). The families performed differently across sites. At SRI, the mean yield was 12.7 t/ha and families of SPKBH008 x Simama and Resisto x Ex-Msimbu-1 had the lowest and highest storage root yield of 6.8 and 24.1 t/ha, respectively. At KATRIN, the mean yield was 13.6 t/ha. At this site, the families Ukerewe x SPKBH008 and Resisto x Simama had the lowest and highest yields of 8.8 and 19.2 t/ha, respectively. Similarly, families of Mataya x 03-03 and 03-03 x Ex-Msimbu-1 had the lowest and highest yield of 8.1 and 21.0 t/ha at SUA with a site mean of 12.4 t/ha. For the parents, Mataya and Simama had the lowest and highest yield of 8.2 and 21.8 t/ha, respectively.

There were highly significant differences (p<0.001) in storage root dry matter content among families and across sites (Table 5.2). Dry matter content ranged from 31.1-39.6% with a mean of 36% (Table 5.3). The crosses Ukerewe x Simama and 03-03 x Ukerewe had the highest dry matter content, while crosses 03-03 x Ex-Msimbu-1 had the lowest. Among the three sites, SRI and KATRIN had the lowest and highest average dry matter content of 34.8 and 37.4%, respectively. Crosses Ukerewe x Simama, SPKBH008 x Simama and 03-03 x Ukerewe had the highest dry matter content of 44.5, 38.9 and 40.2% for SRI, KATRIN and SUA, respectively. Conversely, cross 03-03 x Ex-Msimbu-1 had the lowest dry matter content of 32, 29.8 and 31.5%

at SRI, KATRIN and SUA, respectively (Table 3). The parents SPKBH008 and Ukerewe had the lowest and highest DMC of 32.1 and 40.7%, respectively.

There was highly significant difference (p<0.001) with regard to SPVD resistance among families and across sites (Table 5.2). The SPVD symptoms ranged from 1-4 with the overall mean score of 2 (Table 5.3). There were no definite relationships of F1s with respect to their parents with regard to reaction to SPVD, indicating variable sources of resistance to the disease among sweetpotato genotypes. Generally, most of the families showed relatively low scores to SPVD; however, families of Mataya x 03-03, Mataya x SPKBH008, SPKBH008 x Simama and Ex-Msimbu-1 x Gairo were the best genotypes with lowest SPVD scores. Conversely, Resisto and Mataya were the most susceptible parents with SPVD mean scores of 3 and 4, respectively.

Table 5.3. Mean number of roots per plant yield of storage root, dry matter content, and reaction to sweetpotato virus disease of sweetpotato families evaluated across three sites of eastern Tanzania.

Crosses	Number of roots per plant				Yield (t/ha)				DMC (%)				SPVD			
	SRI	KATRIN	SUA	Mean	SRI	KATRIN	SUA	Mean	SRI	KATRIN	SUA	Mean	SRI	KATRIN	SUA	Mean
Mataya x 03-03	2	2	3	2	11.6	13.0	8.1	10.9	38.2	35.6	36.3	36.7	1	1	2	1
Mataya x Resisto	3	2	3	2	9.0	15.3	10.6	11.7	33.8	36.5	31.8	34.0	2	3	2	2
Mataya x Ukerewe	2	3	3	3	12.0	14.8	9.0	11.9	38.7	37.5	37.3	37.8	2	2	1	2
Mataya x SPKBH008	4	2	3	3	9.1	10.0	8.9	9.3	38.5	36.1	37.1	37.2	2	1	1	1
Mataya x Simama	2	3	3	3	15.9	14.7	14.0	14.9	38.4	38.8	36.3	37.8	2	2	4	3
Mataya x Ex-Msimbu-1	2	3	3	3	17.8	13.5	16.6	16.0	40.9	35.1	36.8	37.6	2	2	2	2
Mataya x Gairo	6	3	3	4	8.9	14.9	10.7	11.5	38.6	35.6	34.0	36.1	3	2	1	2
03-03 x Resisto	3	2	6	3	14.6	12.6	19.9	15.7	35.1	33.8	31.3	33.4	2	2	3	2
03-03 x Ukerewe	3	2	3	3	12.4	14.4	10.8	12.5	39.0	35.3	40.2	38.2	2	2	2	2
03-03 x SPKBH008	5	2	4	3	11.3	14.6	10.6	12.2	37.2	34.2	36.6	36.0	2	3	2	2
03-03 x Simama	5	2	4	4	14.5	18.5	15.4	16.1	35.9	31.3	36.4	34.5	3	1	1	2
03-03 x Ex-Msimbu-1	2	2	3	3	19.9	10.6	21.0	17.2	32.0	29.8	31.5	31.1	1	2	1	2
03-03 x Gairo	4	2	3	3	11.5	16.1	16.7	14.7	35.4	35.0	36.8	35.7	2	4	3	3
Resisto x Ukerewe	2	3	3	3	10.6	14.6	12.4	12.5	36.3	34.1	37.9	36.1	3	2	2	2
Resisto x SPKBH008	3	3	3	3	10.7	15.1	13.1	13.0	36.9	37.7	36.5	37.1	2	3	1	2
Resisto x Simama	3	3	4	3	16.9	19.2	13.6	16.6	36.0	35.6	35.1	35.6	2	2	2	2
Resisto x Ex-Msimbu-1	3	2	3	3	24.1	10.5	11.4	15.3	37.8	35.4	32.8	35.3	1	2	2	2
Resisto x Gairo	3	5	4	4	21.1	14.5	11.0	15.5	40.1	32.8	35.1	36.0	2	2	2	2
Ukerewe x SPKBH008	3	2	5	3	14.1	8.8	14.8	12.6	33.4	32.7	32.6	32.9	3	2	2	2
Ukerewe x Simama	4	4	3	3	10.3	16.3	10.5	12.3	44.5	35.5	38.9	39.6	3	3	3	3
Ukerewe x Ex-Msimbu-1	3	2	4	3	7.8	13.7	8.9	10.1	36.3	33.4	38.6	36.1	2	4	1	2
Ukerewe x Gairo	4	3	3	3	12.1	14.5	9.0	11.9	40.3	35.4	38.4	38.0	2	2	2	2
SPKBH008 x Simama	3	2	3	3	6.8	12.6	9.7	9.7	39.2	38.9	35.1	37.7	1	2	1	1
SPKBH008 x Ex-Msimbu-1	2	3	3	3	13.9	16.1	10.7	13.6	38.9	35.6	36.4	37.0	1	3	1	2
SPKBH008 x Gairo	4	3	4	4	12.6	13.1	13.6	13.1	38.1	34.6	37.6	36.8	1	2	1	2
Simama x Ex-Msimbu-1	3	3	3	3	13.2	14.9	13.5	13.9	36.6	33.7	35.3	35.2	1	3	1	2
Simama x Gairo	10	2	5	6	12.7	16.9	17.6	15.8	38.8	32.6	35.9	35.8	1	3	1	2
Ex-Msimbu-1 x Gairo	2	2	4	3	12.1	11.0	15.4	12.8	42.9	31.1	38.4	37.4	1	2	1	1
Parents																
Mataya	3	3	2	2	7.7	10.8	5.9	8.2	36.0	30.7	32.5	33.1	5	2	4	4
O3-03	2	3	4	3	10.3	11.9	11.8	11.3	34.6	34.1	38.2	35.6	1	2	1	1
Resisto	2	2	4	3	5.9	10.0	10.9	8.9	32.0	32.9	32.2	32.4	3	2	3	3
Ukerewe	3	2	3	3	8.1	9.1	9.2	8.8	42.7	37.8	41.4	40.7	2	2	1	2
SPKBH008	2	3	2	2	10.2	8.7	10.6	9.9	32.1	34.4	29.8	32.1	2	1	1	1
Simama	2	3	3	3	22.7	24.1	18.7	21.8	39.5	35.1	39.6	38.1	1	2	1	1
Ex-Msimbu-1	3	3	2	3	9.8	9.1	10.6	9.8	38.8	36.1	38.0	37.6	1	1	1	1
Gairo	2	2	2	2	13.6	10.2	9.6	11.1	34.7	37.0	33.6	35.1	1	2	1	1
Mean	3.2	2.6	3.3	3.1	12.7	13.6	12.4	12.9	37.4	34.8	35.9	36.0	1.9	2.2	1.7	1.9
CV (%)	50.1	23.3	21.6	36.3	13.9	14.1	14.1	14.1	4.5	6.6	4.4	5.2	39	37.1	48.1	41.1
R² (%)	66.1	77.0	80.2	72.1	92.3	86.9	89.4	90.0	86.2	65.1	86.4	82.7	70.3	66.3	66.3	69.0
LSD(0.05)	5.34	2.03	2.38	0.35	5.85	6.36	6.76	0.58	5.58	7.57	5.26	0.61	2.4	2.64	2.63	0.25

CV = Coefficient of variation, DMC = dry matter content, LSD = Least significant difference, R^2 = Coefficient of determination,

129

5.3.3. Combining ability effects

There was significant (P≤0.001) general combining ability (GCA) and specific combining ability (SCA) effects for number of storage roots, root yield and dry matter content and resistance to sweetpotato virus disease (SPVD) (Table 5.4). Similarly, there were highly significant interaction (P≤0.001) of GCA x site and SCA x site for number of storage root, root yield and dry matter content and SPVD except SCA x site effect for SPVD was not significant (Table 5.4).

Table 5.4. Mean squares and significant tests of combining ability effects for number and yield of storage roots, dry matter content and resistance to Sweetpotato virus disease of sweetpotato clones evaluated at three sites in eastern Tanzania.

Source	DF	Mean squares			
		Nrpp	Yield	DMC	SPVD
GCA	7	2.26***	120.08***	47.66***	3.16***
GCA x Env	14	3.17***	28.83***	22.99***	1.41**
SCA	28	3.72***	56.07***	32.78***	1.37***
SCA x Env	56	2.56***	27.08***	8.33***	0.77[ns]
Error	210	0.61	3.62	3.664511	0.56

DF: degree of freedom, DMC = dry matter content, GCA = general combining ability, SCA = specific combining ability, Env = environment, *. ***, *** = significant at 0.05, 0.01 and 0.001, respectively, [ns] = Not significant at 0.05.

5.3.3.1. General combining ability effects

Parents Simama and Gairo showed significant GCA effects of 0.26 and 0.23 at P≤0.01 and P≤0.05, respectively for number of roots per plant, while the other parents had negative and non-significant GCA effects (Table 5.5).

Positive and highly significant (P≤0.001) GCA effects of 2.05 and 0.70 were recorded for storage root yields for parents Simama and 03-03, respectively which were in a desirable direction. Negative and highly significant (P≤0.001) GCA effects of 1.39 and 1.25 were detected for parents Ukerewe and SBKBH008, respectively (Table 5.5). The rest of the parents had non-significant GCA effects.

A positive and highly significant ($P \le 0.001$) GCA effect of 1.37 for dry matter content was recorded for parent Ukerewe (Table 5.5). Also, a significant ($P \le 0.05$) and positive GCA effect of 0.55 was reported for parent Simama for the same trait. Conversely, a highly significant ($P \le 0.001$) but negative GCA effect of 1.05 was estimated for parent Resisto for dry matter content. Likewise, parent 03-03 had a negative and significant ($P \le 0.05$) GCA effect of 0.78. The GCA estimates for parents Mataya, SPKBH008, Ex-Msimbu-1 and Gairo were non-significant.

In a desirable direction, a negative and significant ($P \le 0.01$) GCA effect of 0.24 and 0.21 for resistance to SPVD was reported for the parents Ex-Msimbu-1 and Gairo (Table 5.5). Conversely, a positive and highly significant ($P \le 0.01$) GCA effect of 0.27 was reported for parent Mataya. Similar, parent Ukerewe had a positive and significant ($P \le 0.01$) GCA effect of 0.27 for the same trait. The GCA effects for other parents were non-significant.

Table 5.5. Estimates of GCA effects for number of storage roots, yield, dry matter content and resistance to sweetpotato virus disease among eight sweetpotato parents.

Genotype	Nrpp	Yield	DMC	Resistance to SPVD
Mataya	-0.15^{ns}	-1.16ns	0.08^{ns}	0.27^{***}
03-03	-0.04^{ns}	0.70***	-0.78**	-0.10^{ns}
Resisto	-0.02^{ns}	0.59ns	-1.05***	0.05^{ns}
Ukerewe	-0.01^{ns}	-1.25***	1.37***	0.26**
SPKBH008	-0.11^{ns}	-1.39***	-0.41^{ns}	-0.09^{ns}
Simama	0.23^{*}	2.05***	0.55^{*}	0.06^{ns}
Ex-Msimbu-1	-0.18^{ns}	0.38^{ns}	-0.03^{ns}	-0.24**
Gairo	0.26**	-0.01^{ns}	0.23^{ns}	-0.21**

DMC = dry matter content, Nrpp = number of roots per plant, SPVD = Sweetpotato virus disease, *. **, *** = Significant at 0.05, 0.01 and 0.001, respectively, ^{ns} = not significant at 0.05.

5.3.3.2. Specific combining ability effects

The specific combining ability effects for number of storage root, root yield, dry matter content and resistance to SPVD are presented in Table5. 6. Crosses Mataya x Gairo and Simama x Gairo had highly significant ($P \le 0.001$) SCA effects of 2.03 and 1.88, respectively.

Table 5.6. Estimates of SCA effects for number of storage roots, yield, dry matter content and resistance to sweetpotato virus disease among 28 sweetpotato families.

Crosses	Nrpp	Yield (t/ha)	DMC (%)	SPVD
Mataya x 03-03	-0.38[ns]	-2.22**	1.45[ns]	-0.29[ns]
Mataya x Resisto	-0.28[ns]	-0.39[ns]	-1.25ns	-0.11[ns]
Mataya x Ukerewe	0.25[ns]	1.70[ns]	0.20[ns]	-0.43[ns]
Mataya x SPKBH008	0.25[ns]	-0.99ns	0.87[ns]	-0.63**
Mataya x Simama	-0.54[ns]	1.39[ns]	0.51[ns]	0.33[ns]
Mataya x Ex-Msimbu-1	0.31[ns]	4.11***	1.69*	-0.04[ns]
Mataya x Gairo	2.03[***]	2.78[ns]	3.20**	-1.29***
03-03 x Resisto	0.61[ns]	1.56[ns]	-0.69[ns]	-0.07[ns]
03-03 x Ukerewe	0.02[ns]	0.37[ns]	2.06**	-0.05[ns]
03-03 x SPKBH008	-0.27[ns]	-0.27[ns]	1.23[ns]	0.41[ns]
03-03 x Simama	0.25[ns]	-0.07[ns]	-0.68[ns]	0.15[ns]
03-03 x Ex-Msimbu-1	-0.57[ns]	3.44***	-4.09***	-0.11[ns]
03-03 x Gairo	-0.19[ns]	3.75**	-0.27[ns]	0.89*
Resisto x Ukerewe	-0.21[ns]	0.27[ns]	-0.11[ns]	-0.09[ns]
Resisto x SPKBH008	-0.02[ns]	0.74[ns]	2.61***	0.04[ns]
Reisto x Simama	0.12[ns]	1.07[ns]	-0.21[ns]	0.11[ns]
Resisto x Ex-Msimbu-1	-0.14[ns]	0.54[ns]	0.83[ns]	-0.04[ns]
Resisto x Gairo	1.16*	7.68***	2.40*	-0.29[ns]
Ukerewe x SPKBH008	0.32[ns]	2.22**	-4.30***	0.61**
Ukerewe x Simama	0.20[ns]	-1.20[ns]	1.34[ns]	0.34[ns]
Ukerewe x Ex-Msimbu-1	0.27[ns]	-1.97*	-1.64*	0.31[ns]
Ukerewe x Gairo	0.08[ns]	1.53[ns]	-1.35[ns]	0.81*
SPKBH008 x Simama	-0.46[ns]	-3.80***	0.96[ns]	-0.30[ns]
SPKBH008 x Ex-Msimbu-1	0.28[ns]	1.60[ns]	1.72*	0.11[ns]
SPKBH008 x Gairo	0.67[ns]	1.87[ns]	3.29**	0.29[ns]
Simama x Ex-Msimbu-1	0.16[ns]	-1.91*	-1.48*	-0.16[ns]
Simama x Gairo	1.88***	-3.82**	-1.58[ns]	0.21[ns]
Ex-Msimbu-1 x Gairo	-0.11[ns]	3.35*	-0.52[ns]	0.08[ns]

DMC = dry matter content, Nrpp = number of roots per plant, SPVD = Sweetpotato virus disease, *. **, ***, *** = Significant at 0.05, 0.01 and 0.001, respectively, [ns] = Not significant at 0.05

Cross Resisto x Gairo had significant (P≤0.05) SCA effects of 1.16 for number of roots per plant. The SCA effects for other parents were non-significant. A positive and highly significant (P≤0.001)

SCA effect of 2.61 for dry matter content was reported for cross Resisto x SPKBH008. Crosses SPKBH008 X Gairo, Mataya x Gairo and 03-03 x Ukerewe had positive and highly significant (P≤0.01) SCA effects of 3.29, 3.20 and 2.05, respectively. Also, a positive and significant (P≤0.05) SCA effects of 2.40, 1.72 and 1.69 were reported for crosses Resisto x Gairo, SPKBH008 x Ex-Msimbu-1 and Mataya x Ex-Msimbu-1, respectively.

Conversely, crosses 03-03 x Ex-Msimbu-1 and Ukerewe x SPKBH008 had negative and highly significant (P≤0.001) SCA effects of -4.03 and -4.30, respectively (Table 6). Also, Simama x Ex-Msimbu-1 and Ukerewe x Ex-Msimbu-1 had negative and significant (P≤0.05) of -1.48 and -1.64, respectively. The rest of the crosses did not produce statistically significant SCA effects for dry matter content.

The SCA effects for storage root yield for crosses Mataya x Ex-Msimbu-1 and 03-03 x Ex-Msimbu-1 and Resisto x Gairo were positive and highly significant (P≤0.001) (Table 5.6). Also, there were positive and highly significant (P≤0.01) SCA effects for crosses 03-03 x Gairo and Ukerewe x SPKBH008 (Table 6). Moreover, cross Ex-Msimbu-1 x Gairo had positive and significant (P≤0.05) SCA effect for storage root yield. Likewise, negative and significant SCA effects were reported for crosses SPKBH008 x Simama (P≤0.001), Simama x Gairo and Mataya x 03-03 (P≤0.01) and, Ukerewe x Ex-Msimbu-1 and Simama x Ex-Msimbu-1 (P≤0.05). The rest of the crosses were not significant.

The cross Mataya x Gairo had negative and highly significant (P≤0.001) SCA effect of -1.29 and Mataya x SPKBH008 had a negative and significant (P≤0.001) SCA effect of 0.63 for resistance to SPVD (Table 5.6). Conversely, cross Ukerewe x SPKBH008 had positive and significant (P≤0.01) SCA effect of 0.61 and, Ukerewe x Gairo and03-03 x Gairo, had positive and significant (P≤0.05) SCA effects of 0.89 and 0.81, respectively for resistance to SPVD (Table 5.6). The rest of the crosses had statistically non-significant SCA effects for resistance to SPVD.

5.3.3.3.   Heritability estimates

The narrow sense heritability estimates for number of storage root per plant, storage root yield, DMC and resistance to SPVD were 0.1, 0.22, 0.16 and 0.27, respectively. Conversely, the broad sense heritability estimates of these traits were 0.98, 0.99, 0.99 and 0.96, in that order.

5.3.3.4.   Heterosis

The percent heterosis for the 28 progenies are presented in Table 5.7. High and positive heterosis for number of roots per plant were recorded for the families of Mataya x Gairo and Simama x Gairo with %MPH and %BPH of 142.4 and 122 and 113.7 and 72.8, in that order. Only one progeny, 03-03 x Ex-Msimbu-1 had negative %MPH and two progenies (03-03 x Ex-msimbu-1 and Mataya x 03-03) had negative %BPH for number of roots per plant (Table 5.7). About 82 and 71% of the progenies had positive MPH and BPH, respectively for storage root yield. The family from the cross of Mataya x Ex-msimbu-1 had the highest %BPH, while the cross SPKBH008 x Ex-Msimbu-1 had the lowest for root yield. Progenies from the crosses of Resisto x SPKBH008 and Mataya x SPKBH008 had the highest MPH of 15.9 and 12.7%, respectively for dry matter content. The same progenies had the highest BPH of 15.7 and 11.3%, respectively for the same trait. Overall, 29 and 64% of the progenies had negative MPH and BPH, respectively for DMC. Most crosses showed lower mean scores for SPVD reaction displaying 32 and 4% mean negative MPH and BPH. Only one family from the cross of Mataya x Resisto had negative BPH. Likewise, the following crosses: SPKBH008 x Simama and Mataya x SPKBH008 had zero MPH and BPH. The progeny derivied from the cross Mataya x SPKBH008 had the highest MPH for resistance to SPVD.

Table 5.7. Estimates of percentage mid-parent (MPH) and better parent heterosis (BPH) for number of roots per plant, root yield, dry matter content and resistance to SPVD among 28 F1 families of sweetpotato.

Cross	Nrpp Mean	%MPH	%BPH	Yield Mean	%MPH	%BPH	DMC Mean	%MPH	%BPH	SPVD Mean	%MPH	%BPH
Mataya x 03-03	2.6	2.2	-14.8	10.5	10.7	-7.9	36.9	8.43	5.2	1.7	-28.6	50.0
Mataya x Resisto	2.7	20.0	9.1	12.1	50.6	42.2	33.9	4.04	2.9	2.0	-29.4	-5.3
Mataya x Ukerewe	3.2	38.1	20.8	12.4	48.27	35.5	37.7	2.50	-7.3	1.9	-26.1	21.4
Mataya x SPKBH008	3.1	47.4	40.0	9.6	11.0	-0.8	36.7	12.73	11.3	1.3	-45.5	0.0
Mataya Simama	2.7	14.3	0.0	15.4	6.2	-28.1	37.3	5.34	-1.4	2.4	-4.4	57.1
Mataya x Ex-Msimbu-1	3.1	33.3	16.67	16.4	94.9	77.2	37.9	7.01	0.0	1.8	-25.6	45.5
Mataya x Gairo	4.4	142.4	122.2	11.5	26.0	7.7	36.3	6.82	3.7	1.8	-23.8	60.0
03-03 x Resisto	3.7	34.7	22.2	16.0	60.9	40.6	33.6	-0.12	-4.2	1.7	3.5	50.0
03-03 x Ukerewe	3.1	9.8	3.7	13.0	26.6	14.1	38.7	2.29	-4.8	1.9	41.7	70.0
03-03 x SPKBH008	3.2	23.4	7.4	12.2	16.3	7.3	36.2	7.69	3.1	2.0	63.6	80.0
03-03 x Simama	3.7	29.4	22.2	15.9	-3.2	-25.8	35.2	-3.33	-6.8	1.8	37.7	65.3
03-03 x Ex-Msimbu-1	2.3	-17.7	-22.2	17.7	71.4	55.3	31.3	-14.30	-17.5	1.4	22.7	28.9
03-03 x Gairo	3.1	33.3	3.7	14.4	29.9	25.8	35.8	2.17	2.1	1.9	70.0	70.0
Resisto x Ukerewe	2.9	14.0	8.3	12.7	43.7	48.9	36.3	-0.44	-10.8	2.0	9.1	28.6
Resisto x SPKBH008	3.0	29.8	25.0	13.0	43.6	52.8	37.3	15.89	15.7	1.8	3.2	33.3
Resisto x Simama	3.4	36.0	29.2	16.8	12.3	-21.4	35.4	1.16	-6.3	2.0	9.1	28.6
Resisto x Ex-Msimbu-1	2.8	9.75	4.2	14.6	64.1	57.6	35.9	2.44	-5.3	1.6	-6.7	27.3
Resisto x Gairo	3.9	91.3	62.0	15.6	62.4	46.0	35.9	6.81	2.6	1.6	-3.5	40.0
Ukerewe x SPKBH008	3.3	35.4	23.5	12.7	35.1	31.7	32.7	-10.03	-19.6	2.6	76.9	91.7
Ukerewe x Simama	3.6	32.5	31.7	12.7	-16.8	-40.6	39.4	0.28	-3.3	2.4	57.1	57.1
Ukerewe x Ex-Msimbu-1	3.2	20.1	19.3	10.3	11.4	10.6	35.8	-8.81	-11.9	2.1	52.0	72.7
Ukerewe x Gairo	3.0	37.4	11.1	11.9	20.1	11.4	38.2	1.01	-6.1	1.9	41.7	70.0
SPKBH008 x Simama	2.8	14.2	4.2	10.0	-35.8	-53.5	37.2	6.50	-1.5	1.4	0.0	8.3
SPKBH008 x Ex-Msimbu-1	3.1	27.9	16.7	13.7	44.8	42.1	37.4	6.98	-1.2	1.6	21.7	27.3
SPKBH008 x Gairo	3.4	78.2	56.6	12.8	26.2	19.9	36.0	7.35	2.9	1.4	18.2	30.0
Simama x Ex-Msimbu-1	3.3	24.2	23.5	13.6	-11.1	-36.3	35.2	-6.97	-7.1	1.4	4.0	18.2
Simama x gairo	4.7	113.7	72.8	15.9	-1.2	-25.9	35.9	-1.42	-5.1	1.6	16.7	40.0
Ex-Msimbu-1 x Gairo	3.0	37.4	11.1	12.2	22.6	14.4	37.6	3.11	-0.9	1.3	14.3	20.0
Mataya	2.0			7.6			32.9			3.6		
03-03	3.0			11.4			35.1			1.1		
Resisto	2.4			8.5			32.2			2.1		
Ukerewe	2.7			9.1			40.7			1.6		
SPKBH008	2.2			9.6			32.1			1.3		
Simama	2.7			21.4			37.8			1.6		
Ex-Msimbu-1	2.7			9.3			37.9			1.2		
Gairo	1.7			10.7			35.0			1.1		

135

5.4. Discussion

5.4.1. Analysis of variance

There were significant differences in the performance of the families for number of storage roots per plant, yield of storage roots, dry matter content and reaction to SPVD implying variations among genotypes. Also, there were significant genotype by environment interaction for number of roots per plant, yield and DMC. Similarly, sites had significant effect on the performance of the traits evaluated. However, sites and site by family interactions were not significant for reaction of the families to SPVD. Similar to this study, Kanju (2000), Chiona (2009) and Tumwegamire et al. (2011) reported significant differences in the performance of number of storage roots, fresh root yield and dry matter content in newly developed sweetpotato clones in South Africa, Zambia and Uganda, in that order. Ngailo et al. (2015) reported similar findings for root yield and DMC. Furthermore, Manrique and Hermann (2000) and Mbwaga et al. (2007) reported significant differences in root yield and their interactions among genotypes. Similar findings were reported for sweetpotato storage roots in Peru and Uganda (Grüneberg et al., 2005; Osiru et al., 2009a). Nakitandwe et al. (2005) found that, sweetpotato genotypes grown in multi-location trials performed differently with regard to yield and disease resistance. The G x E interactions could have largely contributed to break down of resistance in improved varieties grown in agro-ecologies with high SPVD pressure (Gibson et al., 1998; Karyeija et al., 1998). Also, Yada et al. (2011) reported significant differences in response to SPVD for Ugandan sweetpotato germplasm evaluated in different sites. Caliskan et al. (2007) and Mwololo et al. (2009) suggested that, newly developed cultivars need to be evaluated across target agro-ecologies to ascertain their reaction to SPVD as different genotypes will respond differently. Similar to the present study, significant differences in yield and variety by season interaction were reported in Uganda (Bua et al., 2006; Osiru et al., 2009b). Manrique and Hermann (2000) reported significant effects of genotypes, environment and their interactions for storage root yield with genotypes contributing more to total variability compared to other effects. Significant genotypic effects were reported for root yield, dry matter content and their genotype x season interactions by Mcharo et al. (2001). While Yildirim et al. (2011) reported significant differences among genotypes for yield and number of storage roots in Turkey. Also, Mcharo and Ndolo (2013) reported significant differences in storage root yield and dry matter content and their interactions across locations in Kenya. Further, significant differences in root yield in different environments were reported by Laurie (2010). The same author reported highly significant effects due to genotypes, environments and their interactions in South Africa.

5.4.2. General and specific combining ability effects

The GCA and SCA effects were statistically significant for the total variability reported in the genotypic performance which implies that both additive and non-additive effects were important in the expression of the trait. While the GCA was highly significant for all traits, the SCA was highly significant for DMC, root yield and number of roots per plant and significant ($P \le 0.05$) for SPVD. However, the GCA variances for all traits except DMC were much larger than their respective SCA variances. The effects of their interaction with environment were statistically significant indicating that the magnitude of differences among the combining ability of the parents was significantly changed when evaluated across environments. Significant GCA x site and SCA x site for DMC, yield and number of roots per plant indicates that the expression of gene actions are significantly affected by environmental conditions.

The GCA effects of parents and SCA effects of crosses revealed significant differences among genotypes for number of storage roots, root yield, dry matter content and resistance to SPVD. The magnitudes of both GCA and SCA effects (Table 4) imply the roles of both additive and non-additive gene actions in controlling the expression of the traits evaluated. Also, the GCA and SCA interaction with the environment were highly significant for all traits except resistance to SPVD. According to Baker (1978), the closer the combining ratio is to unity, the larger the importance of additive genetic control, and hence, the greater the capacity to predict progeny performance based on GCA effects. Similar to this study, Musembi et al. (2015) and Mwije et al. (2014) reported significant GCA and SCA effects for storage root yields and dry matter content. Consistently, Musembi (2013) reported significant GCA and SCA effects for number of roots and fresh root yield. On the other hand, Chiona (2009) reported a highly significant GCA and SCA effects for root yield and dry matter content except SCA effect for DMC which was non-significant.

5.4.2.1.   Number of root per plant

The GCA and SCA effects for number of roots per plant were statistically significant for the total variability reported in the genotypic performance suggesting that both additive and non-additive effects were important in the expression of the trait. The ratio of GCA to SCA variance mean squares was 0.80, implying the predominance of additive gene action to non-additive in expression of the trait. Only two parents had significant GCA effects. All crosses had non-significant SCA except one cross which had a negative significant ($P \le 0.05$) SCA effect (Table 6). Similar to this study, Sseruwu (2012) reported both negative and positive non-significant GCA effects for number of roots in most of the parents used in breeding programme in Uganda. Also, Kanju (2000) reported non-significant SCA effects for number of roots in South Africa. On the other hand, Saad (1993) reported larger contribution of SCA effects in

controlling number of roots than GCA effects. Absence of SCA effects for the parents and crosses calls for further confirmation.

5.4.2.2. Storage root yield

The GCA variance component was larger than that for SCA for storage root yield indicating that the additive gene action played a major role than non-additive gene action in the inheritance of sweetpotato yield. Similar to this study, Chiona (2009) and Musembi et al. (2015) reported significant GCA to SCA effects in the expression of sweetpotato storage root yield. Similar findings were reported in Malaysia (Saad, 1993) where the GCA effects were larger than SCA effects for sweetpotato root yield. Also, significant contribution of both GCA and SCA effects on expression of root yield were reported by Mwije et al. (2014). According to Musembi et al. (2015) positive contribution of non-additive action to the expression of fresh storage root yield may not necessarily depend on parental GCA; therefore in breeding programmes, parents should not be disqualified based on negative GCA.

5.4.2.3. Dry matter content

The GCA and SCA mean squares for DMC were significant. Accordingly, gene action controlling this trait was predominantly additive and to some extent non-additive gene action contributed to the expression of the trait. Based on GCA values, the high DMC parent Ukerewe had highest, positive and significant GCA effect. Consistently, the low DMC parent Resisto had the lowest, negative and significant GCA effect. The genetic effects of the other parents were minimal with their GCA estimates showing non-significant effect. Genotype Ukerewe appears to be the best parent to be used in future breeding programme with high potential to transmit the desirable trait to other complementary parents. Some of the crosses had positive and significant SCA effects and others had negative and significant SCA effects implying good and bad combiners (Table 6). The findings from the present study corroborate those reported by Shumbusha et al. (2014) who reported that both GCA and SCA were highly significant for DMC in Uganda. The result concurs with that of Chiona (2009) and Musembi et al. (2015). On the contrary, Sseruwu (2012) reported non-significant GCA effects in either of the parents studied. Therefore, both additive and non-additive gene action play a vital role in the inheritance of DMC in sweetpotato.

5.4.2.4. Resistance to SPVD

Parents and crosses had significant GCA and SCA effects for resistance to SPVD, in that order. The ratio of GCA to SCA variance mean squares for resistance to SPVD was 0.76, implying that additive gene action was more important than non-additive in expression of the trait. The parent, Ex-Msimbu-1, had negative and highly significant GCA effects (Table 5).

Similar to this study, Mwanga et al. (2002) reported significant GCA and SCA effects for resistance to SPVD with GCA:SCA variance components ratios 0.51-0.87 indicating that additive gene effects were predominant in the inheritance of resistance to SPVD. Similarly, Mihovilovich et al. (2000) reported significant GCA effects and non-significant SCA effects for resistance to sweetpotato feathery mottle virus, one of the components of SPVD. On the contrary, Sseruwu (2012) reported non-significant parents' GCA effects for SPVD. According to Sseruwu (2012), negative GCA effect for a given parent indicates a contribution to an increased disease resistance in its progenies based on the rating scale used 1-5, where, 1 = resistant and 5 = susceptible (Mwanga et al., 2013). Equally, a positive GCA effect indicates undesirable contribution to an increased susceptibility to the disease in the progenies. Consequently, parent Ex-Msimbu-1 can be incorporated in future breeding programmes for developing new SPVD resistant varieties. However, the ratio of GCA/SCA effects of sweetpotato could not be solely used as a criterion to select the best recombining parents on improving targeted traits (Chiona, 2009).

5.4.2.5. Heritability estimates

Estimates of narrow-sense heritability ranged from 0.1 to 0.3 for the characters studied. Narrow sense heritability for number of roots per plant estimated at 0.1. Similar to this study, Teresa et al. (1994) reported the narrow sense heritability of 0.03-0.72 for number of roots per plant. Also, Ernest et al. (1994) reported heritability of 0.62 for the same trait. Conversely, Lestari et al. (2010) reported high broad-sense heritability of 0.87 for number of storage roots per plant. Despite that the narrow sense heritability estimate for this trait was within reported range but was relatively low.

Narrow sense heritability estimates for storage root yield were 0.22. Similar to the present study, Teresa et al. (1994) reported narrow sense heritability for root yield from 0.11-0.75. Similarly, Chiona (2009) reported narrow and broad sense heritability of 34.9 and 96.9%, respectively for the same trait. Mwije et al. (2014) reported high heritability for most of the traits including root yield. According to Chiona (2009), the broad sense heritability estimate was high.

Narrow and broad sense heritability for DMC was 0.16 and 0.99, respectively. Similar to this study, Shumbusha et al. (2014) reported broad sense heritability of 0.70-0.73 for dry matter content. Further, narrow and broad sense heritability of 76.3% and 89.6%, respectively were reported by Chiona (2009). Teresa et al. (1994), reported the heritability ranging from 0.26-0.49. The narrow sense heritability from this was unexpectedly low.

The narrow sense heritability estimate for resistance to SPVD was 0.27, while the broad sense heritability estimate was 0.96. Similar to this study, Mwanga et al. (2002) reported the narrow

sense heritability ranging 0.31-0.60 and broad sense heritability of 0.73-0.98 for resistance to SPVD. On the other hand, Yada (2014) reported the broad sense heritability of 0.51 for resistance to SPVD.

5.4.2.6.   Estimates of heterosis

The present study found variable degree of mid-parent and better-parent heterosis for number of roots per plant, root yield, dry matter content and resistance to SPVD. Similar to this findings, Chiona (2009) reported the presence of heterosis for dry matter and root yield of sweetpotato studied in Zambia. Lin et al. (2007) reported heterotic effect in F1 of sweetpotato families for root yield. Also, Iwanga et al. (1998) reported heterosis in hybrids generated from diverse genetic sources for root yields where the F1s yielded more than the female parents and local checks. Gruneberg et al. (2009) suggested that, exploitation of heterosis is an important strategy to achieve high genetic gain for yield, yield stability and adaptability. According to Singh (1993) cited in Sibiya (2009), heterosis is largely attributed to dominance gene action though epistasis and over-dominance gene actions are also important. The presence of heterosis in the studied traits indicates the role of non-additive gene action in the inheritance of these traits suggesting the possibility of improving these traits through hybridization.

5.5. Conclusions

There were significant differences in the performance among families and across sites. The GCA and SCA effects were statistically significant for the total variability reported in the genotypic performance which implies that both additive and non-additive effects were important in the expression of the trait. All parents except Gairo had non-significant GCA effects for number of roots per plant. Parents 03-03 and Simama had positive and highly significant GCA effects for storage root yield. While parent Ukerewe had positive and significant GCA effects for DMC, parents Ex-Msimbu-1 and Gairo had a negative and highly significant GCA effect for SPVD resistance. On the other hand, none of the crosses had significant SCA effects for number of roots. Two crosses: Mataya x Gairo and Simama x Gairo had positive and significant SCA for number of roots per plant. Crosses Mataya x Ex-Msimbu-1, 03-03 x Ex-Msimbu-1 and Resisto x Gairo had positive and highly significant SCA effect for storage root yield. Crosses Resisto x SPKBH008, Mataya x Gairo, 03-03 x Ukerewe and SPKBH008 x Gairo had positive and significant SCA effects for DMC. Negative and significant SCA effect for SPVD was estimated for crosses Mataya x SPKBH008 and Mataya x Gairo.

Since the number of roots is an integral component of sweetpotato root yield, parent Gairo could be recommended to be incorporated in future breeding programmes due to its positive

and significant GCA effect for the trait. Parents 03-03 and Simama are recommended for yield improvement due to positive and significant GCA effects to the expression of the trait. Genotype Ukerewe is recommended for future breeding programme for DMC due to its positive contribution to the expression of the trait as its GCA effect estimate was positive and significant. On the other hand, genotypes Ex-Msimbu-1 and Gairo are recommended for future breeding programmes for SPVD resistance. These clones had negative and highly significant GCA effects. Based on the SCA effects, Mataya x Ex-Msimbu-1, 03-03 x Ex-Msimbu-1 and Resisto x Gairo were the best combiners for storage root yield; Resisto x SPKBH008, Mataya x Gairo, 03-03 x Ukerewe and SPKBH008 x Gairo were best combiners for DMC and Mataya x SPKBH008 and Mataya x Gairo were best combiners for resistance to SPVD.

References

Bridgwater, F., L. Fins, S. Friedman, and J. Brotschol 1992. Mating designs. Handbook of quantitative forest genetics. Kluwer Academic Publishers, The Netherlands.

Bua, B., E. Adipala, and R. Gibson. 2006. Reaction of sweetpotato landraces to sweetpotato virus disease in Uganda. African Crop Science Journal 14:197-205.

Buteler, M.I., D.R. Labonte, R.L. Jarret, and R.E. Macchiavelli. 2002. Microsatellite-based paternity analysis in polyploid sweetpotato. Journal of the American Society for Horticultural Science 127:392-396.

Caliskan, M.E., E. Erturk, T. Sogut, E. Boydak, and H. Arioglu. 2007. Genotype x environment interaction and stability analysis of sweetpotato (*Ipomoea batatas*) genotypes. New Zealand Journal of Crop and Horticultural Science 35:87-99.

Carey, E.E. and D. Reynoso 1999. Procedure for evaluation of pathogen-tested sweetpotato clones. In*:* Huamán, Z. editor, Sweetpotato germplasm management. Training manual 3. Evaluation and breeding. International potato Centre (CIP), Lima

Chiona, M. 2009. Towards enhancement of β-carotene content of high drymass sweetpotato genotypes in Zambia. PhD Thesis, University of KwaZulu Natal, Pietermaritzburg.

Ernest, J., I.E. Wagih, and V. Kesavan. 1994. Genetic evaluation of polycross hybrids of sweetpotato. African Crop Science Journal 2:29-34.

Ferreira, F.M., J.I.R. Júnior, C.P. Pacheco, C.H.O. Silva, and M.F. Sebastião. 2004. Genetic components of combining ability in a complete diallel. Crop Breeding and Applied Biotechnology 4:338-343.

Falconer, D.S. and T.F.C. Mackay. 1996. Introduction to quantitative genetics. 4th edition. Prentice Hall, Harlow, UK.

Fonseca, C., J.P. Molina, and E.E. Carey. 1999. Farmers' participation in the selection of new sweetpotato varieties. In: Huamán, Z. editor, Sweetpotato germplasm management. Training manual 3.0. Evaluation and breeding. CIP, Lima.

Gibson, R.W., I. Mpembe, T. Alicai, E.E. Carey, R.O.M. Mwanga, S.E. Seal, and H.J. Vetten. 1998. Symptoms, aetiology and serological analysis of sweetpotato virus disease in Uganda. Plant Pathology 47:95-102.

Griffing, B. 1956. Concept of general and specific combining ability in relation to diallel crossing systems. Australian Journal of Biological Sciences 9:463-493.

Grüneberg, W.J., K. Manrique, D. Zhang, and M. Hermann. 2005. Genotype × environment interactions for a diverse set of sweetpotato clones evaluated across varying ecogeographic conditions in Peru. Crop Science 45:2160-2171.

Hallauer, A.R., M.J. Carena, and J.B.M. Filho 2010. Quantitative genetics in maize breeding, 6th. Springer Science + Business Media, LLC, New York, USA.

Hayman, B. 1954. The theory and analysis of diallel crosses. Genetics 39:789-809.

Huaman, Z. 1999. Botany, origin, evolution and biodiversity of the sweetpotato. Sweetpotato Germplasm Management Training Manual. International Potato Center, Lima Peru:1-11.

Johnson, G.R. and J.N. King. 1997. Analysis of half-diallel mating designs: I - A practical analysis procedure for ANOVA approximation. Silvae Genetica 47:74-78.

Kanju, E.E. 2000. Inheritance of agronomic and quality characteristics in sweetpotato (*Ipomoea batatas* (L.) lam). PhD Thesis. University of Orange Free State, Bloemfontein, South Africa.

Karyeija, R., R. Gibson, and J. Valkonen. 1998. The significance of sweetpotato feathery mottle virus in subsistence sweetpotato production in Africa. Plant Disease 82:4-15.

Laurie, S.M. 2010. Agronomic performance, consumer acceptability and nutrient content of new sweetpotato varieties in South Africa. PhD Thesis, Free State University, Bloemfontein, South Africa.

Lestari, S.M., I. Hapsari and Sutoyo. 2012. Improving storage root protein content in sweetpotato through open-mating pollination. Agrivita 34:225-232.

Lin, K., Y.C. Lai, K. Chang, Y. Chen, S.Y. Hwang, and H.F. Lo. 2007. Improving breeding efficiency for quality and yield of sweetpotato. Botanical Studies 48: 283-292.

Manrique, K. and M. Hermann. 2000. Effect of GxE interaction on root yield and beta carotene content of selected sweetpotato (*Ipomoea batatas* (L) Lam.) varieties and breeding clones. CIP program report:281-287.

Mbwaga, Z., M. Mataa, and M. Msabaha 2007. Quality and yield stability of orange fleshed sweetpotato *(Ipomoea batatas)* varieties grown in different agro-ecologies. The Eighth African Crop Science Society Conference. African Crop Science Soceity, El-minia, Egypt 339-345.

Mcharo, M. and P. Ndolo. 2013. Root-yield performance of pre-release sweetpotato genotypes in Kenya. Journal of Applied Biosciences 65:4914-4921.

Mcharo, M., E. Carey, and S. Gichuki. 2001. Performance of selected sweetpotato varieties in Kenya. African Crop Science Journal 9:49-57.

Mihovilovich, E., H.A. Mendoza, and L.F. Salazar. 2000. Combining ability for resistance to sweetpotato feathery mottle virus. HortScience 35:1319-1320.

Mukasa, S., P. Rubaihayo, and J. Valkonen. 2004. Viral synergism: a crinivirus enhances virulence of a potyvirus and an ipomovirus in sweetpotato plants. Ph. D. Thesis. Swedish University of Agricultural Sciences.

Musembi, B. (2013). Breeding sweetpotato *(Ipomoea batatas* [L.] Lam.) for drought tolerance in Kenya. PhD Thesis, University of KwaZulu-Natal, Pietermaritzburg.

Musembi, K., S. Githiri, G. Yencho, and J. Sibiya. 2015. Combining ability and heterosis for yield and drought tolerance traits under managed drought stress in sweetpotato. Euphytica 201:423-440.

Mwanga, R., G. Yencho, and J.W. Moyer. 2002. Diallel analysis of sweetpotatoes for resistance to sweetpotato virus disease. Euphytica 128:237-248.

Mwanga, R.O.M., C.G.C. Yencho, R.W. Gibson, and J.W. Moyer. 2013. Methodology for inoculating sweetpotato virus disease: Discovery of tip dieback, and plant recovery and reversion in different clones. Plant Disease 97:30-36.

Mwije, A., S. Mukasa, P. Gibson, and S. Kyamanywa. 2014. Heritability analysis of putative drought adaptation traits in sweetpotato. African Crop Science Journal 22:79-87.

Mwololo, J.K., P.W. Muturi, M.W.K. Mburu, R.W. Njeru, N. Kiarie, J.K. Munyua, E.M. Ateka, R.W. Muinga, R.E. Kapinga, and B. Lemaga. 2009. Additive main effects and multiplicative interaction analysis of genotype × environmental interaction among sweetpotato genotypes. Journal of Animal and Plant Sciences (JAPS) 2:148-155.

Nakitandwe, J., E. Adipala, R. El-Bedewy, W. Wagoire, and B. Lemaga. 2005. Adaptability of SIFT potato genotypes in different agro-ecologies of Uganda. African Crop Science Journal 13:107-116.

Ngailo, S.E., H. Shimelis, J. Sibiya, and K. Mtunda. 2015. Screening of Tanzanian sweetpotato germplasm for yield and related traits and resistance to sweetpotato virus disease. Acta Agriculturae Scandinavica, Section B — Soil & Plant Science DOI: 10.1080/09064710.2015.1063684.

Njeru, R.W., M.W.K. Mburu, E. Cheramgoi, R.W. Gibson, Z.M. Kiburi, E. Obudho, and D. Yobera. 2004. Studies on the physiological effects of viruses on sweetpotato yield in Kenya. Annals of Applied Biology 145:71-76.

Osiru, M.O., M.O. Olanya, E. Adipala, B. Lemaga, and R. Kapinga. 2009a. Stability of sweetpotato cultivars to *Alternaria* leaf and stem blight disease. Journal of Phytopathology 157:172-180.

Osiru, M.O., O.M. Olanya, E. Adipala, R. Kapinga, and B. Lemaga. 2009b. Yield stability analysis of *Ipomoea batatus* L. cultivars in diverse environments. Australian Journal of Crop Science 3:213-220.

Saad, M.S. 1993. Variability, divergence, heterosis, combining ability and yield component studies in sweetpotatoes (*Ipomoea batatas* (L) Lam.) from Sabah and Sarawak, Malaysia. PhD Thesis, Universiti Pertanian Malaysia.

SAS 2008. SAS software, version 9.2. SAS Institute Cary, NC, USA.

Shattuck, V.I., B. Christie, and C. Corso. 1993. Principles for Griffing's combining ability analysis. Genetica 90:73-77.

Shumbusha, D., G. Tusiime, R. Edema, P. Gibson, E. Adipala, and R.O.M. Mwanga. 2014. Inheritance of root dry matter content in swrrtpotato. African Crop Science Journal 22:69-78.

Sibiya, J. 2009. Breeding investigations for resistance to Phaeosphaeria leaf spot (PLS) and other important foliar diseases and a study of yield stability in African maize germplasm. PhD Thesis. University of KwaZulu-Natal, Pietermaritzburg.

Sseruwu, G. 2012. Breeding of sweetpotato (*Ipomoea batatas* (L.) Lam.) for storage root yield and resistance to Alternaria Leaf Petiole and Stem Blight (*Alternaria spp.*) in Uganda. PhD Thesis, University of KwaZulu-Natal, Pietermaritzburg.

Sughroue, J.R. and A.R. Hallauer. 1997. Analysis of the Diallel Mating Design for Maize Inbred Lines. Crop Sci. 37:400-405.

Tairo, F., E. Mneney, and A. Kullaya. 2008. Morphological and agronomical characterization of sweetpotato [*Ipomoea batatas* (L.) Lam.] germplasm collection from Tanzania. African Journal of Plant Science 2:077-085.

Teresa, M.L., G.S. Cruz, and E. Chujoy. 1994. Heritability estimates for some root characters in sweetpotatoes. Philippine Journal of Crop Science 19:27-32.

Tumwegamire, S., R. Kapinga, P.R. Rubaihayo, D.R. Labonte, W.J. Grüneberg, G. Burgos, T. Zum Felde, R. Carpio, E. Pawelzik, and R.O. Mwanga. 2011. Evaluation of dry matter, protein, starch, sucrose, β-carotene, iron, zinc, calcium, and magnesium in East African sweetpotato [*Ipomoea batatas* (L.) Lam] germplasm. HortScience 46:348-357.

Van Buijtenen, J.P. 1976. Mating designs. p. 11-27. *In* Proceedings of the IUFRO (International Union of Forestry Research Organizations) Joint Meeting onAdvanced Genetic Breeding. Bordeaux, France.

Viana, J.M.S., C.D. Cruz, and A.A. Cardoso. 1999. Theory and analysis of partial diallel crosses. Genetics and Molecular Biology 22:591-599.

Yada, B. (2014). Genetic analysis of agronomic traits and resistance to sweetpotato weevil and Sweetpotato virus disease in a bi-parental sweetpotato population. PhD. Thesis, North Carolina State University, USA.

Yada, B., P. Tukamuhabwa, A. Alajo, and R.O.M. Mwanga. 2011. Field evaluation of Ugandan sweetpotato germplasm for yield, dry matter and disease resistance. South African Journal of Plant and Soil 28:142-146.

Yildirim, Z., Ö. Tokuşoğlu, and G. Öztürk. 2011. Determination of Sweetpotato [*Ipomoea batatas* (L.) Lam.] genotypes suitable to the Aegean Region of Turkey. Turkish Journal of Field Crops 16:48-53.

Zhang, Y., M.S. Kang, and K.R. Lamkey. 2005. DIALLEL-SAS05: A comprehensive program for Griffing's and Gardener-Aberhart analyses. Agronomy Journal 97:1097-1106.

Chapter six

6. Genotype-by-environment interaction of yield and related traits and resistance to sweetpotato virus disease among selected sweetpotato clones

Abstract

A study was conducted to determine the magnitude of genotype-by-environment and stability for yield and yield related traits and sweetpotato virus disease (SPVD) resistance among newly developed sweetpotato clones in eastern Tanzania. Experiments were conducted across six diverse environments namely; Gairo, Kilombero Agricultural Training Research Institute (KATRIN), Sokoine University of Agriculture (SUA), Sugarcane Research Institute (SRI), Chambezi and Mkuranga. Twenty three newly bred clones and three commercially grown varieties were evaluated in a randomized complete block design with three replications. The Additive Main Effect and Multiplicative Interaction (AMMI) and genotype and genotype-by-environment interaction (GGE) biplot analyses were used to determine the GxE and stability of the genotypes. Environment, genotype and GxE interaction variances were highly significant (p ≤ 0.01) for all traits. The mean number of roots per plant ranged from 2.1-5.8 with an overall mean of 3.6. Mean root yield ranged from 7.5-17.2 t/ha for G24 and G5, respectively with a mean of 10.7 t/ha. Dry matter content (DMC) varied from 30.3-40.8% for G25 and G26, respectively with a mean of 36%. The severity of SPVD symptoms differed from 1.2-3.1 for G12 and G25, respectively with a mean of 1.6. AMMI analysis of variance revealed significant (p ≤ 0.001) differences among genotypes, environments and genotype x environment interaction (GEI) effects for all traits evaluated. The interaction principal component analysis axes (IPCAs) contributed significantly to the GEI. Both AMMI and GGE biplot identified the following genotypes: G5, G11, G23, G9, G7, G18 and G17 as high yielding and resistant to SPVD. These genotypes could be further evaluated in multi-environment yield trials (MEYTs) in eastern Tanzania. Furthermore, both models isolated the genotypes G22 and G3 as high yielding and resistant to SPVD but specifically suited to two environments; E5 and E1. Overall, the selected test environments were sufficiently capable of discriminating the candidate genotypes with respect to the traits studied. Further MEYTs are required for selection and recommendation of high yielding and stable sweetpotato varieties.

Keywords: Additive main effects and multiplicative interaction, Genotype x environment interactions. GGE biplot, Sweetpotato, Yield stability

6.1. Introduction

Expression of economic traits of crop varieties is determined by the genotype, environment and genotype x environment interaction. Often genotype and environment are not additive but they interact (Mwololo et al., 2009). Genotype-by-environment interaction (GEI) refers to the changes in the relative performance of genotypes across different growing environments (Acquaah, 2011; Xu, 2010). Baker (1988) defined GEI as the failure of genotypes to achieve the same relative performance in different environments. The GEI plays a key role in formulating strategies for crop improvement (Singh et al., 1999). According to Annicchiarico (2009), existence of GEI has significantly influenced the efficiency of crop improvement through plant breeding. In the event of a large GEI, the selection process and recommendations for a given genotype becomes slow and difficult (Caliskan et al., 2007; Mwololo et al., 2009). Ceccarelli (2012) reported that GEI is one of the major factors limiting the efficiency of plant breeding programmes. Consequently, multi-locational trials are necessary for proper separation and ranking of genotypes for reliable selection of high and stable yielding genotypes. Multi-locational trials are mandatory before the release of superior genotypes for target production environments (Ilker et al., 2009).

Sweetpotato is grown in diverse environments across the world (Haldavanekar et al., 2011; Caliskan et al., 2007). Several important traits are a composite reflection of multiple genetic and environmental factors in the crop (Vuylsteke and van Eeuwijk, 2008). Despite its adaptability to diverse and harsh growing conditions, the crop is very sensitive to environmental variations (Bryan et al., 2003). This influences expression of most of economically important traits which are largely quantitatively inherited (Ngeve, 1993; Lebot, 2010). Genotype-by-environment interactions are of great interest when evaluating the stability of breeding clones under different environmental conditions (Manrique and Hermann, 2000). Nakitandwe et al. (2005) found that sweetpotato genotypes grown in multi-location trials performed differently with regard to yield and disease resistance. Progress in sweetpotato breeding depends amongst others, the presence and extent of genotype-by-environment interaction on traits expression. Development of sweetpotato genotypes with high and stable yield and other agronomic traits of economic importance remains an important component in sweetpotato breeding programmes.

Owing to widespread cultivation and utilization of sweetpotato as a food security crop in many developing countries, knowledge of the cultivar's stability and reaction to disease is vital (Osiru et al., 2009). The same authors suggested that, knowledge of genotype performance in

different agro-ecologies is critical in cultivar development. Identification of superior cultivars for yield, disease resistance and other important traits may be confounded by GEI (Ngeve, 1993). Therefore, newly developed sweetpotato cultivars need to be evaluated across target agro-ecologies to ascertain their performances such as reaction to yield and yield components and pest and disease resistance notably to the sweetpotato virus disease (SPVD) (Caliskan et al., 2007; Mwololo et al., 2009). According to Laurie (2010), study of GEI is particularly important in countries with multiple agro-ecologies such as Tanzania. Therefore, knowledge of GEI is necessary to select genotypes either for wide or specific adaptation (Grüneberg et al., 2005).

Several statistical approaches are currently available for GEI analysis. The Additive Main Effect and Multiplicative Interaction (AMMI) (Gauch, 1992) and genotype and genotype-by-environment interaction (GGE) biplot (Yan and Tinker, 2006; Yan and Kang, 2003) analyses are the most commonly applied methods. The AMMI model combines the analysis of variance of genotype by environment main effects, principal component analysis and the interaction of the main effects, while GGE biplot analysis is an effective method based on principal component analysis (PCA) to fully explore MET data. It is an effective tool for: mega-environment analysis (e.g. "which-won-where" pattern), where by specific genotypes can be recommended to specific mega-environments (Yan and Kang, 2003; Yan and Tinker, 2006), genotype evaluation (the mean performance and stability) and environmental evaluation (the power to discriminate among genotypes in target environments) (Ding et al., 2008). The GGE biplot analysis is a useful tool for identifying locations that optimized the genotypes performance and for making better use of limited resources available for the testing programme. In an attempt to develop high yielding and SPVD resistant sweetpotato cultivars for eastern Tanzania regions, 23 promising clones were selected and the objective this study was to determine the magnitude of GxE and stability for yield and yield related traits and SPVD resistance among these newly developed sweetpotato clones in eastern Tanzania.

6.2. Materials and methods

6.2.1. Study sites and planting materials

The study was conducted at six environments namely; Gairo, Kilombero Agricultural Training Research Institute (KATRIN), Sokoine University of Agriculture (SUA), Sugarcane Research Institute (SRI), Chambezi and Mkuranga. The description of the study sites is summarized in

Table 6.1. The sites represent low to high altitude ranges with diverse agro-ecologies in Tanzania where sweetpotato is widely grown.

Twenty three clones were selected from families developed through a diallel cross. The F1 seedling plants were originally field evaluated along with other three commercially grown sweetpotato. The experimental clones were selected based on various attributes including orange, yellow or white flesh colour of roots, low to high root dry matter content (RDMC), high fresh root yields or resistance to sweetpotato disease (SPVD) or a combination of these traits (Table 6.2).

Table 6.1. Description of the experimental sites used for the study.

Location	Code	Coordinates		Altitude (masl)	Soil textural class	pH (H2O)	OC (%)	TN (%)	Av. P (meq/100g)	Exchangeable bases (meq/100g)			
										Ca	Mg	K	N
Gairo	E1	E036o54'787",	S06o08'156"	1310	Sandy clay loam	5.9	0.81	0.08	5.9	4.1	1.9	0.66	0.2
SRI	E2	E038o58'315",	S06o46'701"	169	Clay	6.7	0.71	0.07	3.9	6.2	2.1	0.48	0.26
KATRIN	E3	E036o39'945",	S08o03'612"	288	Sandy loam	6	1.15	0.06	6	9.9	2.1	0.53	0.25
SUA	E4	E037o38'756",	S06o50'252''	518	Clay	5.3	2.1	0.11	5.3	5.1	2.5	0.95	0.3
Chambezi	E5	E038o28'59",	S06o33'302"	47	Loamy sand	6.4	0.39	0.05	6.4	2.7	0.7	0.24	0.21
Mkuranga	E6	E039o11'689",	S06o08'306"	119	Sandy loam	6.4	0.37	0.06	6.4	2.0	0.4	0.24	0.17

masl = metres above sea level, meq 100g^{-1} = milli-equivalent per 100 g of soil. Av. P = Available phosphorus, OC = organic carbon, TN = total nitrogen, Ca = calcium, Mg = Magnesium, K = potassium, Na = Sodium; KATRIN = Kilombero Agricultural Training and Research Institute, SRI = Sugarcane Research Institute, SUA = Sokoine University of Agriculture.

Table 6.2. Description of sweetpotato genotypes used for the study.

Sr.No.	Cross/Name of genotypes	Genotype code	Flesh colour	DMC (%)	Root yield (t/ha)	Response to SPVD
1	Resisto x Ukerewe	G1	Yellow	35.7	14.6	Moderately resistant
2	Resisto x Ukerewe	G2	Orange	35.7	14.6	Moderately resistant
3	Ukerewe x Ex-Msimbu-1	G3	Cream	36.1	13.0	Resistant
4	03-03 x SPKBH008	G4	Cream	35.8	18.3	Resistant
5	Ukerewe x SPKBH008	G5	White	32.9	10.7	Resistant
6	Mataya x Gairo	G6	Yellow	36.1	12.3	Resistant
7	Simama x Ex-Msimbu-1	G7	Pale orange	36.1	12.3	Resistant
8	SPKBH008 x Ex-Msimbu-1	G8	Cream	37.0	16.7	Resistant
9	Mataya x Ukerewe	G9	Cream	37.8	16.3	Resistant
10	Resisto x Simama	G10	Pale orange	36.1	16.9	Resistant
11	Resisto x Simama	G11	Pale orange	36.1	16.9	Resistant
12	03-03 x SPKBH008	D12	Orange	36.0	16.7	Resistant
13	Mataya x Gairo	G13	Orange	36.1	17.0	Resistant
14	Resisto x Gairo	G14	Orange	35.7	14.7	Resistant
15	Ukerewe x Simama	G15	Cream	39.6	15.9	Resistant
16	Mataya x Ukerewe	G16	Yellow	37.8	13.7	Resistant
17	Mataya x Resisto	G17	Orange	34.0	15.3	Resistant
18	Resisto x Simama	G18	Cream	35.6	21.7	Resistant
19	Ukerewe x Simama	G19	Cream	39.6	17.5	Resistant
20	03-03 x Ukerewe	G20	Yellow	38.2	14.9	Moderately resistant
21	03-03 x Resisto	G21	Orange	33.4	15.4	Resistant
22	Ukerewe x Gairo	G22	Cream	37.0	16.0	Resistant
23	SPKBH008 x Ex-Msimbu-1	G23	Cream	37.0	16.0	Resistant
24	Simama	G24	Cream	38.1	21.4	Resistant
25	Mataya	G25	Orange	33.1	15.5	Susceptible
26	Ukerewe	G26		40.7	10.5	Resistant

Sr.N = serial number

6.2.2. Experimental design and field establishment

The experimental clones and check varieties were field evaluated using a randomized complete block design with three replications. Experimental plots consisted of two rows of six metre long for each genotype. The intra-row and inter-row spacing were 0.3 m and 1 m, respectively. Four to six node vine cuttings were planted on ridges. At Mkuranga, the trial was replanted following severe dry spell immediately after the first planting. Agronomic practices such as weeding and fertilization were done as per recommendation for sweetpotato production in Tanzania.

6.2.3. Data collection

Sweetpotato virus disease reactions were assessed visually at 60, 90 and 120 days after planting using a 1 to 5 scale; where 1 = no visible symptoms, 2 = mild symptoms (a few local lesions on a few leaves), 3 = moderate symptoms (mosaic symptoms on leaves), 4 = severe symptoms (mosaic symptoms with plants showing stunted growth) and 5 = very severe symptoms of purpling/yellowing or mosaic on leaves, severe leaf distortion, reduced leaf size and severe stunting (Mwanga et al., 2013). The genotypes Mataya and Ukerewe were used as susceptible and resistant checks, respectively. The field trials were harvested 120 days after planting. At harvesting, storage roots were grouped into marketable and un-marketable types, counted and their fresh weight (kg) per plot was recorded. The number of roots was expressed per plant basis. The root yield were collected on plot basis and later converted to tonnes per hectare (t/ha). From each plot, a sample of three to four medium to large storage roots was collected to determine root dry matter content. The dry matter content was determined using methods described by Carey and Reynoso (1999) and Tairo et al. (2008) with some modifications. Briefly, a sample of 250 g was chopped from undamaged roots for each entry in each replication. The samples were air-dried and then oven dried at 70°C until constant weight. The dried samples were weighed using an electronic balance and the resultant figures were used to calculate dry matter content as percentage of the fresh weight.

6.2.4. Data analysis

6.2.4.1. Analysis of variance

The data for number of storage roots, root yield, dry matter content and SPVD across the six sites were subjected to analysis of variance using Statistical Analysis System version 9.2 (SAS, 2008). A separate analysis was done for each site; however, due to homogeneity in

error variances, a combined analysis of variance for the six sites was conducted (Gomez and Gomez, 1984).

The presence of GxE interaction was detected using ANOVA and consequently stability analysis was conducted using AMMI and GGE biplot models.

6.2.4.2. GxE and stability analysis

The data on number of storage roots per plant, storage root yield, dry matter content and SPVD scores for the six environments were analysed using AMMI and GGE biplots in GenStat 17th edition (Payne et al., 2014) to determine the effects of genotypes, environments and their interaction.

The GxE and stability analysis were conducted using additive main effects and multiplicative interaction (AMMI) (Gauch, 1988; Gauch and Zobel, 1988), AMMI stability value (ASV) (Purchase, 1997) and genotype main effect and genotype x environment interaction (GGE) biplot (Kempton, 1984; Yan et al., 2000; Yan, 2001; Yan et al., 2001).

The AMMI statistical model is given below:

$$\overline{Y}_{ijk} = \mu + G_i + E_j + \sum_{k=1}^{m} \lambda_k \alpha_{ik} \gamma_{jk} + \rho_{ij}$$

Where: $\overline{Y}_{ijk}$ = the yield of the ith genotype in the jth environment, G_i = the mean of the ith genotype minus the grand mean, E_j = the mean of the jth environment minus the grand mean, λ_k = the square root of the eigen value of the kth IPCA axis, α_{ik} and γ_{jk} = the principal component scores for IPCA axis k of the ith genotypes and the jth environment, ρ_{ij} = the deviation from the model. According to Zobel et al. (1988), AMMI with only two interaction principal component axes could be the best predictive model. Hence, two IPCAs were adopted in this study in AMMI analysis.

Since AMMI model does not make provision for a quantitative stability, AMMI stability value (ASV) was calculated to quantify and rank genotypes (Rezene et al., 2014). This was carried out using a formula suggested by Purchase (1997);

AMMI Stability Value (ASV) = $\sqrt{\left[\left(\dfrac{SSIPCA1}{SSIPCA2}(IPCA1)\right)^2 + [IPCA2]^2\right]}$; where, $\dfrac{SSIPCA1}{SSIPCA2}$

represents the weighted value assigned to the first interaction principal component score due to its high contributions in the GXE model, SSIPCA1 and SSIPCA2 are the sum of squares for IPCA1 and IPCA2, respectively, IPCA1 and IPCA2 are the first and second IPCA scores for

each genotype. The larger the ASV value the more specifically adapted the genotype to a certain environment and the smaller ASV indicates a more stable genotype across environments (Purchase, 1997; Farshadfar et al., 2011; Thiyagu et al., 2012). The AMMI stability value was calculated using Microsoft excel 2013 programme.

The model for a GGE biplot (Yan, 2002; Yan et al., 2007) based on singular value decomposition (SVD) of *t* principal components is:

$$\bar{Y}_{ij} - \mu_i - \beta_j = \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

Where: $\bar{Y}_{ij}$ is the performance of genotype *i* in environment *j*, μ is the grand mean, β_j is the main effect of environment *j*, *k* is the number of principal components (PC); λ_k is singular value of the kth PC; and α_{ik} and γ_{jk} are the scores of ith genotype and j^{th} environment, respectively for PC$_k$; ε_{ij} is the residual associated with genotype *i* in environment *j*. AMMI and GGE biplot were performed with GenStat 17th edition (Payne et al., 2014).

6.3. Results

6.3.1. Analysis of variance

Results from analysis of variance of data from each environment for number of roots per plant, root yield, dry matter content and resistance to SPVD indicated significant (p ≤ 0.001) differences among genotypes for each environment. Similarly, combined analysis of variance showed highly significant (p ≤ 0.001) differences among the six test environments and the genotypes (Table 6.3). Significant (p ≤ 0.01) genotype x environment interactions were reported for all traits studied (Table 6.3). Replication within environment contributed significantly to variation in the performance of the traits studied except for dry matter content where replication was not significant (Table 6.3). The analysis of variance depicted the presence of significant genotype x environment interactions for the traits evaluated necessitating assessment of the magnitude of the interaction.

Table 6.3. Analysis of variance for number of roots, root yield, dry matter content and resistance to SPVD for sweetpotato clones evaluated across six environments in eastern Tanzania.

Sources of variation	DF	Nrpp	Yield (t/ha)	DMC (%)	SPVD
		Mean squares			
Environment	5	30.92***	2396.37***	430.26***	6.38***
Rep (Environment)	12	2.26*	28.69***	5.60^{ns}	1.35***
Genotypes	25	13.76***	83.79***	98.09***	2.78***
Genotypes x environment	125	2.86***	38.06***	10.79***	0.78***
Error	300	1.18	10.43	6.13	0.4
Total	467				
Mean		3.61	10.69	35.97	1.62
CV (%)		30.08	30.21	5.65	39.22
R^2 (%)		71.45	85.97	82.93	63.59
LSD		1.34	3.99	2.51	0.78
EMS		1.18	10.43	4.13	0.4

DF = Degrees of freedom, *, *** = significant at 0.05 and 0.001, respectively, ^{ns} = non-significant at 0.05, CV = coefficient of variation, DMC = dry matter content, EMS = error mean square, LSD = least significant difference, Nrpp = number of roots per plant, R^2 = coefficient of determination.

6.3.2. GxE and stability analysis using AMMI

Combined analysis of variance for the six test environments indicated highly significant (p ≤ 0.001) effects for genotypes, environment and their interactions for number of roots per plant, root yield, dry matter content and SPVD (Table 6.4). All the principal components were highly significant.

6.3.2.1.   Number of roots per plant

The AMMI analysis of variance for number of roots per plants in the tested environments showed highly significant (p ≤ 0.001) effects of the genotypes, environment and their interaction (Table 6.4). All IPCAs were highly significant (Table 6.4). IPCA1 and IPCA2 accounted for 47.7 and 20.1% of the GE interaction, respectively. The genotype G10 had high and positive IPCA1 score and G20 had lowest negative score (Table 6.5).

Table 6.4. AMMI analysis of variance for number of roots per plant, root yield, dry matter content and SPVD of 26 sweetpotato clones evaluated across six environments in eastern Tanzania.

Sources of variation	DF	Mean squares			
		Nrpp	Yield (t/ha)	DMC (%)	SPVD
Genotypes (G)	25	13.77***	83.9***	98.1***	2.78***
Environments (E)	5	30.38***	2396.2***	430.3***	5.39***
Block	12	2.34ns	28.7***	5.6ns	1.53***
Interactions (GxE)	125	2.71***	38.0***	10.8***	0.78***
IPCA 1	29	5.57***	107.5***	19.5***	1.40***
IPCA 2	27	2.52***	28.8**	13.0***	1.08***
Residuals	69	1.58	12.4	6.3**	0.41ns
Error	300	1.17	10.4	4.1	0.40

DF = Degrees of freedom, *, **, *** = significant at 0.05, 0.01, and 0.001, respectively, ns = non-significant, DMC = dry matter content, GxE = genotype by environment interaction, IPCA1 and 2 = first and second interaction principal component analysis axes, Nrpp = number of roots per plant.

The means for number of roots per plant of the 26 genotypes (G1-G26) across the six environments (E1-E6) are presented in Table 6.5. Genotype G20 ranked the best across environments with a mean number of roots per plant of 5.8, and performed better than other genotypes in four out of six environments namely, E2, E3, E4 and E6 with mean root number of 7.4, 7, 8.8 and 6.3, respectively. E2 (the site at the Sugar Research Institute) was the best environment with the highest mean number of roots per plant of 4.5 and E1 (the site at Gairo) had the lowest mean number of roots per plant of 2.7.

AMMI stability value (ASV) ranged from 0.14-4.25 for genotypes G5 and G20, respectively (Table 6.5). The smaller the ASV the stable the genotypes and vice versa is true; hence, G5, G15 and G13 were relatively stable and G20 was the least stable genotype.

AMMI biplot for number of roots per plant is presented in Figure 6.1a. In the biplot, the genotypes with IPCA1 scores close to zero were G5, G15, G6 and G13 were most stable in the test environments. Conversely, G20 and G10 were the most responsive genotypes to environment changes. In addition, genotypes with negative first IPCA scores such as G20 were allocated in environments with negative IPCA scores too and the opposite is true for G10 (Figure 6.1; Table 6.5).

Table 6.5. AMMI means for number of roots per plant, IPCA scores and ASV values of 26 sweetpotato clones evaluated across six environments in eastern Tanzania.

Genotype	E1	E2	E3	E4	E5	E6	Mean	IPCA1	IPCA2	ASV
G1	3.6	4.5	3.6	4.1	5.4	4.0	4.2	0.60	0.03	1.4
G2	3.4	5.9	4.8	5.6	3.4	4.2	4.6	-0.51	-0.05	1.2
G3	3.4	5.5	4.9	5.7	3.1	4.5	4.5	-0.60	0.23	1.4
G4	3.2	4.2	4.5	5.1	3.1	4.7	4.1	-0.34	0.70	1.1
G5	2.9	4.8	3.6	4.3	3.9	3.4	3.8	0.04	-0.11	0.1
G6	2.4	4.1	3.0	3.7	3.5	3.0	3.3	0.10	-0.01	0.2
G7	2.1	4.4	2.7	3.4	3.2	2.3	3.0	0.02	-0.34	0.3
G8	2.1	2.5	2.7	3.1	3.1	3.3	2.8	0.29	0.58	0.9
G9	2.7	7.2	4.0	5.1	2.9	2.5	4.1	-0.71	-1.01	2.0
G10	2.6	2.4	2.4	2.7	4.7	3.3	3.0	0.88	0.45	2.1
G11	2.9	5.7	3.4	4.2	4.2	2.8	3.9	0.07	-0.62	0.6
G12	2.6	3.8	3.0	3.6	4.0	3.2	3.4	0.32	0.10	0.8
G13	1.1	2.4	2.0	2.6	1.7	2.1	2.0	-0.05	0.32	0.3
G14	2.4	3.1	3.4	3.9	2.8	3.7	3.2	-0.03	0.63	0.6
G15	2.2	4.0	3.0	3.7	2.9	2.9	3.1	-0.08	0.04	0.2
G16	2.5	4.0	3.1	3.7	3.5	3.1	3.3	0.12	0.04	0.3
G17	1.5	2.7	2.5	3.1	2.0	2.6	2.4	-0.09	0.41	0.5
G18	2.9	6.0	3.6	4.4	4.0	2.8	4.0	-0.11	-0.66	0.7
G19	3.3	4.2	3.9	4.4	4.4	4.3	4.1	0.22	0.35	0.6
G20	4.1	7.7	7.1	8.2	1.7	5.8	5.8	-1.79	0.27	4.3
G21	2.2	3.6	2.1	2.7	4.4	2.3	2.9	0.64	-0.25	1.5
G22	4.3	7.3	5.2	6.0	5.0	4.4	5.3	-0.26	-0.50	0.8
G23	2.3	3.9	2.3	2.8	4.3	2.3	3.0	0.57	-0.30	1.4
G24	2.0	4.3	2.2	2.8	3.7	1.8	2.8	0.32	-0.56	1.0
G25	3.3	4.3	3.2	3.7	5.4	3.5	3.9	0.69	-0.08	1.6
G26	1.8	3.3	3.0	3.6	2.0	2.9	2.8	-0.27	0.33	0.7
Mean	2.7	4.5	3.4	4.1	3.6	3.3	3.6			
IPCA1	0.44	-0.85	-0.76	-1.04	2.18	0.04				
IPCA2	0.14	-1.63	0.43	0.21	-0.44	1.29				

ASV = AMMI stability value, E1, E2, E3, E4, E5 and E6 = Gairo, SRI, KATRIN, SUA, Chambezi and Mkuranga, respectively, IPCA1 and IPCA2 = first and second interaction principal component analysis axes, See codes of genotypes in Table 6.2.
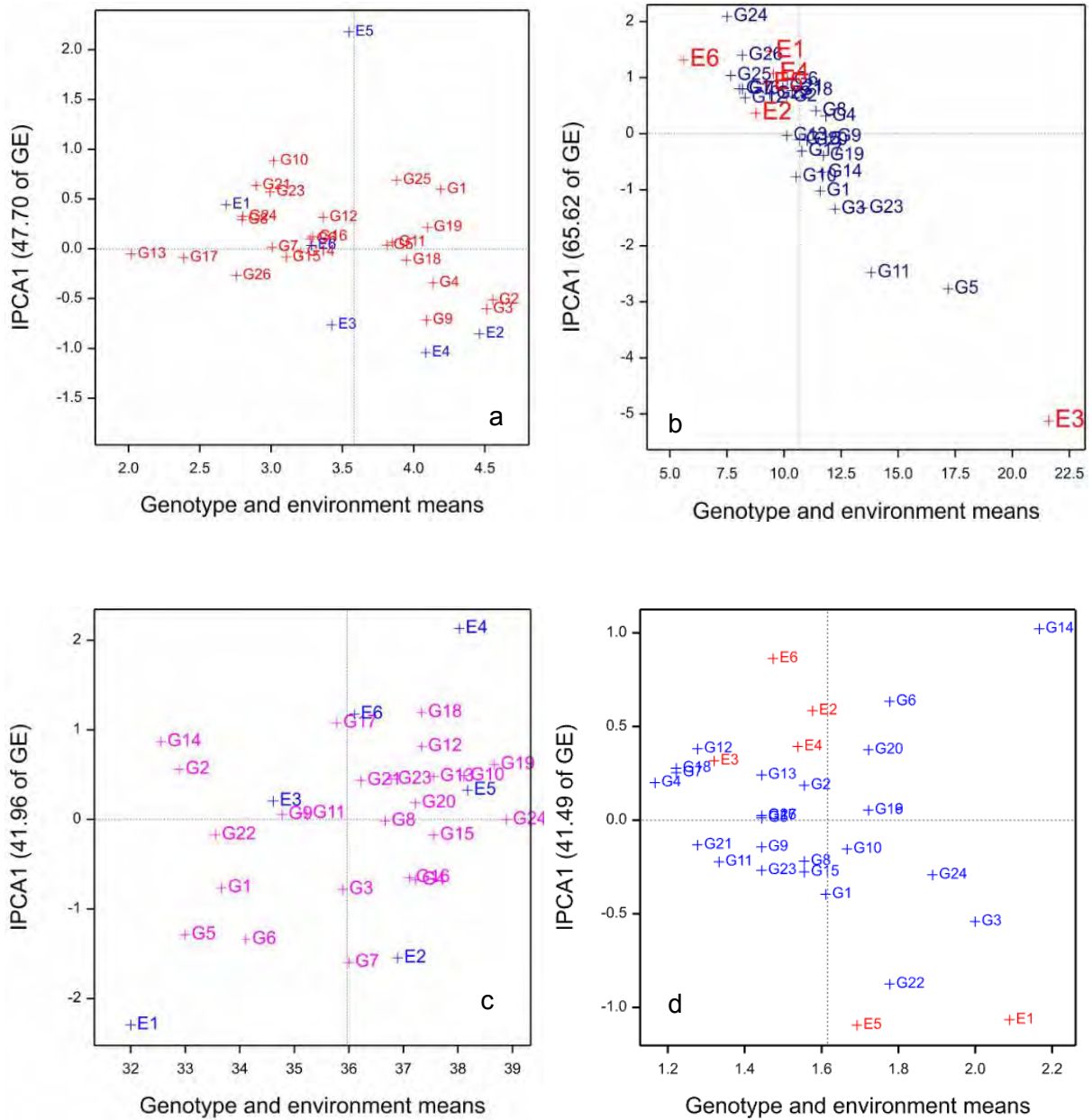
Figure 6.1 AMMI biplot a, b, c and d showing the distribution of 26 sweetpotato clones evaluated across six environments in eastern Tanzania for number of roots per plant, storage root yield, dry matter content and SPVD, respectively. See codes of environments and genotypes in Tables 6.1 and 6.2, respectively.

6.3.2.2.　　Storage root yield

AMMI analysis of variance for storage root yield is presented in Table 6.4 The genotypes, environments and GxE interaction effects were highly significant (p ≤ 0.001) and contributed to 81.9% of the total sum of squares. About 64% of the total sum of squares were attributed

by the environmental effect compared to 11 and 25% accounted by genotypes and their interaction, respectively. Large environment sum of squares relative to other sources of variation suggests that the environments were relatively diverse. The magnitude of the interaction sum of squares was 2.3 times larger than that of the genotypes, indicating that there were substantial differences in genotypic yield response across environments.

The means for storage root yield are presented in Table 6.6. Mean root yield across the six environments ranged from 7.5-17.2 t/ha for G24 and G5, respectively with a mean of 10.6 t/ha. More than 46% of the genotypes yielded above the mean with G5, G11 and G23 being the highest yielder of 17.2, 13.8 and 13.5 t/ha, respectively across the six environment. The test environments Mkuranga (E6) and KATRIN (E3) had the lowest and highest mean yields of 5.6 and 21.6t/ha, respectively. None of the released and commercially grown cultivars performed better than the new clones in all locations.

AMMI analysis of variance showed statistically significant effect of the IPCA1 and IPCA2 ($p \leq$ 0.01), respectively (Table 6.4). The two IPCAs captured 82% of the GE interaction, IPCA1 accounted 65.6% of the interaction. The genotypes G24 and G5 had the highest and lowest IPCA1 scores, respectively (Table 6.6). The ASV values corresponded well with the IPCA scores. ASV values ranged from 0.30-11.16 for G24 and G5, respectively (Table 6.6). Consequently, G9 was the most stable genotype across the test environments (Table 6.6; Figure 6.2).

AMMI biplot of IPCA1 scores against the genotype and environment means is presented in Figure 6.1b. In the biplot, 42% of the tested genotypes yielded above the mean yield. G5 and G11 were the highest yielding genotypes by 61 and 29% above the overall mean. Conversely, G5, G11 and G23 were specifically adapted to E3, while G19 and G2; G6 and G21; and, G12 and G7 were specifically adapted to E1, E4 and E2, respectively. Among the test environments, E3 and E6 were considered as the high and low yielding environments, respectively (Figure 6.2). Likewise, E2, E6 and E3 were regarded as stable environments and E1 and E5 as least stable environments in discriminating genotypes regarding yield (Figure 6.2). The mean yield under environment E3 was 102% above the overall mean.

Table 6.6. AMMI means for fresh root yield (t/ha), IPCA scores and ASV values for 26 sweetpotato clones evaluated across six environments in eastern Tanzania.

Genotype	E1	E2	E3	E4	E5	E6	Mean	IPCA1	IPCA2	ASV
G1	9.6	9.4	27.8	9.0	8.6	5.2	11.6	-1.02	0.29	4.11
G2	14.8	8.8	18.0	7.6	5.4	6.0	10.1	0.66	1.68	3.14
G3	10.7	10.0	30.2	8.9	8.2	5.4	12.2	-1.34	0.59	5.42
G4	8.9	9.9	21.0	11.9	12.3	7.1	11.8	0.31	-0.69	1.44
G5	8.7	14.0	42.0	14.4	15.6	8.4	17.2	-2.77	-1.03	11.16
G6	6.8	8.3	15.9	11.5	12.2	6.3	10.2	0.96	-1.13	4.02
G7	9.1	6.6	15.1	7.4	6.7	4.2	8.2	0.80	0.35	3.21
G8	8.9	9.5	20.1	11.4	11.7	6.8	11.4	0.41	-0.58	1.74
G9	10.0	10.1	23.2	11.1	11.0	6.9	12.1	-0.06	-0.21	0.30
G10	9.2	8.4	25.5	8.1	7.6	4.5	10.5	-0.77	0.38	3.10
G11	10.9	11.1	37.6	9.2	8.6	5.5	13.8	-2.48	0.67	9.97
G12	7.4	6.6	15.9	8.0	7.8	4.0	8.3	0.64	-0.16	2.56
G13	10.2	8.3	21.3	8.3	7.6	5.0	10.1	-0.03	0.49	0.51
G14	6.2	9.2	25.8	11.1	12.0	5.6	11.7	-0.69	-1.04	2.95
G15	10.0	8.8	22.2	9.1	8.5	5.5	10.7	-0.11	0.28	0.51
G16	5.7	6.3	14.7	8.7	9.0	4.0	8.1	0.80	-0.73	3.29
G17	9.0	8.8	23.3	9.3	9.1	5.3	10.8	-0.31	0.01	1.24
G18	13.2	9.0	17.6	8.8	7.3	6.3	10.4	0.77	1.00	3.25
G19	15.4	10.1	25.1	7.8	5.8	6.2	11.7	-0.39	1.83	2.41
G20	9.4	9.0	22.5	9.8	9.6	5.8	11.0	-0.12	-0.05	0.48
G21	6.8	8.1	16.4	11.0	11.6	5.9	10.0	0.83	-1.02	3.48
G22	9.9	7.8	16.7	8.6	8.0	5.2	9.4	0.71	0.28	2.86
G23	7.9	10.9	31.0	11.8	12.5	6.6	13.5	-1.33	-0.74	5.38
G24	11.1	6.5	7.9	7.8	6.6	5.2	7.5	2.09	0.61	8.41
G25	6.2	6.0	13.1	8.3	8.4	3.9	7.7	1.04	-0.54	4.21
G26	7.3	6.6	11.8	9.2	9.2	4.9	8.2	1.40	-0.54	5.64
Mean	9.4	8.8	21.6	9.5	9.3	5.6	10.7			
IPCA1	1.47	0.37	-5.12	1.07	0.89	1.31				
IPCA2	3.03	0.23	0.24	-1.26	-2.29	0.06				

ASV = AMMI stability value, IPCA1 and IPCA2 = first and second interaction principal component analysis axes; See codes of environments and genotypes in Tables 6.1 and 6.2, respectively.

6.3.2.3. Dry matter content (DMC)

The AMMI analysis of variance for root dry matter content is presented in Table 6.4. Genotypes, environments and their interactions had highly significant (p ≤ 0.001) effects on

Table 6.7. AMMI means for dry matter content (%), IPCA scores and ASV values of 26 sweetpotato clones evaluated across six environments in eastern Tanzania.

Genotype	E1	E2	E3	E4	E5	E6	Mean	IPCA1	IPCA2	ASV
G1	31.5	35.6	32.4	34.1	35.5	32.8	33.7	-0.76	-0.10	1.23
G2	28.6	31.1	34.2	36.2	34.4	32.9	32.9	0.56	-1.06	1.39
G3	34.4	36.7	36.2	36.3	37.2	34.5	35.9	-0.78	-0.76	1.47
G4	34.5	39.9	34.8	37.8	39.5	36.9	37.2	-0.68	0.38	1.15
G5	32.8	34.4	33.4	32.4	34.1	31.0	33.0	-1.29	-0.84	2.23
G6	33.0	37.5	32.0	33.3	36.0	32.8	34.1	-1.34	0.20	2.16
G7	34.9	40.9	32.4	34.6	38.4	34.9	36.0	-1.59	0.83	2.70
G8	32.4	38.2	34.5	38.7	39.2	37.1	36.7	-0.02	0.35	0.35
G9	30.2	36.5	32.3	36.9	37.4	35.4	34.8	0.06	0.50	0.51
G10	32.7	38.9	36.0	41.2	40.8	39.1	38.1	0.49	0.36	0.86
G11	30.5	37.1	32.5	37.4	37.9	35.9	35.2	0.07	0.60	0.61
G12	32.0	36.1	37.3	41.2	39.4	38.0	37.3	0.81	-0.50	1.40
G13	31.9	38.8	34.9	40.6	40.4	38.7	37.6	0.48	0.61	0.98
G14	27.3	30.8	33.2	36.5	34.4	33.1	32.6	0.87	-0.79	1.60
G15	34.7	37.3	38.1	39.3	39.1	36.9	37.6	-0.18	-0.80	0.85
G16	35.6	37.2	38.0	37.8	38.3	35.7	37.1	-0.65	-1.02	1.46
G17	29.5	34.8	35.0	40.1	38.2	37.1	35.8	1.08	-0.14	1.74
G18	30.3	37.0	35.5	41.9	40.2	39.1	37.3	1.19	0.31	1.95
G19	32.8	39.5	36.3	42.0	41.5	39.9	38.7	0.61	0.50	1.10
G20	33.0	37.6	36.2	39.7	39.4	37.5	37.2	0.18	-0.13	0.32
G21	31.0	37.0	34.3	39.2	38.8	37.1	36.2	0.44	0.29	0.76
G22	29.2	36.3	30.1	35.2	36.4	34.2	33.6	-0.17	0.86	0.91
G23	31.6	37.4	35.0	39.8	39.3	37.6	36.8	0.45	0.20	0.75
G24	33.7	42.2	34.4	40.9	42.2	40.1	38.9	0.00	1.33	1.33
G25	26.7	29.8	30.6	32.8	32.0	30.1	30.3	0.15	-0.68	0.73
G26	37.2	40.8	40.6	42.9	42.6	40.6	40.8	0.03	-0.48	0.48
Mean	32.0	36.9	34.6	38.0	38.2	36.1	36.0			
IPCA1	-2.29	-1.55	0.21	2.13	0.33	1.18				
IPCA2	-0.94	1.77	-2.36	-0.05	0.8	0.78				

ASV = AMMI stability value, IPCA1 and IPCA2 = first and second interaction principal component analysis axes, See codes of environments and genotypes in Tables 6.1 and 6.2, respectively.

DMC of genotypes across sites. The means for dry matter content are presented in Table 6.7. The mean DMC across the six sites ranged from 30.3-40.8% for G25 and G26, respectively, with an overall mean of 36%. Both G25 and G26 are released and commercially grown cultivars.

Among the newly bred clones, G14 and G19 had the lowest and highest DMC of 32.6 and 38.7%, respectively; G7 had the same DMC to the overall mean. About 54% of test genotypes had DMC above the overall mean (Table 6.7). Test environments E1 and E5 had the lowest and highest DMC of 32 and 38.2%, respectively.

IPCA1 and IPCA2 had significant differences at $p \leq 0.01$. The IPCAs accounted for 68% of the GxE interaction sum of squares. G7 and G18 had the lowest and highest IPCA1 of -1.59 and 1.19, respectively (Table 6.7). Conversely, G24 had zero IPCA1. The ASV for DMC among the test genotypes ranged from 0.32-2.7 for G20 and G7, respectively (Table 6.7). Therefore, G20 was the most stable and G7 the least stable genotype (Figure 6.1c).

An AMMI biplot with IPCA scores against means of genotypes and environments for dry matter content is presented in Figure 6.3A. Genotypes G25 and G26 had the lowest and highest DMC, respectively. G7, G3 and G17 had DMC closer or equal to the overall mean DMC; however, they were least stable. G24, G20, G8, G11, G22, G25 and G15 were relatively stable in the test environments compared to G7, G6, G5, G18 and G17 which were least stable. On the other hand, test environments E3 and E5 were stable. In contrast, E1, E2 and E4 showed great variablity in discriminating test genotypes with regards to dry matter content (Figure 6.1c).

6.3.2.4. Sweetpotato virus disease (SPVD)

The AMMI analysis of variance for SPVD showed highly significant ($p \leq 0.001$) effects of genotypes, environments and their interaction on SPVD response (Table 6.4). IPCA1 and IPCA2 were highly significant ($p \leq 0.001$). The two IPCAs accounted to 71% of the interaction.

The mean SPVD severity scores are presented in Table 6.8. The SPVD scores for the six environments ranged from 1.17-3.11 corresponding to the genotypes G4 and G25, respectively; with an overall mean of 1.62. Therefore, the genotype G4 was the most resistant and G25 the most susceptible. G25 is a released orange fleshed and commercially grown cultivar, while G4 is a newly bred clone. About 62% of the genotypes had SPVD scores less than the overall mean scores of the six environments.

The genotypes G22 and G14 had the lowest and highest IPCA1 score of -0.87 and 1.02, respectively (Table 6.8). The ASVs for the experimental clones ranged from 0-0.38 (Table 6.8). The following genotypes: G16, G19, G5 and G12 had an ASV value of zero; while G14, G6 and G1 had ASV of 0.38. Hence, the genotypes G16, G19, G5 and G12 were stable and G14, G6 and G1 were unstable across the six environments with regards to reaction to SPVD (Table 6.8; Figure 6.1d).

Table 6.8. AMMI means for SPVD reaction, IPCA scores and ASV values for 26 sweetpotato clones evaluated across six environments in eastern Tanzania

Genotypes	E1	E2	E3	E4	E5	E6	Mean	IPCA1	IPCA2	ASV
G1	1.76	1.66	1.32	0.89	2.89	1.14	1.61	-0.39	0.70	0.38
G2	2.16	1.49	1.26	1.76	1.09	1.57	1.56	0.19	-0.30	0.08
G3	3.16	1.60	1.51	1.79	2.55	1.39	2.00	-0.54	-0.11	0.08
G4	1.46	1.23	0.93	1.19	0.99	1.20	1.17	0.20	-0.03	0.01
G5	1.70	1.50	1.19	1.24	1.72	1.32	1.44	0.01	0.19	0.00
G6	1.11	2.31	1.77	1.65	1.64	2.19	1.78	0.63	0.43	0.38
G7	1.40	1.34	1.01	1.23	1.05	1.30	1.22	0.25	0.02	0.01
G8	2.32	1.37	1.18	1.43	1.81	1.23	1.56	-0.22	-0.05	0.02
G9	2.77	1.02	0.98	1.77	0.95	1.17	1.44	-0.14	-0.66	0.13
G10	2.07	1.64	1.37	1.37	2.16	1.40	1.67	-0.15	0.22	0.05
G11	1.84	1.25	1.00	1.03	1.87	1.01	1.33	-0.22	0.19	0.06
G12	1.34	1.47	1.11	1.35	0.94	1.47	1.28	0.38	0.01	0.00
G13	1.85	1.47	1.19	1.59	1.07	1.51	1.44	0.24	-0.17	0.06
G14	1.84	2.60	2.15	2.68	0.83	2.90	2.17	1.02	-0.27	0.38
G15	3.06	1.04	1.05	1.85	1.18	1.16	1.56	-0.28	-0.68	0.26
G16	2.17	1.70	1.44	1.69	1.71	1.63	1.72	0.05	-0.03	0.00
G17	2.29	1.25	1.09	1.64	1.09	1.32	1.44	0.02	-0.37	0.01
G18	1.35	1.37	1.03	1.22	1.05	1.32	1.22	0.28	0.05	0.02
G19	2.17	1.70	1.44	1.69	1.71	1.63	1.72	0.05	-0.03	0.00
G20	1.28	2.13	1.64	1.45	1.93	1.92	1.72	0.38	0.48	0.25
G21	1.46	1.35	1.02	0.87	1.95	1.03	1.28	-0.13	0.40	0.07
G22	3.32	1.17	1.18	1.44	2.68	0.88	1.78	-0.87	-0.12	0.15
G23	2.46	1.14	1.02	1.43	1.55	1.07	1.44	-0.27	-0.24	0.09
G24	2.47	1.77	1.54	1.57	2.49	1.50	1.89	-0.29	0.19	0.08
G25	3.18	3.22	2.86	2.51	4.12	2.78	3.11	-0.23	0.61	0.20
G26	2.37	1.22	1.08	1.69	1.00	1.32	1.44	0.03	-0.44	0.02
Mean	2.09	1.58	1.32	1.54	1.69	1.47	1.62			
IPCA1	-1.06	0.59	0.32	0.39	-1.09	0.86				
IPCA2	-1.07	0.46	0.19	-0.70	1.11	0.02				

ASV = AMMI stability value, IPCA1 and IPCA2 = first and second interaction principal component analysis axes, See codes of environments and genotypes in Tables 6.1 and 6.2, respectively.

AMMI biplot for IPCA1 scores against genotype and environment means for response to SPVD is presented in Figure 6.1d. Genotypes G19, G16, G10, G17, G26 and G5 were relatively stable across sites; however, only G17, G26 and G5 had SPVD scores below the

overall mean. Corresponding to IPCA1 scores and ASV values, G14 and G22 were most responsive across all the test environments. G25 fell out of the range of the biplot due to its high SPVD mean scores and its susceptibility. G22 was highly susceptible at E5 and E1, while G14 and G6 were highly susceptible at E6. On the other hand, G7, G18 and G12 had minimal infection rate at E3. Test environments; E1 and E5 had high infection rates and conducive for SPVD, while E2, E3, E4 and E6 had less infection rates. Two sites, one from each of the two groups could sufficiently be used to evalute the test genotypes for evaluation of genotypes for SPVD resistance.

6.3.3. Best or worst genotypes selected by AMMI per environment

AMMI analysis identified four best test genotypes per environment for number of roots per plant, root yield and DMC. Also, highly SPVD susceptible test genotypes per each environment were identified (Table 6.9). G20 ranked first in four environments for number of roots per plant. G5 was the best in all test environments except E1 where G19 was the best for root yield. Similarly, G26 was the highest at E1, E3, E4, E5 and E6 except E2 where G24 was the highest for DMC. Alternatively, G25 was the most susceptible in all environments, it ranked first at E2, E3 and E5 and, second at E1, E4 and E6. While at E6 where G14 was the highly infected, G22 ranked first at E1. The above ranking corresponds to IPCA1 scores and ASV values previously highlighted in Tables 6.5 to 6.8.

Table 6.9. The first four AMMI selections of sweetpotato genotypes per environment

Traits	Environments	Mean	Scores	1	2	3	4
Nrpp	E2	4.5	-0.85	G20	G22	G9	G18
	E4	4.1	-1.04	G20	G22	G3	G2
	E5	3.5	2.18	G1	G25	G22	G10
	E3	3.4	-0.76	G20	G22	G3	G2
	E6	3.3	0.04	G20	G4	G3	G22
	E1	2.7	0.44	G22	G20	G1	G2
Yield	E3	21.6	-5.12	G5	G11	G23	G3
	E4	9.5	1.07	G5	G4	G23	G6
	E1	9.4	1.47	G19	G2	G18	G24
	E5	9.3	0.90	G5	G23	G4	G6
	E2	8.8	0.37	G5	G11	G23	G19
	E6	5.6	1.32	G5	G4	G9	G8
DMC	E5	38.2	0.33	G26	G24	G19	G10
	E4	38.0	2.13	G26	G19	G18	G10
	E2	36.9	-1.55	G24	G7	G26	G4
	E6	36.1	1.18	G26	G24	G19	G18
	E3	34.6	0.21	G26	G15	G16	G12
	E1	32.0	-2.29	G26	G16	G7	G15
SPVD	E6	1.5	0.86	G14	G25	G6	G20
	E2	1.6	0.59	G25	G14	G6	G20
	E4	1.5	0.39	G14	G25	G15	G3
	E3	1.3	0.32	G25	G14	G6	G20
	E1	2.1	-1.07	G22	G25	G3	G15
	E5	1.7	-1.09	G25	G1	G22	G3

DMC = dry matter content, Nrpp = number of roots per plant, SPVD = sweetpotato virus disease. See codes of environments and genotypes in Tables 6.1 and 6.2, respectively.

6.3.4. GxE and stability analysis using GGE biplot

6.3.4.1. Number of roots per plant

GGE biplot analysis of number of roots per plant using principal component 1 (PC1) and PC2 is presented in Figure 6.2A. The two PCs explained about 78% of the interaction. Large and positive PC scores for given genotypes indicate higher average value while those with large negative PC scores imply lower average value (Yan et al., 2000). Consequently, the following genotypes: G20, G22, G3, G2, G9 and G4 had the highest average number of roots per plant (Figure 6.5). Conversely, genotypes G13, G17, G10, G21 and G8 had the lowest mean number of roots per plant (Figure 6.2A).

Genotypes with PC2 scores near zero indicate that they were more stable. Accordingly, G6, G16, G5, G11 and G12 had relatively low PC2 scores. Unlike genotypes at the polygon vertexes, the clones designated as G1, G22, G20, G10 and G13 were the most responsive to environments. Five out of six environments were located in one sector implying that they discriminated the test genotypes similarly.

Genotypes at the vertices of the polygon performed either best or poorest. Hence, G20, G1 and G22 had highest average number of roots at E3, E5 and E4, respectively. Figure 6.2A shows what genotype won where, consequently G20 and G22 won at E1, E2, E3, E4 and E6, while G1 was best suited for E5.

Moreover, environments with large PC1 scores were better in discriminating the genotypes and those with PC2 scores near zero weare more representative of an average environment (Yan et al., 2000). Therefore, E1, E2, E3, E4 and E6 discriminated the genotypes similarly with regard to number of roots per plant. Conversely, G1 and G25 specifically won at E5. While E5 was not representative in discriminating the test genotypes, the rest were representative. Consequently, this led to two mega-environments for the numbers of roots per plant as depicted in Figure 6.2A.

Figure 6.2a shows the stability of the genotypes across the test environments. The line that passes through the biplot origin is called the average environment coordinate (AEC), it shows the stability of the genotypes (Farshadfar et al., 2011). The stability of the genotypes is measured by their projection to the AEC *y*-axis. Either direction away from the biplot origin, on this axis, indicates greater GE interaction and reduced stability (Farshadfar et al., 2011). Therefore, genotypes G6, G16, G7, G8, G4, G12 and G5 were considered to be stable across the test environments for number of roots per plant. Conversely, G1, G25, G13, G26, G17 and G15 were least stable. Among the test environments, E5 was highly variable compared to E1, E6, E4 and E2 which were relatively stable. The AEC *y*-axis also separates genotypes with mean value of below average and above average. Genotypes to the right of this line are high

performers and those to the left are low performers (Gurmu et al., 2012). Therefore, G20 and G22 were the highest, while G13 and G17 were the lowest (Figure 6.2a).
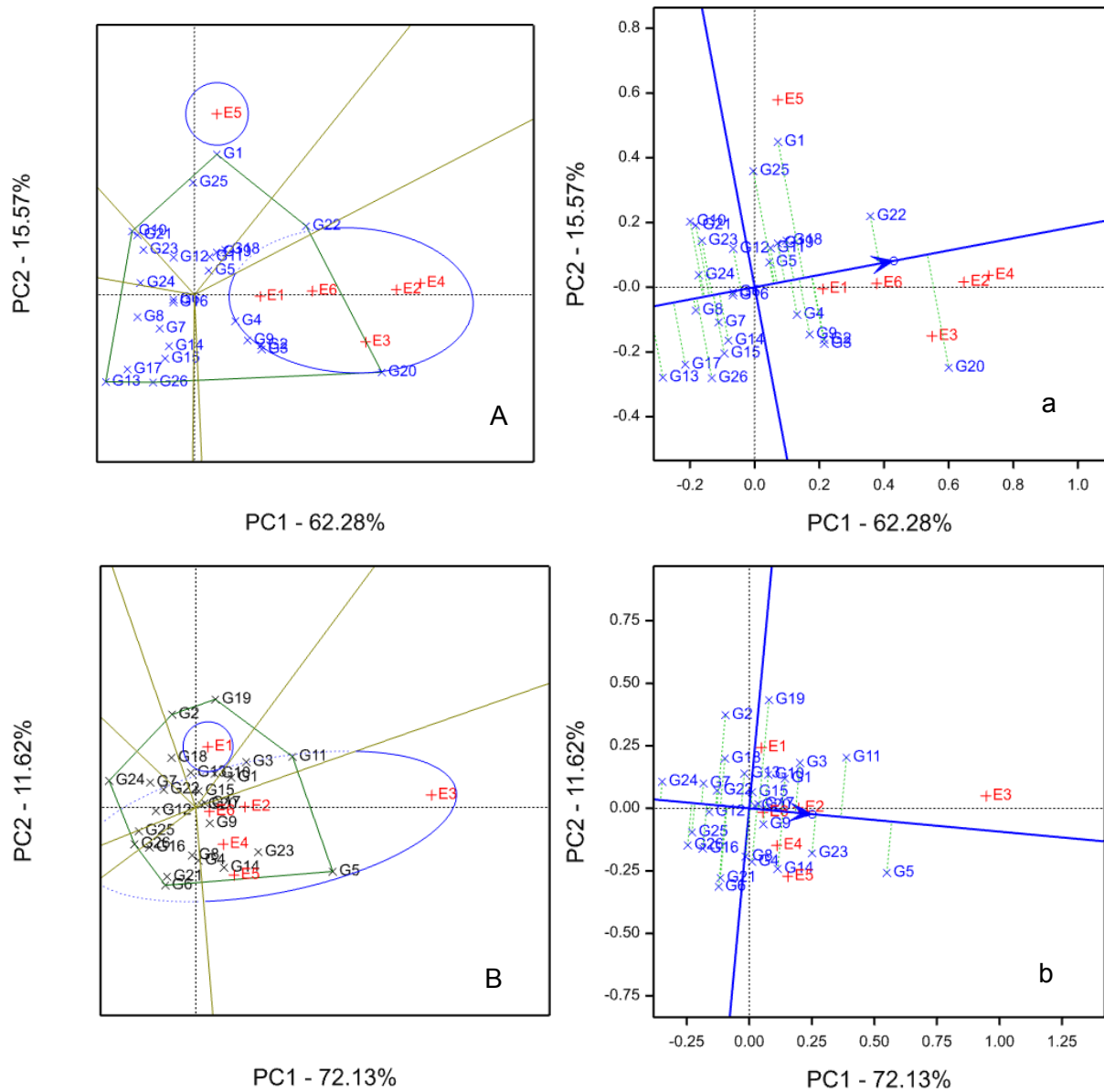

Figure 6.2 GGE biplots showing the 'which won where' view of (A and B) and comparison with ideal genotypes (a and b) of 26 sweetpotato genotypes tested across six environments for number of roots per plant (A and a) and storage root yield (B and b), respectively. See codes of environments and genotypes in Tables 6.1 and 6.2, respectively.

6.3.4.2.   Storage root yield

The GGE biplot showing environments and their respective sweetpotato genotypes for storage root yield is as presented in Figure 6.2B. Genotypes G5, G11, G23, G14 and G3 had positive PC1 scores and were higher yielders compared to the rest in all test environments except E1. Conversely, G24, G25, G26, G7, G16 and G12 had negative PC1 scores and yielded below the overall mean.

The clone G5 won across most of the test environments, while G19 performed better at E1 (Figure 6.2B; Table 6.9). E2 and E6 were more representative of the test environments, while E1 was a non-representative or discriminated the test genotypes differently for root yield. Five out of six environments were contained in the same sector meaning that they discriminated test genotypes similarly and consequently constituting one mega-environment. Uniquely, E1 constituted one mega-environment.

Figure 6.2b shows the stability of the genotypes across the test environments. Genotypes G5, G7, G9, G17, G10 and G22 were most stable across the test environments. However, G5 was the most stable and high yielding. Alternatively, G2, G19, G6 and G21 were least stable. G24 and G5 had the lowest and highest mean yields, respectively. Conversely, E2 and E6 were stable and, E1 and E4 were highly variable test environments with regard to root yield. Therefore, E2 and E6 could be used to test genotypes for a wide adaptation.

6.3.4.3.   Dry matter content (DMC)

Figure 6.3A shows which genotype won where or which is best for which environment with regard to DMC. Both PC1 and PC2 accounted about 81% of the total variation implying that they sufficiently explained the GGE. Genotypes G26, G24, G19, G10 and G13 had high and positive PC1 scores and high mean DMC mean. Conversely, G25, G14, G5, G2, G1, G22 and G6 had negative PC1 scores and had DMC below overall mean. Overall, 54% of the test genotypes had high mean DMC than the overall mean. All the test environments had positive PC1 scores and constituted one mega-environment implying that they were equally similar in discriminating test genotypes with regard to DMC. Nonetheless, E3, E5 and E6 were most representative environments.

Figure 6.3a shows the stability of the genotypes across the test environments for DMC. Genotypes G22, G9, G11, G8, G20, G24, G15 and G26 were most stable across the test environments. G24 and G26 were the highest in DMC across sites. The genotypes including G7, G6, G5, G14, G17 and G18 were least stable. Genotype G26 and G25 had the highest and lowest mean DMC, respectively. E5 and E3 were relatively the most stable environments with regard to DMC.
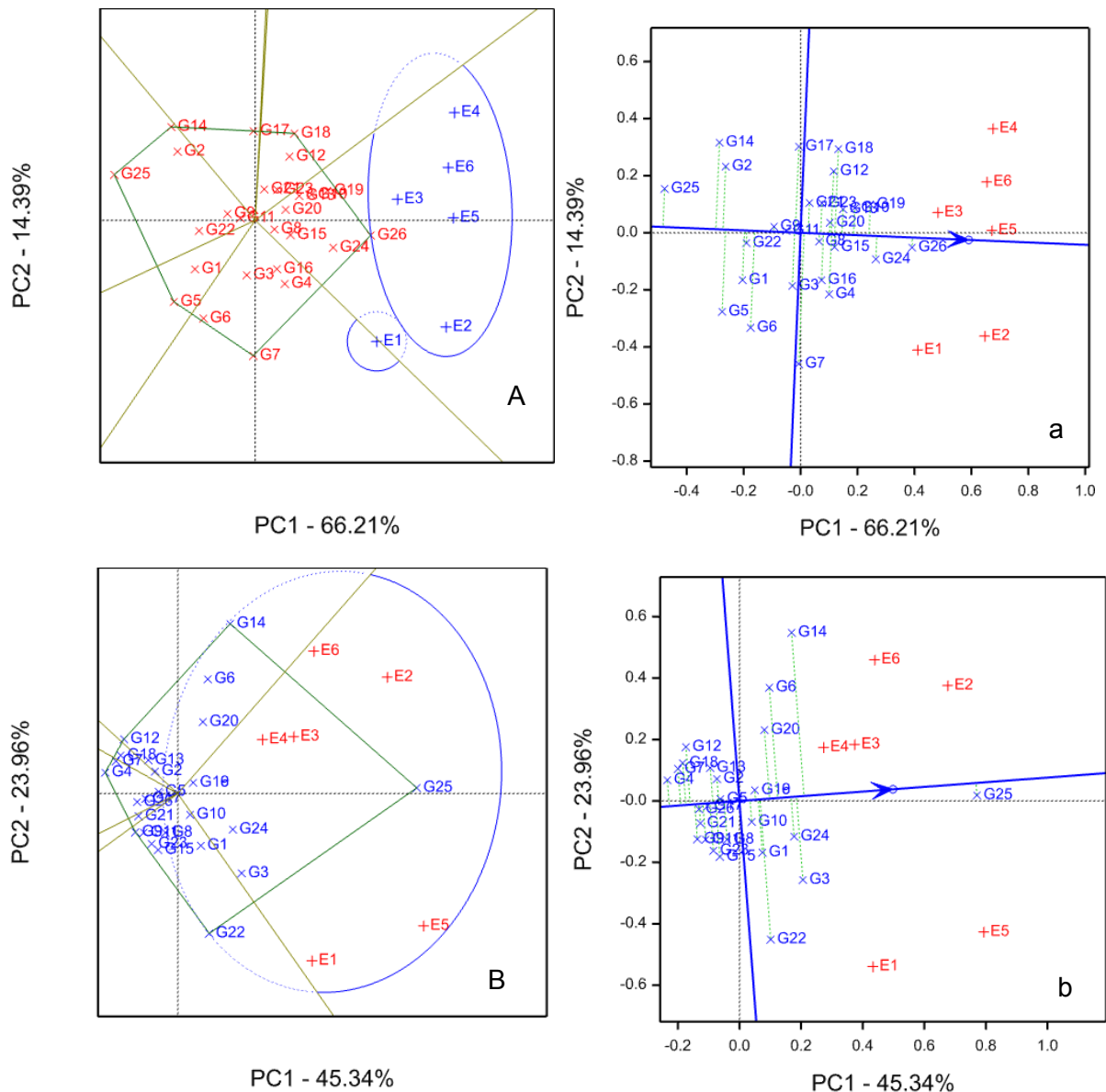
Figure 6.3 GGE biplots showing the 'which won where' view of (C and D) and comparison with ideal genotypes (c and d) of 26 sweetpotato genotypes tested across six environments for dry matter content and SPVD reaction (C and c) and (D and d), respectively. See codes of environments and genotypes in Tables 6.1 and 6.2, respectively.

6.3.4.4. Resistance to sweetpotato virus disease (SPVD)

Figure 6.3B shows which genotype wins where or which is best for which environment with regard to reaction to SPVD. The two PCs accounted for 69% of the total variation with PC1 and PC2 contributing at 45 and 24%, respectively. Contrary to the previously described traits, genotypes with high and positive PC1 scores imply that they were most susceptible and those with negative PC1 are most resistant. Thus genotype G25 was consistently the most susceptible across locations, while G14 was most affected by SPVD at E6. Interestingly, 65% of the genotypes had SPVD scores below the overall mean. Some of the new clones were

more resistant than the resistant check, G26. Overall, the genotypes G4 and G7 had the lowest SPVD scores. Consequently, G25 and G26 could be used as susceptible and resistant checks, in that order, when evaluating new sweetpotato genotypes against SPVD in eastern Tanzania.

The test environments had positive PC1 scores and constituted one mega-environment; hence they were similar in discriminating genotypes for SPVD. However, E3 and E4 were relatively the most representative environments in discriminating genotypes.

Figure 6.3b shows the stability of the genotypes across locations for SPVD. The genotypes indicated as G10, G16, G19, G6, G26, G21, G11, G17, G8 and G25 were stable across test environments. The genotype G25 was the most susceptible. Conversely, the genotypes G14, G22, G6, G3 and G20 were least stable by showing high divergence from the AEC abscissa. G25 had the highest SPVD score, while the remaining genotypes had disease scores less than the mean except G16 and G19.

6.4. Discussion

6.4.1. Analysis of variance

Significant differences were detected in number of roots per plant, storage root yield, dry matter content and resistance to SPVD among the genotypes studied across the six sites. Presence of significant differences in genotypes, environments and GE interaction effects implied differential responses in performances of genotypes across sites. Ngailo et al. (2015) and Placide et al. (2015) reported significant differences among sweetpotato genotypes, environments and their interactions in number of roots per plant, root yield, dry matter content and response to SPVD in Tanzania and Rwanda, respectively. Karuri et al. (2009) reported significant differences in SPVD symptoms severity among genotypes studied in Kenya. The same authors reported significant differences in dry matter content among genotypes studied. Laurie (2010) reported significant differences in yield and dry matter content in newly released and commercially grown sweetpotato varieties in South Africa. Likewise, Nwankwo and Afuape (2013) reported significant differences among orange fleshed sweetpotato genotypes for number of roots per plant, storage root yield, dry matter content and response to pests and diseases including viral diseases. Moreover, Marzouk et al. (2011) reported significant differences in the number of roots per plant in Egyptian sweetpotato germplasm. Similar findings were reported by Ali et al. (2015) for storage root yield and dry matter content in Ethiopia, while Kathabwalika et al. (2013) reported root yield differences in Malawi. Similarly, Mcharo and Ndolo (2013) and Saraswati et al. (2013) reported differential responses of

genotypes across test environments for root yield and dry matter content in sweetpotato genotypes in Kenya and Papua Indonesia, respectively. In Tanzania and Uganda, Mbwaga et al. (2007) and Mwanga et al. (2007), respectively, reported varied yields, dry matter content and SPVD symptoms severity of sweetpotato genotypes in agreement to the present findings. Differential response across sites implied differences in environments, and their interactions with the test genotypes.

6.4.2. AMMI analysis

6.4.2.1. Number of roots per plant

From AMMI analysis of variance (Table 6.4), the main effects and their interaction significantly caused variations in the number of roots per plant. However, the magnitude of their contribution varied. Genotypic and interaction effects were equally important, environments contributed less to the total sum of squares compared to other treatment components. IPCA1 contributed about 46.46% of the interaction and was the most important, while IPCA2 contributed to 21.1% of the interaction variance. Number of roots per plant is an important component of yield; however, the size and weight of the roots determine the final yield. Ngailo et al. (2015) and Placide et al. (2015) reported variations in the number of roots per plant across test sites in east Africa. This suggests that, the number and size of the roots is determined not only by genotypes but also by soil properties and other management practices during growth and development processes.

6.4.2.2. Storage root yield

The AMMI analysis of variance on storage root yield showed great contribution of environments and GE interactions to the variation in storage root yield compared to the main effect of genotypes. The contribution of environment to total sum of squares was larger compared to other sources of variations implying that the environments were diverse with large differences causing most of variations in root yields. IPCA1 and IPCA2 accounted for 66 and 16% of the interaction variance, respectively. There was a decrease in the contribution to GE interaction sum of squares with an increase in number of IPCAs. Similar to this study, Mwololo et al. (2009), Oduro (2013) and Kivuva et al. (2014) reported significant effects of genotypes, environments and their interactions in sweetpotato genotypes performance in Kenya and Ghana. Amare et al. (2014) reported significant effects of the genotypes, locations and their interaction on total sweetpotato root yields in Ethiopia. Adebola et al. (2013) reported similar findings in South Africa. Congruent to this study, Kivuva et al. (2014) reported large proportion of IPCA1 to GE interaction. However, Niringiye et al. (2014) reported higher contribution of genotypic effects than environment and GE interaction effects in variation of

sweetpotato root yields Uganda. Also, Kathabwalika et al. (2013) reported larger contribution of the interaction than genotype and environment in the variation of root yield in Malawi. The presence of interaction between genotypes and environments on the performance of candidate genotypes emphasizes the need to ascertain the influence of GE interaction in evaluation, selection and release of new varieties.

6.4.2.3. Dry matter content (DMC)

The AMMI analysis of variance showed that, genotypes and environment and their interaction were highly significant. The two IPCAs contributed to 68% of GE interaction. Caliskan et al. (2007) reported great variation in dry matter across locations in Turkey. Similar to this study, Oduro (2013) reported larger contribution of genotypic effects compared to environment and interaction effects in variation of dry matter content and other quality attributes. Likewise, most of sweetpotato quality traits were reported to have high dependence on environment main effects except dry matter content (Moussa et al., 2011). Shumbusha et al. (2014) reported little differences in dry matter content across locations among sweetpotato families in Uganda. Placide et al. (2015) reported significant genotype-environment interaction for sweetpotato dry matter content in Rwanda. Likewise, Wera et al. (2014) argued that significant GE interaction for dry matter content was attributed by genotypic effect. Contrary to this study and other reports, Chiona (2009) reported absence of environment effects and only 3% contribution of GE interaction on the variation of dry matter content in newly bred sweetpotato clones in Zambia. The mean DMC reported in this study resembles those reported by Tairo et al. (2008) and Chiona (2009) of 26.9-45.3% and 30.5-42.1%, respectively. In general, dry matter content of sweetpotato is the most preferred attribute by both farmers and consumers.

6.4.2.4. Resistance to sweetpotato virus disease (SPVD)

There were highly significant differences for genotypes, environments and their interactions. The IPCAs sufficiently explained the interaction of the main effects and accounted for 71% of GE interaction. The high IPCA scores in any direction and in any environment indicated the high degree of severity of SPVD for such particular genotype. For instance, genotypes G1 and G25 had high mean SPVD scores at E5 and, G14 and G22 at E6 and E1 respectively (Table 6.10; Figure 6.4). As opposed to yield and possibly other traits, high IPCA scores did not indicate responsiveness and specific adaptation but rather high degree of disease severity. The high GEI might be most useful in testing accessions' adaptability and resistance to pest and diseases (Tumwegamire et al., 2011). Byamukama et al. (2002) reported the variation of SPVD incidences with environments and that GE interaction effects for SPVD existed among sweetpotato clones in Uganda. Mwololo et al. (2012) reported significant variations in SPVD incidences due to sites, seasons and genotypes. The environmental mean SPVD severity

scores reported in this study were slightly lower than those reported by Niringiye et al. (2014). Forbes et al. (2005) argued that, stability of resistance over time is difficult to study as it requires historical data for stability inferences to be drawn over a significant period. Differential responses of genotypes to SPVD across sites could imply differences in disease inoculum pressure, hence testing of genotypes for resistance to the disease is vital to identify either for specific or wide adaptation to SPVD and possibly other diseases.

6.4.3. GGE biplot analysis

6.4.3.1. Number of roots per plant

From the GGE biplot, G20 and G22 had the highest number of roots per plant but very responsive to environment changes (Figure 6.2a). Also, G1, G25, G13, G26 and G17 were responsive and unstable genotypes with specific provisional adaptation to specific environments. E1 was the most stable but low yielding environment compared to E2, E3 and E4 were stable and high number of roots. Alternatively, E5 was unstable environment and mainly for specific adaptation. The findings indicated that genotypes were different and the environments were diverse in discriminating the test genotypes for number of roots.

6.4.3.2. Storage root yield

Genotypes G5 and G11 were high yielding in most of test environment. E2 and E6 were most stable but low yielding compared to E3 was the stable and high yielding. On the other hand, E1 and E4 were relatively less stable in discriminating the test genotypes. GGE biplot analysis resulted into two mega-environments implying that only two sites, one from each mega-environment could sufficiently be used to evaluate the genotypes. According to Yan et al. (2000), genotypes closer to the origin within the biplot polygon were considered stable and those at the polygon vertexes were responsive to environment changes. Hence, G5, G11 and G19 were very responsive to environment changes unlike G8 and G22. Laurie and Booyse (2015) reported similar trend among ten sweetpotato varieties selected for multiple traits in South Africa. Also, Kivuva (2013) reported similar findings where high yielding genotypes were positioned at the vertices of the polygon and most of the test environments were contained in one sector when working for drought tolerance in sweetpotato in Kenya. Therefore, different genotypes are likely to perform differently when tested in diverse environments.

6.4.3.3. Dry matter content (DMC)

All the test environments had positive PC1 scores and were contained in one sector which indicated their similarity in discriminating the test genotypes with regard to dry matter content. However, E3 and E5 were stable compared to the other four environments. Genotypes G25

and G26, both check varieties, had the lowest and highest DMC, respectively. Likewise, G7 had mean DMC similar to the overall mean DMC of genotypes. Alternatively, G7, G17, G18 and G14 were responsive to environment changes hence least stable compared to other genotypes. Besides GE interactions, variations in dry matter content among genotypes could be due to genetic constitution (Ali et al., 2015).

6.4.3.4.   Resistance to sweetpotato virus disease (SPVD)

SPVD resistant genotypes with low severity scores were found to be close to the origin of the biplot hence most stable compared to their counterparts. Genotypes G25, G14 and G22 were the most susceptible in the test environments in descending order. The environments were similar in discriminating the test genotypes for SPVD. E2, E3 and E4 were moderately stable, the rest were highly variable. Resistant genotypes are claimed to be stable unlike the susceptible counterparts (Mulema et al., 2008). Nakitandwe et al. (2005) found that, sweetpotato genotypes grown in multi-location trials performed differently with regard to yield and disease resistance. Since resistance to SPVD is quantitatively inherited (Diaz-Pendon et al., 2004); it is likely to be relatively stable across environments (Forbes et al., 2005). However, it is a long term endeavour as the presence of GxE interactions is claimed to have largely contributed to break down of resistance in improved varieties grown in agro-ecologies with high SPVD pressure (Gibson et al., 1998; Karyeija et al., 1998). However, further evaluation would be useful for certainty. Likewise, the results insist the need to breeders and agronomists to breed and evaluate new genotypes in multiple environments to identify resistant genotypes for either specific or wide adaptation for SPVD or other diseases.

6.5. Conclusions

There were significant differences in the performance among genotypes and across sites. AMMI analysis of variance showed significant differences for additive main effects and their interaction. Genotype, environment and their interaction contributed significantly to the variations in the traits studied though in varying proportions. The two IPCAs sufficiently explained the GEI. Both AMMI and GGE biplot identified G5, G11, G23, G9, G7, G18 and G17 being high yielding and resistant to SPVD and could be further evaluated in multi-environment yield trials (MEYTs) in eastern Tanzania. Likewise, both models identified G22 and G3 as high yielding and resistant to SPVD but specifically suited to E5 and E1. The presently used environments sufficiently discriminated the test genotypes with respect to traits studied. However, further MEYTs will be useful.

References

Acquaah, G. 2011. Principles of plant genetics and breeding. Malden, USA, Blackwell Publishing.

Adebola, P.O., A. Shegro, S.M. Laurie, , L.N. Zulu, and M. Pillay. 2013. Genotype x environment interaction and yield stability estimate of some sweetpotato [*Ipomoea batatas* (L.) Lam] breeding lines in South Africa. Journal of Plant Breeding and Crop Science 5:182-186.

Afuape, S., I. Nwankwo, R. Omodamiro, J. Njoku, C. Ogbonna, and D. Uzuegbu. 2013. Targeted breeding for sweetpotato-based enterprises: Variability, genotype-by-environment interaction, heritability and correlation studies of important sweetpotato root processing quality traits. International Journal of Plant Breeding and Genetics. DOI: 10.3923/ijpbg.2015.

Ali, S., W. Mohammed, and B. Shimelis. 2015. Agronomic and physicochemical evaluation of sweetpotato [*Ipomoea batatas* (L.) Lam] collections in Ethiopia. Advances in Crop Science and Technology DOI: 104172/2329-8863 1000172.

Amare, B., F. Abay, and Y. Tsehaye. 2014. Evaluation of sweetpotato (*Ipomoea batatas*, L.) varieities for total storage root yield in South and South East zones of Tigray, Ethiopia. American Journal of Trade and Policy 1**:**27-32.

Annicchiarico, P. (ed.). 2009. Coping with and exploiting genotype-by-environment interactions, Rome, Italy: FAO.

Baker, R.J. 1988. Tests for crossover genotype-environmental interactions. Canadian Journal of Plant Science 68**:**405-410.

Bryan, A.D., J.R. Schultheis, Z. Pesic-VanEsbroeck and G.C. Yencho. 2003. Cultivar decline in sweetpotato: II. Impact of virus infection on yield and storage root quality in 'Beauregard' and 'Hernandez'. Journal of the American Society for Horticultural Science 128**:**856-863.

Byamukama, E., E. Adipala, R.W. Gibson and V. Aritua. 2002. Reaction of sweetpotato clones to virus disease and their yield performance in Uganda. African Crop Science Journal 10**:**317-324.

Caliskan, M.E., E. Erturk, T. Sogut, E. Boydak and H. Arioglu. 2007. Genotype x environment interaction and stability analysis of sweetpotato (*Ipomoea batatas*) genotypes. New Zealand Journal of Crop and Horticultural Science 35**:**87-99.

Carey, E.E. and D. Reynoso. 1999. Procedure for evaluation of pathogen-tested sweetpotato clones. *In:* Huamán, Z. (ed.) Sweetpotato germplasm management. Training manual 3. Evaluation and breeding. Lima International potato Centre (CIP).

Ceccarelli, S. 2012. Plant breeding with farmers – a technical manual. Aleppo, ICARDA, Syria.

Chiona, M. 2009. Towards enhancement of β-carotene content of high drymass sweetpotato genotypes in Zambia. PhD Thesis, University of KwaZulu-Natal.

Diaz-Pendon, J.A., V. Truniger, C. Nieto, J. Garcia-Mas, A. Bendahmane, and M. Aranda. 2004. Advances in understanding recessive resistance to plant viruses. Molecular Plant Pathology 5:223-233.

Ding, M., B. Tier, W. Yan, H.X. Wu, M.B. Powell, and T.A. McRae. 2008. Application of GGE biplot analysis to evaluate genotype (G), environment (E), and G×E interaction on Pinus radiata: A case study. New Zealand Journal of Forestry Science 38**:**132-142.

Farshadfar, E., N. Mahmudi, and A. Yaghotipoor. 2011. AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (*Triticum aestivum* L.). Australian Journal of Crop Science 5:1837-1844.

Forbes, G.A., M.G. Chacon, H.G. Kirk, M.A. Huarte, M. van Damme, S. Distel, G.R. Mackay, H.E. Stewart, R. Lowe, J.M. Duncan, H.S. Mayton, W.R. Fry, D. Andrivon, D. Allisseche, R. Pelle, W.H. Platt, G. Mackenzie, T.R. Tarn, L.T. Colon, D.J. Budding, H. Lozoya-Saldana, A. Hernandez-Vilchis, and S. Capezio. 2005. Stability of resistance to Phytophthora infestans in potato: An international evaluation. Plant Pathology 54:364-372.

Gauch, H.G. 1988. Model selection and validation for yield trials with interaction. Biometrics 44**:**705-715.

Gauch, H.G. and R.W. Zobel. 1988. Predictive and postdictive success of statistical analysis of yield trials. Theoretical and Applied Genetics 76**:**1-10.

Gauch, H.G., Jr. 1992. Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Amsterdam, Elsevier Science Publishers.

Gibson, R.W., I. Mpembe, T. Alicai, E.E. Carey, R.O.M. Mwanga, S.E. Seal, and H.J. Vetten. 1998. Symptoms, aetiology and serological analysis of sweetpotato virus disease in Uganda. Plant Pathology 47:95-102.

Gomez, K.A. and A.A. Gomez. 1984. Statistical procedures for agricultural research. John Wiley and Sons.

Grüneberg, W.J., K. Manrique, D. Zhang, and M. Hermann. 2005. Genotype × environment interactions for a diverse set of sweetpotato clones evaluated across varying ecogeographic conditions in Peru. Crop Science 45**:**2160-2171.

Gurmu, F., E. Lire, A. Asfaw, F. Alemayehu, Y. Rezene, and D. Ambachew. 2012. GGE-biplot analysis of grain yield of Faba bean genotypes in Southern Ethiopia. Electronic Journal of Plant Breeding 3:898-907.

Haldavanekar, P.C., S.G. Bhave, R.G. Kahandekar, S.G. Kadam, and S.S. Sawant. 2011. Stability analysis in sweetpotato (*Ipomea batatas* L.). Karnataka Journal of Agricultural Sciences 24**:**358-361.

Ilker, E., F.T. Aykut, O. Caylak, M. Tosun, and I. Ozmen. 2009. Assessment of genotype x environment interactions for grain yield in maize hybrids using AMMI and GGE biplot analysis. Turkish Journal of Field Crops 14**:**123-135.

Karuri, H.W., E.M. Ateka, R. Amata, A.B. Nyende, and A.W.T. Muigai. 2009. Characterization of Kenyan sweetpotato genotypes for SPVD resistance and high dry matter content using simple sequence repeat markers. African Journal of Biotechnology 8**:**2169-2175.

Kathabwalika, D., E. Chilembwe, V. Mwale, D. Kambewa, and J. Njoloma. 2013. Plant growth and yield stability of orange fleshed sweetpotato (*Ipomoea batatas*) genotypes in three agro-ecological zones of Malawi. International Research Journal of Agricultural Science and Soil Science 3**:**383-392.

Karyeija, R., R. Gibson, and J. Valkonen. 1998. The significance of sweetpotato feathery mottle virus in subsistence sweetpotato production in Africa. Plant Disease 82:4-15.

Kempton, R.A. 1984. The use of biplots in interpreting variety by environment interactions. Journal of Agricultural Science 103**:**123-135.

Kivuva, B.M. 2013. Breeding sweetpotato [*Ipomoea batatas* (L.) Lam] for drought tolerance in Kenya. PhD Thesis. School of Agricultural, Earth and Environmental Sciences, University of KwaZulu-Natal, Pietermaritzburg.

Laurie, S.M. 2010. Agronomic performance, consumer acceptability and nutrient content of new sweetpotato varieties in South Africa. PhD Thesis, Free Sttate University.

Laurie, S.M. and M. Booyse. 2015. Employing the GGE SREG model plus Elston index values for multiple trait selection in sweetpotato. Euphytica 204:1-10.

Lebot, V. 2010. Sweetpotato. *In:* Bradshaw, J.E. (ed.). Root and tuber crops: Handbook of plant breeding. London: Springer.

Manrique, K. and M. Hermann. 2000. Effect of GxE interaction on root yield and beta carotene content of selected sweetpotato (*Ipomoea batatas* (L) Lam.) varieties and breeding clones. CIP program report 281-287.

Marzouk, N.M., A.S. El-Beltagy, U.A. EL-Behairy, S.D. Abou-Hussein, R. EL-Bedawy, and S.O. El-Abd. 2011. Performance of selected sweetpotato germplasms under Egyptian conditions. Australian Journal of Basic and Applied Sciences 5:18-21.

Mbwaga, Z., M. Mataa, and M. Msabaha. 2007. Quality and yield stability of orange fleshed sweetpotato *(Ipomoea batatas)* varieties grown in different agro-ecologies. *The Eighth African Crop Science Society Conferenc*e. El-minia, Egypt: African Crop Science Soceity.

Mcharo, M. and P. Ndolo. 2013. Root-yield performance of pre-release sweetpotato genotypes in Kenya. Journal of Applied Biosciences 65:4914-4921.

Moussa, S.A.M., H.A. Abd El-Aal, and N.I. Abo El-Fadl. 2011. Stability study of sweetpotato yield and its component characters under different environments by regression analysis. Journal of Horticultural Science and Ornamental Plants 3:43-54.

Mulema, J.M.K., E. Adipala, O.M. Olanya, and W. Wagoire. 2008. Yield stability analysis of Late bright resistant potato selections. Experimenta Agriculture 14**:**145-155.

Mwanga, R.O.M., C.G.C. Yencho, R.W. Gibson, and J.W. Moyer. 2013. Methodology for inoculating sweetpotato virus disease: Discovery of tip dieback, and plant recovery and reversion in different clones. Plant Disease 97**:**30-36.

Mwanga, R.O.M., B. Odongo, C. Niringiye, R. Kapinga, and S. Tumwegamire. 2007. Sweetpotato selection releases: Lessons learnt from Uganda. African Crop Science Journal 15:11-23.

Mwololo, J.K., M.W.K. Mburu, and P.W. Muturi. 2012. Performance of sweetpotato varieties across environments in Kenya. International Journal of Agronomy and Agricultural Research 2:1-11.

Mwololo, J.K., P.W. Muturi, M.W.K. Mburu, R.W. Njeru, N. Kiarie, J.K. Munyua, E.M. Ateka, R.W. Muinga, R.E. Kapinga, and B. Lemaga. 2009. Additive main effects and multiplicative interaction analysis of genotype × environmental interaction among sweetpotato genotypes. Journal of Animal and Plant Sciences (JAPS) 2**:**148-155.

Nakitandwe, J., E. Adipala, R. El-Bedewy, W. Wagoire, and B. Lemaga. 2005. Adaptability of SIFT potato genotypes in different agro-ecologies of Uganda. African Crop Science Journal 13**:**107-116.

Ngailo, S.E., H. Shimelis, J. Sibiya, and K. Mtunda. 2015. Screening of Tanzanian sweetpotato germplasm for yield and related traits and resistance to sweetpotato virus disease. Acta Agriculturae Scandinavica*,* Section B — Soil and Plant Science DOI: 10.1080/09064710.2015.1063684.

Ngeve, J.M. 1993. Regression analysis of genotype × environment interaction in sweetpotato. Euphytica 71**:**231-238.

Niringiye, C.S., G.N. Ssemakula, J. Namakula, C.B. Kigozi, A. Alajo, I. Mpembe, and R.O.M. Mwanga. 2014. Evaluation of promising orange fleshed sweetpotato genotypes in

different agroecological zones of Uganda. International Journal of Agriculture and Crop Science 7**:**1312-1321.

Nwankwo, I.I.M. and S.O. Afuape. 2013. Evaluation of high altitude orange fleshed sweetpotato (*Ipomoea batatas*) genotypes for adaptability and yield in lowland rainforest ecology of Umudike southeastern Nigeria. *I*OSR Journal of Agriculture and Veterinary Sciences 5**:**77-81.

Oduro, V. 2013. Genetic control of sugars, dry matter and bete-carotene in sweetpotato [*Ipomoea batatas* (L.) Lam]. PhD Thesis. School of Agriculture and Consumer Services, University of Ghana, Legon.

Osiru, M.O., M.O. Olanya, E. Adipala, B. Lemaga, and R. Kapinga. 2009. Stability of sweetpotato cultivars to *Alternaria* leaf and stem blight disease. Journal of Phytopathology 157**:**172-180.

Payne, R.W., D. Murray, S. Hardings, D. Baird, and D. Souter. (2014). GenStat for windows 17th edition. VSN International, Hemel, Hempstead, UK.

Placide, R., H. Shimelis, M. Laing, and D. Gahakwa. 2015. Phenotypic characterization of sweetpotato genotypes grown in East and Central Africa. South African Journal of plant and Soil 32:77-86.

Purchase, J.L. 1997. Parametric analysis to describe GxE interaction and stability in winter wheat. PhD Thesis. Department of Agronomy, Faculty of Agriculture, University of the Orange Free State, Bloemfontein, South Africa.

Rezene, Y., A. Bekele, and Y. Goa. 2014. GGE and AMMI biplot analysis for field pea yield stability in SNNPR state, Ethiopia. International Journal of Sustainable Agricultural Research 1:28-38.

Saraswati, P., A. Soplanit, A.I. Syahptura, L. Kossay, N. Muid, E. Ginting, and G. Lyons. 2013. Yield trial and sensory evaluation of sweetpotato cultivars in Highland Papua and West Papua Indonesia. Journal of Tropical Agriculture 51:74-83.

SAS 2008. SAS software, version 9.2. SAS Institute Cary, NC.

Shumbusha, D., G. Tusiime, R. Edema, P. Gibson, E. Adipala, and R.O.M. Mwanga. 2014. Inheritance of root dry matter content in sweetpotato. African Crop Science Journal 22:69-78.

Singh, M., S. Ceccarelli, and S. Grando. 1999. Genotype x environment interaction of crossover type: detecting its presence and estimating the crossover point. Theoretical and Applied Genetics 99**:**988-995.

Tairo, F., E. Mneney, and A. Kullaya. 2008. Morphological and agronomical characterization of sweetpotato [*Ipomoea batatas* (L.) Lam.] germplasm collection from Tanzania. African Journal of Plant Science 2**:**077-085.

Thiyagu, D., M.Y. Rafii, T.M.M. Mahmud, M.A. Lath, M.A. Malek, and G. Sentoor. 2013. Genotype by environment assessment in sweetpotato as a leafy vegetable using AMMI model. Pakistan Journal of Botany 45**:**843-852.

Tumwegamire, S., R. Kapinga, P.R. Rubaihayo, D.R. LaBonte, W.J. Grüneberg, G. Burgos, T. zum Felde, R. Carpio, E. Pawelzik, and R.O. Mwanga. 2011. Evaluation of dry matter, protein, starch, sucrose, β-carotene, iron, zinc, calcium, and magnesium in East African sweetpotato [*Ipomoea batatas* (L.) Lam] germplasm. HortScience, 46:348-357.

Vuylsteke, M. and F. van Eeuwijk. 2008. The use of general and specific combining abilities in a context of gene expression relevant to plant breeding. Euphytica 161:115-122.

Wera, B., A. Yalu, A. Ramakrishna, and M. Deros. 2014. Genotypic variability estimates of agronomic traits for selection in a sweetpotato (*Ipomoea batatas*) polycross population in Papua Guinea. Journal of Plant breeding and Genetics 2:131-136.

Xu, Y. 2010. Molecular plant breeding, Oxfordshire, UK, CABI.

Yan, W. 2001. GGE Biplot: A Windows Application for Graphical Analysis of Multi-Environment Trial Data and Other Types of Two-way Data. Agronomy Journal 93**:**1111-1118.

Yan, W. 2002. Singular-value partitioning in biplot analysis of multienvironment trial data. Agronomy Journal 94**:**990-996.

Yan, W. and M.S. Kang. 2003. GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists. Boca Raton, FL., CRC Press.

Yan, W. and N.A. Tinker. 2006. Biplot analysis of multi-environment trial data: principles and applications. Canadian Journal of Plant Science 86**:**623-645.

Yan, W., P.L. Cornelius, J. Crossa, and L.A. Huntt. 2001. Two Types of GGE biplots for analyzing multi-environment trial data. Crop Science 41**:**656-663.

Yan, W., L.A. Hunt, Q. Sheng, and Z. Szlavnics. 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Science 40**:**597-605.

Yan, W., M.S. Kang, B. Ma, S. Woods, and P.L. Cornelius 2007. GGE Biplot vs. AMMI analysis of genotype-by-environment data. Crop Science 47**:**643-655.

Zobel, W.R., W.J. Wright, and H.G. Gauch. 1988. Statistical analysis of a yield trial. Agronomy Journal 80**:**388-393.Chapter seven

7.   General overview

7.1. Introduction

Sweetpotato production contributes significantly to food security and incomes of subsistence farmers in Tanzania. However, its production is constrained by several biotic, abiotic and socio-economic factors. Sweetpotato virus disease (SPVD) is amongst the major biotic constraints and causes significant yield losses in the country. Both improved cultivars and landraces that are grown succumb to SPVD. Continued use of susceptible varieties and lack of effective control measures to SPVD has contributed to low yields and disease build up, development and persistence. Several SPVD control strategies such as cultural practices, phytosanitary measures, control of vectors and deployment of genetic resistance to prevent or limit the extent of damage have been recommended singly or in combinations. Both chemical and biological control methods are not effective against SPVD. The use of resistant varieties remains the most effective and cheapest method for subsistence farmers. The use of resistant varieties is cheap, easy, safe, effective and environmentally friendly. Therefore, breeding for SPVD resistance and high yields is an important consideration to develop and release improved sweetpotato varieties with end users preferences. This overview presents the summary of major findings of each objective. Finally, the implications of the findings are presented for sweetpotato breeding to SPVD resistance and improved yield and related traits.

The specific objectives of the study were:

1. To assess the present sweetpotato farming systems, farmers' preferences, production constraints and breeding priorities in eastern Tanzania

2. To determine genetic variation among diverse sweetpotato germplasm with regard to yield, dry matter content and sweetpotato virus disease (SPVD) resistance and to identify suitable clones for breeding.

3. To investigate the genetic diversity of 48 Tanzanian sweetpotato genotypes using nine selected polymorphic simple sequence repeat (SSR) markers to determine genetic relationship and select unique parents for breeding

4. To determine the general combining ability (GCA) and specific combining ability (SCA) effects of selected sweetpotato clones for the number of storage roots, fresh storage root yield, dry matter content (DMC) and resistance to sweetpotato virus disease (SPVD) for further selection and breeding.

5. To determine the magnitude of genotype-by-environment and stability for yield and yield related traits and sweetpotato virus disease (SPVD) resistance among newly developed sweetpotato clones in eastern Tanzania.

7.2. Summary of major findings

The first study assessed the present sweetpotato farming systems, farmers' preferences, production constraints and breeding priorities in eastern Tanzania. A participatory rural appraisal was conducted at Gairo, Kilosa and Kilombero districts of Morogoro Region and Mkuranga district of the Coast Region of Tanzania. A total of 138 and 149 farmers were sampled for household interviews and focus group discussion, respectively. The main findings of this study indicated that:

- More than 94% of the respondents depended on crop farming for their livelihoods.
- The main sweetpotato production constraints were Sweetpotato virus disease (SPVD) and pests, drought, unavailability of markets and lack of transport, low prices, inadequate extension services and postharvest losses.
- High yield, high dry matter content, tolerance to diseases and early maturity were the most preferred sweetpotato attributes.
- Farmers expressed their persuasive needs towards improved extension service delivery, SPVD tolerant cultivars and reliable and coordinated market systems of sweetpotato.

The second study determined phenotypic variation among diverse sweetpotato collections with regard to yield, dry matter content and sweetpotato virus disease resistance and identified suitable clones for breeding. A total of 144 sweetpotato genotypes were evaluated at two sites in Tanzania using a 12x12 simple lattice design in 2013. The main findings are listed hereunder:

- Genotypes differed in time to 50% flowering, number of roots per plant, root yield, dry matter content and resistance to SPVD.
- Fifty eight percent of the genotypes showed resistant reaction to SPVD, while 31% and 11% were moderately susceptible and susceptible to the disease, respectively.
- Seven clones including Simama, Ukerewe, Mataya, Resisto, 03-03, Ex-Msimbi-1 and Gairo were selected for high storage root yield and related traits or SPVD resistance. The selected genotypes are recommended as potential parents for sweetpotato breeding.

The third study determined genetic relationship and selected unique parents useful for future breeding. A total of 48 Tanzanian sweetpotato genotypes were genotyped using nine polymorphic simple sequence repeat markers. Genetic diversity parameters, cluster analysis, and analysis of molecular variance were calculated to determine genetic diversity and relationships. The following were the outcomes:

- The SSR markers used were highly polymorphic with the mean polymorphic information content (PIC) of 0.78, while allelic richness per locus ranged from 4-17 with a mean of 10.0 and the number of effective alleles varied from 2.2-6.1 with a mean value of 3.5.
- The un-weighted pair group method with arithmetic mean allocated the germplasm collection into three major genetic clusters.
- Ex-Ramadhani, Kibakuli, Mkombozi, Mjomba, Ex-Halima-3 and Kabuchenji were identified as genetically unrelated and complementary genotypes and recommended for future breeding programmes.

The fourth experiment determined combining ability effects for yield and related traits, and resistance to SPVD. Eight genotypes selected for their high yield, dry matter content or SPVD resistance were crossed using an 8x8 half diallel mating design. The generated families were evaluated in the field at Sugarcane Research Institute (SRI) at Kibaha, Kilombero Agricultural Training and Research Institute (KATRIN) and Sokoine University of Agriculture (SUA) in Tanzania. Results showed:

- Highly significant differences among families for all studied traits across sites.
- Highly significant GCA and SCA effects of parents for all traits studied.
- Both GCA and SCA interacted significantly with sites indicating environmental influence on the gene action for respective traits.
- Clonal parent Gairo had positive and significant GCA effect for number of roots per plant.
- Clonal parents 03-03 and Simama had significantly positive GCA effects for storage root yield, while Ukerewe displayed positive and significant GCA effect for DMC.
- The parental clones Ex-Msimbu-1and Gairo displayed negative and significant GCA effect for SPVD resistance. Therefore, the following parents: 03-03, simama, Ukerewe, Ex-Msimbu-1 and Gairo could be used for future sweetpotato breeding programmes poised to improve yield, dry matter content and resistance to SPVD.
- Families that were best combiners displaying positive and significant SCA effects: Mataya x Gairo and Simama x Gairo for number of roots per plant, Mataya x Ex-Msimbu-1, 03-03 x Ex-Msimbu-1 and Resisto x Gairo for root yield and, Resisto x

SPKBH008, Mataya x Gairo, 03-03 x Ukerewe and SPKBH008 x Gairo for DMC and Mataya x SPKBH008 and Mataya x Gairo had negative and significant SCA effect for resistance to SPVD.

- The selected parents and families were the best candidates to develop improved sweetpotato varieties with high root yield, DMC and SPVD resistance.

Finally, the magnitude of genotype-by-environment interaction among newly developed sweetpotato clones was determined for yield and related traits and SPVD resistance in eastern Tanzania. Experiments were conducted across six diverse environments, namely Gairo, Kilombero Agricultural Training Research Institute (KATRIN), Sokoine University of Agriculture (SUA), Sugarcane Research Institute (SRI), Chambezi and Mkuranga. Twenty three newly developed clones and three released and commercially grown check varieties were evaluated using a randomized complete block design with three replications. The Additive Main Effect and Multiplicative Interaction (AMMI) and genotype and genotype-by-environment interaction (GGE) biplot analyses were used to determine the GxE interaction and stability of the genotypes.

- AMMI analysis of variance revealed highly significant differences among genotypes, environments and genotype x environment interaction effects for all traits evaluated.
- Both AMMI and GGE biplots identified genotypes: G5, G11, G23, G9, G7, G18 and G17 being high yielding and resistant to SPVD which could be further evaluated in multi-environment yield trials (MEYTs) in eastern Tanzania.
- Also, both models isolated genotypes G22 and G3 as high yielding and resistant to SPVD but specifically suited to Chambezi and Gairo.
- Test environments sufficiently discriminated the candidate genotypes for traits studied.
- Further MEYTs are required for selection and recommendation of high yielding, SPVD resistant and stable sweetpotato clones for eastern Tanzanian or similar environments.

7.3. Implications of the research findings

The following implications were noted from this study:

- Farmers' participation in sweetpotato varietal selection and identification of breeding priorities is important for adoption of newly developed and improved varieties.

- Participatory germplasm conservation and utilization is fundamental for maintenance of useful genetic resources and diversity for future sustainable uses.

- The SSR genetic markers are useful in genetic diversity analysis studies.

- Presence of both additive and non-additive gene effects for yield and resistance to SPVD suggests that breeding gain can be realized through hybridization and selection strategies.

In general, the study identified constraints and brreding priorities for improving sweetpotato production, presence of distantly sweetpotato genotypes which are valuable genetic resources for future crop breeding and generated valuable sweetpotato families with high combining ability for number and yield of storage roots, dry matter content and SPVD resistance from which new clones can be selected for future evaluation and release as new cultivars.