Genetic Enhancement of Sweetpotato for Weevil (*Cylas* spp.) Resistance, Storage Root Yield and Yield-related Traits

By

Filson Mbezi Kagimbo

BSc. Agronomy (Sokoine University of Agriculture, Morogoro, Tanzania)
MSc. Agricultural Science (The University of Melbourne, Melbourne, Australia)

A thesis submitted in partial fulfilment of the requirements for the degree of Doctor of Philosophy (PhD) in Plant Breeding

African Center for Crop Improvement (ACCI)

School of Agricultural, Earth and Environmental Sciences
College of Agriculture, Engineering and Science
University of KwaZulu-Natal
Republic of South Africa

November 2017

THESIS ABSTRACT

Sweetpotato (*Ipomoea batatas* [L.] Lam.) is an important crop providing livelihood and economic opportunities for millions of smallholder farmers in sub-Saharan Africa (SSA). Weevil infestation caused by sweetpotato weevil (*Cylas* spp.) is one of the main factors contributing to the low storage yields of the crop in SAA, including Tanzania. Field sanitation, early planting, early harvesting and chemical treatments are the suggested control options to manage sweetpotato weevils. However, these strategies are less effective and unsustainable. Breeding sweetpotato varieties with durable resistance to weevils and enhanced yield and yield components is advocated as an economic and environmentally friendly strategy to control weevils and to boost production and productivity of the crop. Therefore, the objectives of this study were: (i) to identify farmers' perceptions on sweetpotato weevil damage, production constraints and criteria used to select and grow the best sweetpotato varieties in western Tanzania, (ii) to determine variation among Tanzanian sweetpotato germplasm for dry yield and yield-related traits, (iii) to assess Tanzanian sweetpotato germplasm for resistance to weevils in western Tanzania and (iv) to determine inheritance of weevil resistance, yield and yield-related traits in newly developed sweetpotato clones. The first study was undertaken using a participatory rural appraisal (PRA) method in four selected districts of western Tanzania. Data were collected using a structured questionnaire, focus group discussions and transect walk involving 122 sweetpotato farmers. Farmers identified weevil damage to be the overriding constraint to sweetpotato production followed by sweetpotato diseases and drought. Farmers' preferred agronomic traits of sweetpotato included high yield, drought tolerance and disease and weevil resistance. Dry matter content was the most important quality trait followed by reduced cooking time, taste and fiber content.

Seventy six sweetpotato accessions collected from Tanzania and 20 accessions received from International Potato Centre (CIP) in Lima/Peru were field characterized in two seasons using a 16 x 6 triple lattice design to determine their genetic diversity. Genotypes New Kawogo, Kiti cha Nyerere and Kisu cha Masai had the highest root yields of 10.14, 9.85, 9.67 t/ha, respectively The following genotypes were identified with high dry matter content: Ngw'anangusa (43.50%), Rugomoka (43.30%) and Secondary (43.30%). Two major genetic groups with genetic diversity of 0.54 were distinguished for further selection.

A total of 96 sweetpotato genotypes were screened for weevil resistance and yield and yield-related traits in two selected sites in western Tanzania using a 12 x 8 lattice design with three replications at each site. Nine sweetpotato genotypes (Kibandule, Malulumba, Utitiri, 3-CIP, Madebe, Magunhwa, 5-CIP, Kafu and Chuchu ya nesi) expressing weevil resistance and 10

genotypes (Nyamvuva, sengi, 22-CIP, Rugomoka, Tumauma, Ejumla, Carot C, New Kawogo 2, Haraka and 4-CIP) with moderate resistance to weevils were identified. Magunhwa, Chuchu ya Nesi, Rugomoka, Tumauma and New Kawogo were the best five genotypes selected displaying promising weevil resistance and desirable yield and yield-related traits.

The last experiment determined gene action and heritability of weevil resistance, yield and yield components and dry matter content and selected best parents and families. Six weevil resistant and six susceptible parents were crossed using a 6 x 6 North Carolina Design II mating design. The 36 families were evaluated at three locations using a 3 x 12 lattice design with two replications. Results showed that additive gene action showing a >0.5 general predicted ratio (GPR) was more influential for total root number (TRN), root yield (RY), dry matter content (DMC), percentage of infested root number (PIRN), percentage infested root yield (PIRY) and weevil damage score (WDS). Non-additive gene action was more influential for percentage of marketable root number (PMRN) and percentage of marketable root yield (PMRY) with a <0.5 GPR. The narrow sense heritability for TRN, RY, DMC, PIRN and WDS were 0.24, 0.56, 0.84, 0.62 and 0.62, while the broad sense heritability for these traits were 0.58, 0.72, 0.93, 0.78 and 0.77, in that order. Good combiner parents for RY were Simama, 2-CIP, 8-CIP and 17-CIP, while good combiner parents for DMC were Burenda, Kasinia, Masinia and 8-CIP. Genotypes Burenda, Kasinia, Masinia, 4-CIP and 5-CIP were good combiners for weevil resistance assessed through WDS. The best selected families for RY were Kasinia x 8-CIP, Simama x 2-CIP, Jewel x 5-CIP and Masinia x 18. The following families: Burenda x 2-CIP, Kasinia x 8-CIP, Masinia x 17-CIP and Simama x 17-CIP were superior for high DMC. The families Jewel x 18-CIP, Simama x 4-CIP, Masinia x 2-CIP and Kasinia x 5-CIP were selected for improved WDS.

In general, the study selected good combining sweetpotato parents that can be used to develop recombinant populations for future breeding. Further, best families were selected with promising root yield, dry matter content and weevil resistance which will be subjected to multi-environmental evaluation for cultivar release in western Tanzania.

DECLARATION

I, Filson Mbezi Kagimbo, 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: 

……..

Filson Mbezi Kagimbo

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

……

Prof. Hussein Shimelis (Supervisor)

……

Dr. Julia Sibiya (Co-Supervisor)

ACKNOWLEDGEMENTS

Above all, I thank The God Almighty for bringing me to this level and making my study a success.

I express special thanks and appreciation to my main supervisor, Prof. Hussein Shimelis, for his close supervision, guidance, positive criticism, inspiration and support all the way through my study. I am also grateful to my co-supervisor, Dr. Julia Sibiya, for her guidance, encouragement, support, genuine criticism and valuable comments. I recognize the contribution of Dr. Paul Shanahan for support and valuable comments during proposal development and implementation in the field.

I express my deepest gratitude to the Alliance for a Green Revolution in Africa (AGRA) for the scholarship through the African Centre for Crop Improvement (ACCI) and the University of KwaZulu-Natal for enrolling me as a PhD Scholar. The staff of ACCI are highly recognized for their hospitality and facilitation of logistics.

The Tanzania Ministry of Agriculture, Livestock and Fisheries is duly acknowledged for granting me a study leave. The Director for Research and Development-Western Zone Mr. Deusdedit Byamungu is especially acknowledged for his inspiring words and support throughout my study. Mr. Godson Bugingo, Accountant of Tumbi Agricultural Research Institute (ARI-Tumbi), is also highly appreciated for his positive support in managing research funds. Mr. Elias Issack Shinanda, Field officer at ARI-Tumbi is duly acknowledged for close supervision of all field work and trials of my research at ARI-Tumbi. I thank Mr. Living Kilawe of Urambo agricultural district office and Mr. Mtakakwa of Kasulu agricultural district office for close supervision of trials in their respective districts. I sincerely acknowledge Mr. Abdalla Cheyo, Timotheo Mugalegale and Baraka Stephen for their help in undertaking the daily activities in research fields at ARI-Tumbi.

The International Potato Center (CIP) staff in Lima, Peru especially Dr. Genoveva Rossel, Dr. Rosario Falcon and Dr. Davis Ellis are duly acknowledged for their assistance during acquisition of sweetpotato genotypes for my crosses. Staffs of Sugarcane Research Institute (SRI)-Kibaha, Dr. Stephan Ngailo, Dr Kiddo Mtunda and Mr. Tollano are highly appreciated for their assistance in receiving in *vitro* sweetpotato material from CIP-Lima and raising them in *situ*.

My beloved wife Irene Filson always has special place in my heart. It would be difficult for me to smoothly complete my study without her care of our beloved kids, Jonathan Agasha and Joshua Kamugisha. Dear Irene, I know you always wish to see my success, I thank you. I am

grateful to all my family members who have directly or indirectly contributed to the success of my study. God bless you all.

DEDICATION

I dedicate this thesis to: God almighty in Jesus Christ name; my family, my wife Irene and sons, Jonathan and Joshua; my parents, Rev. Phillemon Kagimbo and Fredina Kagimbo; my guardians, Fidelis Kabigiza and Christina Kabigiza; my brothers, sisters, nephews, nieces and friends.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

PUBLICATION PERTAINING THIS THESIS

Chapter 2

Filson Kagimbo, Hussein Shimelis & Julia Sibiya. 2018. Sweet Potato Weevil Damage, Production Constraints, and Variety Preferences in Western Tanzania: Farmers' Perception, Journal of Crop Improvement, 32 (1): 107-123, doi: 10.1080/15427528.2017.1400485

Chapter 3

Kagimbo, F.M., H. Shimelis and J. Sibiya. 2017. Diversity assessment of sweetpotato germplasm collections for yield and yield-related traits in western Tanzania. Acta Agriculturae Scandinavica, Section B — Soil & Plant Science: 1-9. doi:10.1080/09064710.2017.1372516.

Chapter 5

Filson Kagimbo, Hussein Shimelis & Julia Sibiya. 2018. Combining ability, gene action and heritability of weevil resistance, storage root yield and yield-related traits in sweetpotato. Under review in Euphytica.

THESIS INTRODUCTION

Background

Sweetpotato (*Ipomoea batatas* [L.] Lam.) is the world's seventh most important multipurpose food crop (Elameen et al., 2008; Nelles, 2009). Globally 106.60 million tonnes of sweetpotao is produced from an estimated area of 8.37 million hectares (FAOSTAT, 2017). China and Africa contribute 95.80% of the world's sweetpotato production. The crop is grown for food, source of cash incomes, feed and as industrial raw material for starch, alcohol and biofuel extraction (Schafleitner et al., 2010; Clark et al., 2012). Sweetpotato storage root is consumed in various forms such as fried chips, boiled root or baked products (Engoru et al., 2005). Young and succulent leaves of the crop are used as leaf vegetable. The above ground biomass of the crop is used as fodder. The orange-fleshed sweetpotato (OFSP) varieties are rich in β-carotene that is a precursor of vitamin 'A' useful in combating vitamin A deficiency (Mwanga et al., 2007; Burri, 2011). The purple-fleshed sweetpotato are reported to contain high antioxidant levels of anthocyanin, a pigment which gives root flesh a purple colour.

Sub-Saharan Africa (SSA) produces a mean of 22.63 million tonnes sweetpotato annually from an estimated area of 3.80 million hectares (FAOSTAT, 2017). In SSA sweetpotato is cultivated as a food security crop. It is a highly preferred crop by smallholder farmers owing to its ability to grow under marginal soil and dryland environmental conditions yet attaining higher yield per unit area compared to rice (*Oryza sativa*), wheat (*Triticum aetsivum*), maize (*Zea mays*) and cassava (*Manihot esculenta*) (Schafleitner et al., 2010). The crop is early maturing (3 to 4 months) hence able to escape drought under short rainfall condition.

Tanzania is amongst the top 5 leading world producers of sweetpotato (FAOSTAT, 2017). In the country sweetpotato is cultivated on an approximately 690 239.40 ha of agricultural lands with a mean national yield of 4.62 t ha^{-1} (FAOSTAT, 2017). Sweetpotato is cultivated in almost all agro-ecological zones in Tanzania (Kapinga et al., 1995; Ngailo et al., 2016). It is a vital food crop in the country after maize, rice and cassava (Tairo et al., 2008). Sweetpotato is cultivated under mono-cropping or inter-cropping systems. Typically, it is intercropped with cassava, maize, beans, cowpea and ground nuts. Due to postharvest deterioration and a lack of post-harvest storage facilities most sweetpotato farmers in the country practice sequential harvesting of storage roots, while leaving a considerable proportion of the produce in the field (Tairo et al., 2008; Ngailo et al., 2016). Despite the importance of sweetpotato in food and nutrition security in Tanzania, production and productivity of the crop is affected by an array of constraints. The major constraints contributing to low yields or quality losses include biotic and abiotic stresses, and socio-economic factors (Kapinga et al., 1995; Kulembeka et al., 2005; Ndunguru and Kapinga, 2007; Tairo et al., 2008; Ngailo et al., 2016; Kagimbo et al., 2017).

Constraints to sweetpotato production

Biotic constraints

Sweetpotato is vulnerable to damages caused by biotic factors such as pests (sweetpotato weevils and vertebrates) and diseases (mainly viruses) (Kapinga et al., 2009; Schafleitner et al., 2010; Ngailo et al., 2013). Sweetpotato yield loss due to weevils can reach up to 98% in susceptible varieties (Stathers et al., 1999; Lebot, 2009; Anyanga et al., 2013). Sweetpotato weevils including *Cylas puncticollis* Boheman and *C. brunneus* Fabricius are the major pests of the crop in SSA, whereas *C. formicarius* is the major production constraint in the Americas and Asia (Smit et al., 2001; Anyanga et al., 2017). Adult *Cylas* spp. feed on the storage root surface, leaves and epidermis of the vines, whereas the larvae (which are the most destructive stage) tunnel into the storage root and feed on the inside tissue. Infested storage roots produce bitter toxins and tarpenoids in response to weevil infestation reducing the quality of the storage roots for domestic use or market (Muyinza et al., 2012). Weevil infestation tend to peak under dry conditions because weevils become active and get access to the storage roots through cracked soils (Reynolds et al., 2015). Early planting and harvesting, crop rotation, hilling up, field sanitation, chemical treatment and flooding are some of the recommended weevil control measures (Stathers et al., 2003; Muyinza et al., 2012; Anyanga et al., 2017).

Amongst sweetpotato diseases, sweetpotato virus disease (SPVD) causes significant yield loss of 56 to 98% (Mukasa et al., 2003; Ndunguru and Kapinga, 2007). More than 15 different types of virus have been identified to cause SPVD in SSA and Asia (Ndunguru and Kapinga, 2007; Reynolds et al., 2015). SPVD causes stunted growth of the crop, reduces the storage time of the root in the field and after harvest (Kapinga et al., 2009). SPVD can be managed through the use of healthy planting material from symptomless plants or the use of virus free vines to reduce inoculum.

Other biotic factors affecting sweetpotato production in SSA are vertebrate pests which include moles (*Talpidae* family), wild pigs (*Sus scrofa*), porcupines (*Erethizontidae* family), rats (*Rattus* spp.), monkeys (*Primates* order) and hippopotamus (*Hippopotamus amphibious*) in areas near lakes and rivers (Kulembeka et al., 2005). In Tanzania farmers use various techniques to manage vertebrate pests such as trapping, hunting and use of repellent shrubs locally referred to as ‘intwitwi’ (Kapinga et al., 1995).

Abiotic constraints

The major abiotic constraints to sweetpotato production include drought and low soil fertility (Tairo et al., 2008; Reynolds et al., 2015). Farmers in East Africa considered drought tolerance as the main preferred trait in sweetpotato production (Fuglie, 2007). Drought conditions are associated with high

weevil infestation (Anyanga et al., 2013) and shortage of planting material (Mbithe et al., 2016) and reduced yields (Rukundo et al., 2013). Low soil fertility is associated with reduced sweetpotato yields because smallholder farmers rarely use inorganic fertilizers. Under wetland sweetpotato production systems some farmers incorporate organic residues (Reynolds et al., 2015).

Socio-economic constraints

Socio-economic constraints affecting sweetpotato production include shortage of planting material, limited access to improved varieties with pest and disease resistance, and poor market access, among others, (Kapinga and Carey, 2003; Engoru et al., 2005; Gibson et al., 2008). Kapinga and Carey (2003) reported that poor consumer acceptance of improved sweetpotato cultivars was attributed to low starch content, infestation by pests and diseases and poor taste. This has led to continuous use of landraces by farmers. This can be partly solved by participatory plant breeding involving farmers in setting breeding goals and selecting their preferred traits in potential varieties (Gibson et al., 2008). There is a lack of processing and storage facilities of sweetpotato harvests which is one of the overriding constraints for wide production and adoption of the crop in SSA (Engoru et al., 2005).

There is low investment by national research programs in sweetpotato research and development in SSA. This is the main cause of the limited breeding efforts in releasing varieties with pest and disease resistance (Kapinga and Carey, 2003). Sweetpotato breeding program in Tanzania is in its developmental stage. Thus far there are limited number of improved sweetpotato cultivars released to farmers in the country. The slow release of cultivars by breeders and poor extension services has led to limited availability and distribution of improved sweetpotato cultivars. Hence farmers still rely on their local landraces which are low yielding with low dry matter content (Fuglie, 2007).

Problem statement

The mean storage root yield of sweetpotato in Tanzania is 4.62 t ha^{-1} which is far below the potential productivity of the crop varying from 15 to 23 t ha^{-1} (Sebastiani et al., 2007). Sweetpotato weevils are key pests of the crop causing significant losses. Field sanitation, early planting and early harvesting are some of the recommended cultural practices to minimise losses associated with weevil infestation which peaks up during the dry season. Chemical control is another control option against weevils but it is unaffordable to small-scale farmers and this approach is not environmentally friendly. Cultural practice such as early planting is a difficult weevil management approach for many farmers due to shortage of planting materials during the onset of rainfall. Early harvesting is also a challenge since farmers practice sequential and piecemeal harvesting to minimise post-harvest losses. Chemical treatment is less effective because the juvenile weevils develop in roots and vines (Lebot, 2009).

Breeding sweetpotato varieties with durable resistance to weevils is advocated as an economic and sustainable strategy to control weevils under smallholder production systems (Muyinza et al., 2012; Anyanga et al., 2013). However, weevil resistance varieties are yet to be developed and released in Tanzania.

Genetic diversity present in a breeding population is vital for selecting promising genotypes with desirable and complementary traits. Thus far there is no report on the genetic diversity of the crop using germplasm collections from western Tanzania. Recently, the existence of sweetpotato varieties with reasonable level of resistant to weevils has been reported. This indicates that more resistance varieties can possibly be selected among the local landraces. So far Tanzania's sweetpotato germplasm collections have not been effectively screened for weevil resistance. Farmers have their own selection criteria for sweetpotato varieties such as high storage root yield and dry matter content; neglect of which in plant breeding programs can lead to rejection of the developed varieties. Therefore this study seeks to develop sweetpotato cultivars resistant to *Cylas* spp. and with improved dry matter content, yield and yield-related traits.

Overall objective

The overall objective of this study was to contribute to the development of improved sweetpotato cultivars that are both resistant to *Cylas* spp. and have high dry matter content, yield and yield-related traits.

Specific objectives

The specific objectives of the study were:

i To identify farmers' perceptions on sweetpotato weevil damage, production constraints and criteria used to select and grow the best sweetpotato varieties in western Tanzania.

ii To determine the variation among Tanzanian grown sweetpotato germplasm for dry yield and yield related traits

iii To asses Tanzanian sweetpotato germplasm for resistance to weevils in western Tanzania.

iv To determine inheritance of weevil resistance, yield and yield related traits in newly developed sweetpotato clones.

Hypotheses

The main hypotheses of the study were:

i. Farmers in the western Tanzania have no varied criteria for sweet potato selection, different priorities for sweetpotato production and constraints to sweetpotato production.

ii. Genetic diversity does not exists among sweetpotato germplasm in western Tanzania for yield and yield-related traits and dry matter content.

iii. A source of resistance against *Cylas* spp. does not exist among sweetpotato landraces grown in Tanzania.

iv. Inheritance of *Cylas* spp. resistance and dry matter content in sweetpotato is not controlled by both additive and non-additive gene action.

Thesis outline

This thesis consists of six distinct chapters (Table 0.1) reflecting a number of activities related to the above-mentioned objectives. Chapters 2 to 5 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 Crop Science Journal system of referencing. This is the dominant 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 3 has been published in the journal of Acta Agriculturae Scandinavica, Section B - Soil & Plant Science; Chapter 2 has been published in the Journal of Crop Improvement and Chapter 5 is under review in Euphytica.

Table 0.1. Outline of this thesis.

Chapter	Title
-	Introduction to thesis
1	A review of the literature
2	Farmers' perception on sweetpotato weevil damage, production constraints and variety preferences in western Tanzania
3	Variations of sweetpotato germplasm collections for yield and yield-related traits in western Tanzania
4	Screening of sweetpotato germplasm collections for sweetpotato weevil (*Cylas* spp.) resistance in Tanzania
5	Combining ability, gene action and heritability of weevil resistance, storage root yield and yield-related traits in sweetpotato
6	An overview of research findings

References

Anyanga, M.O., H. Muyinza, H. Talwana, D.R. Hall, D.I. Farman, G.N. Ssemakula, R.O.M. Mwanga and P.C. Stevenson. 2013. Resistance to the weevils *Cylas puncticollis* and *Cylas brunneus* conferred by sweetpotato root surface compounds. Journal of Agricultural and Food Chemistry 61: 8141-8147.

Anyanga, M.O., B. Yada, G.C. Yencho, G.N. Ssemakula, A. Alajo, D.I. Farman, R.O.M. Mwanga and P.C. Stevenson. 2017. Segregation of hydroxycinnamic acid esters mediating sweetpotato weevil Resistance in storage roots of Sweetpotato. Frontiers in Plant Science 8. doi:10.3389/fpls.2017.01011.

Burri, B.J. 2011. Evaluating sweet potato as an intervention food to prevent vitamin A deficiency. Comprehensive Reviews in Food Science and Food Safety 10: 118-130.

Clark, C.A., J.A. Davis, J.A. Abad, W.J. Cuellar, S. Fuentes, J.F. Kreuze, R.W. Gibson, S.B. Mukasa, A.K. Tugume and F.D. Tairo. 2012. Sweetpotato viruses: 15 years of progress on understanding and managing complex diseases. Plant Disease 96: 168-185.

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

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

FAOSTAT. 2017. Food and Agriculture Organisation of the United Nations: Crop production data. FAOSTAT Division, Rome.

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

Gibson, R.W., E. Byamukama, I. Mpembe, J. Kayongo and R.O. Mwanga. 2008. Working with farmer groups in Uganda to develop new sweet potato cultivars: decentralisation and building on traditional approaches. Euphytica 159: 217-228.

Kagimbo, F.M., H. Shimelis and J. Sibiya. 2017. Diversity assessment of sweetpotato germplasm collections for yield and yield-related traits in western Tanzania. Acta Agriculturae Scandinavica, Section B — Soil & Plant Science: 1-9. doi:10.1080/09064710.2017.1372516.

Kapinga, R. and E. Carey. 2003. Present status of sweetpotato breeding for eastern and southern Africa. Sweetpotato post-harvest Assessment: Experiences from East Africa. Chatham, United Kingdom. NRI/CPHP/DFID/CIP/Ministry of Agriculture. Natural Resources Institute: The University of Greenwich. ISBN 0 859554: 2.

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.E., P.T. Ewell, S. Jeremiah and R. Kileo. 1995. Sweetpotato in Tanzanian farming and food systems: implications for research. International Potato Center, Tanzanian Ministry of Agriculture, Nairobi and Dar-Es-Salaam.

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

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.

Lebot, V. 2009. Tropical root and tuber crops: cassava, sweet potato, yams and aroids. CABI, Wallingford

Mbithe, M.J., R. Steven, S. Agili, M.B. Kivuva, W.F. Kioko and E. Kuria. 2016. Morphological Characterisation of Selected Ugandan Sweet potato (*Ipomoea batatas* L) Varieties for Food and Feed. Phylogen Evolution Biology 4. doi:10.4172/2329-9002.1000163.

Mukasa, S.B., P.R. Rubaihayo and J.P. Valkonen. 2003. Incidence of viruses and virus like diseases of sweetpotato in Uganda. Plant Disease 87: 329-335.

Muyinza, H., H.L. Talwana, R.O.M. Mwanga and P.C. Stevenson. 2012. Sweetpotato weevil (*Cylas* spp.) resistance in African sweetpotato germplasm. International Journal of Pest Management 58: 73-81.

Mwanga, R., B. Odongo, C. Niringiye, R. Kapinga, S. Tumwegamire, P. Abidin, E. Carey, B. Lemaga, J. Nsumba and D. Zhang. 2007. Sweetpotato selection releases: lessons learnt from Uganda. African Crop Science Journal 15: 11 - 23.

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.

Nelles, W. 2009. Sweetpotato Education, Research and Capacity Development through a CIP-Orissa Learning Site. CTCRI, Bhubaneswar, Orissa, India.

Ngailo, S., H. Shimelis, J. Sibiya and K. Mtunda. 2013. Sweet potato breeding for resistance to sweet potato virus disease and improved yield: Progress and challenges. African Journal of Agricultural Research 8: 3202-3215.

Ngailo, S., H.A. Shimelis, J. Sibiya and K. Mtunda. 2016. Assessment of sweetpotato farming systems, production constraints and breeding priorities in eastern Tanzania. South African Journal of Plant and Soil 33: 105-112.

Reynolds, T.W., S.R. Waddington, C.L. Anderson, A. Chew, Z. True and A. Cullen. 2015. Environmental impacts and constraints associated with the production of major food crops in Sub-Saharan Africa and South Asia. Food Security 7: 795-822.

Rukundo, P., H. Shimelis, M. Laing and D. Gahakwa. 2013. Storage root formation, dry matter synthesis, accumulation and genetics in sweet potato. Australian Journal of Crop Science 7: 2054-2061.

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. doi.org/10.1186/1471-2164-11-604.

Sebastiani, S., 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. *8th African Crop Science Society Conference*, El-Minia, Egypt, 27-31 October 2007.

Smit, N.E.J.M., M.C.A. Downham, P.O. Laboke, D.R. Hall and B. Odongo. 2001. Mass-trapping male Cylas spp. with sex pheromones: a potential IPM component in sweetpotato production in Uganda. Crop Protection 20: 643-651.

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

Stathers, T.E., D. Rees, S. Kabi, L. Mbilinyi, N. Smit, 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 sweet potato [*Ipomoea batatas* (L.) Lam.] germplasm collection from Tanzania. African Journal of Plant Science 2: 77-85.

CHAPTER 1 REVIEW OF THE LITERATURE

Abstract

Sweetpotato (*Ipomoea batatas* [L.] Lam.) is an important food crop ranking seventh globally and fifth in developing countries. The crop is grown for food, source of cash incomes, feed and industrial raw material for starch, alcohol and biofuel extraction. Weevil (*Cylas* spp.) infestation is one of the main constraints to sweetpotato production and productivity globally. Cultural practice and chemical control against the weevil are less effective. The use of sweetpotato varieties with durable resistance to weevils is advocated as the best strategy to control the pest. Yield, yield components and dry matter content are some of the key farmer's selection criteria for sweetpotato varieties which are the ultimate determinants of cultivar adoption. This review highlights the economic importance of sweetpotato, constraints limiting its production and productivity with emphasis on sweetpotato weevils. The review also covers the overall challenges and successes in sweetpotato breeding in general and in weevil resistance breeding in particular. Lastly, factors affecting adoption of newly developed sweetpotato varieties by farmers are presented. Information presented in this review can be a useful reference in breeding sweetpotato varieties with weevil resistance and enhanced storage root yields incorporating farmers preferred traits.

Keywords: *Cylas spp*., resistance breeding, sweetpotato, weevils.

1.1 Introduction

Sweetpotato (*Ipomoea batatas* (L.) Lam.; 2n=6x=90) is a dicotyledonous herbaceous crop. It has perennial growth habit but cultivated as an annual crop. Sweetpotato belongs to the family *Convolvulacea*, genus *Ipomoea* and section *Batatas*. About 12 other species belong to section *batatas* (Loebenstein and Thottappilly, 2009). There are about 500 species in the genus *Ipomoea* but *I. batatas* is the only domesticated species (Austin and Huáman, 1996). The origin of sweetpotato is still debatable. Ugent et al. (1982) reported that sweetpotato could have originated from the Chilca Canyon of Peru supported by archaeological evidence from dried roots. Woolfe (1992) postulated that sweetpotato could have originated in tropical America where it was domesticated over 5000 years ago. However, most of the literature supports Central America as the primary centre of diversity and centre of origin of the crop especially areas encompassing southern Mexico, Central America and northern South America (Onwueme, 1978; Jones et al., 1986; Loebenstein and Thottappilly, 2009). Detailed genomic analysis indicated that sweetpotato collections from Central America showed extensive genetic diversity supporting the proposed centre of diversity of the crop (Huang and Sun, 2000).

Sweetpotato is an important food crop ranking seventh globally. In developing countries it is the fifth important crop next to rice (*Oryza sativa*), wheat (*Triticum aetsivum*), maize (*Zea mays*) and cassava (*Manihot esculenta*) (Elameen et al., 2008; Nelles, 2009). The average global sweetpotato production from 2010 to 2014 was 106.60 million tonnes of which Asia and Africa produced 76.70% and 19.10%, respectively, while the rest of the world produced 4.20% (FAOSTAT, 2017). In sub-Saharan Africa (SSA), sweetpotato is grown on about 2.1 million ha and with annual production of 9.9 million tonnes storage roots (Anyanga et al., 2013). Three countries in SSA (Nigeria, Tanzania and Uganda) are amongst the top five largest world producers of sweetpotato (Table 1.1). In SSA, sweetpotato is grown as a food security crop and highly preferred by smallholder farmers due to its ability to grow under low rainfall condition and marginal soils yet attaining relatively higher yields per unit area (Schafleitner et al., 2010).

Table 1.1. World largest sweetpotato producing countries from 2010 to 2014.

Region/country	Area harvested (ha)	Total production (tonnes)	Productivity (tonnes/ha)
World	8 366 704.80	106601602	12.52
Africa	3 803 553.20	22630750	5.27
China	3 420 382.00	72 512 099.20	21.20
Nigeria	1 375 908.20	3 596 911.60	2.62
Tanzania	690 239.40	3 197 336	4.62
Indonesia	171 219.40	2 296 986.60	13.51
Uganda	520 737.60	2 183 400	4.17
Mozambique	65 900.20	335664	22.20
Vietnam	141 033.60	1 373 433.40	9.77
Ethiopia	57 482.40	1 359 171.60	24.79
United States of America	50 309.20	1 194 400	23.74
Angola	154 006.20	1 161 044.8	7.38

Source: FAOSTAT (2014)

Sweetpotato is used for food, source of cash incomes, and feed in SSA (Fuglie, 2007). The roots are rich in carbohydrates, starch, sugars, pectin and cellulose making up to 90% of the root dry weight (Lebot, 2009). The purple-fleshed sweetpotato contains high antioxidant levels of anthocyanin, a natural pigment which gives root flesh purple colour while the orange-fleshed sweetpotato varieties (OFSPs) contain high levels of β-carotene that is a precursor of vitamin 'A' useful in combating vitamin A deficiency in humans (Mwanga et al., 2007; Burri, 2011). Storage roots are used for food in various forms such as fried chips, boiled roots or baked products (Engoru et al., 2005b). Young and succulent leaves of the crop are used as leaf vegetable. In some instances the entire canopy of the crop can be used as fodder for livestock (Woolfe, 1992). Sweetpotato roots are also used as industrial raw material for starch and alcohol extraction (Schafleitner et al., 2010; Clark et al., 2012). The crop's ability to produce high amount of starch makes it an ideal candidate in the biofuel industry. Extracted starch can be fermented and converted into ethanol (Grüneberg et al., 2009; Cervantes-Flores et al., 2011).

In Tanzania sweetpotato is an important subsistence crop cultivated in almost all agro-ecological zones (Kapinga et al., 1995; Ngailo et al., 2016). It is an important food crop next to maize, rice and cassava (Tairo et al., 2008). In the country sweetpotato is cultivated on approximately 0.69 million ha with a mean yield of 4.62 t ha^{-1} (FAOSTAT, 2017). The crop is grown both in a mono-crop and inter-crop systems with cassava, maize, beans, cowpea and ground nuts. Given the high degree of postharvest perishability of sweetpotato storage roots, most farmers practice sequential harvesting leaving a considerable proportion of the produce in the field (Kapinga et al., 1995; Tairo et al., 2008; Ngailo et al., 2016).

In Tanzania sweetpotato production and productivity is affected by a range of constraints including biotic, abiotic and socio-economic factors. The current national yield of the crop is 4.62 t ha^{-1} which is far below potential yields of 15 to 23 t ha^{-1} (Sebastiani et al., 2007). Sweetpotato weevil infestation caused by the sweetpotato weevils (*Cylas* spp.) is one of the main biotic constraints causing yield losses in Tanzania. Agronomic practices such as field sanitation, early planting and early harvesting, chemical control are some of the options used by farmers to manage sweetpotato weevils. However, cultural practices are less effective and chemical control method is expensive and not an environmentally friendly approach (Stathers et al., 2003; Lebot, 2009; Muyinza et al., 2012; Anyanga et al., 2017). Breeding sweetpotato varieties with durable resistance to weevils is advocated as the best strategy to control weevils (Muyinza et al., 2012; Anyanga et al., 2013). However, weevil resistant varieties are yet to be developed and released in Tanzania. The objective of this review was to highlight the economic importance of sweetpotato, constraints limiting its production and productivity with emphasis on sweetpotato weevils. The review also covers the overall challenges and success in sweetpotato breeding in general and in weevil resistance breeding in particular. Lastly, factors affecting the adoption of newly developed sweetpotato varieties by farmers are presented. Information presented in this review can be a useful reference in breeding sweetpotato varieties with weevil resistance and enhanced storage root yields incorporating farmers' needs and preferences.

.

1.2 Constraints to sweetpotato production

1.2.1 Biotic constraints

Sweetpotato is vulnerable to damages caused by biotic factors such as pests (sweetpotato weevils and vertebrates) and diseases (viruses) (Kapinga et al., 2009; Schafleitner et al., 2010; Ngailo et al., 2013). Sweetpotato weevils including *Cylas puncticollis* Boheman and *C. brunneus* Fabricius are the major pests of the crop in SSA, whereas *C. formicarius* is the major production constraint in the Americas and Asia (Smit et al., 2001; Anyanga et al., 2017). Figure 1.1 presents an example of *Cylas* spp (*Cylas puncticollis*). Adult *Cylas* spp. feed on the storage root surface, leaves and epidermis of the vines, whereas the larvae (which are the most destructive stage) tunnel into the storage root and feed on the inside tissue. Infested storage roots produce bitter toxins and terpenoids in response to weevil infestation reducing the quality of the storage roots for domestic use or market (Muyinza et al., 2012). Weevil infestation tend to peak under dry conditions because weevils become active and get access to the storage roots through cracked soils (Reynolds et al., 2015). Sweetpotato yield loss due to weevils can reach up to 98% in susceptible varieties (Stathers et al., 1999; Lebot, 2009; Anyanga et al., 2013). Early planting and harvesting, crop rotation, hilling up, field sanitation, chemical

treatment and flooding are some of the recommended weevil control measures (Stathers et al., 2003; Muyinza et al., 2012; Anyanga et al., 2017).

Amongst sweetpotato diseases, sweetpotato virus disease (SPVD) causes the most yield loss ranging from 56-98% (Mukasa et al., 2003; Ndunguru and Kapinga, 2007). More than 15 different types of viruses have been identified to cause SPVD in SSA and Asia (Ndunguru and Kapinga, 2007; Reynolds et al., 2015). SPVD causes stunted growth of the crop, reduces the storage time of the root *in situ* (in the field) and after harvest (*ex situ*) (Kapinga et al., 2009). SPVD can be managed through the use of healthy planting material from symptomless plants or the use of virus free vines to reduce inoculum.

Other biotic factors affecting sweetpotato production in SSA are vertebrate pests which include moles (*Talpidae* family), wild pigs (*Sus scrofa*), porcupines (*Erethizontidae* family), rats (*Rattus* spp.), monkeys (*Primates* order) and hippopotamus (*Hippopotamus amphibious*) in areas near lakes and rivers (Kapinga et al., 2003b; Kulembeka et al., 2005). In Tanzania farmers use various techniques to manage vertebrate pests such as trapping, hunting and use of repellent shrubs locally referred to as 'intwitwi' (Kapinga et al., 1995).

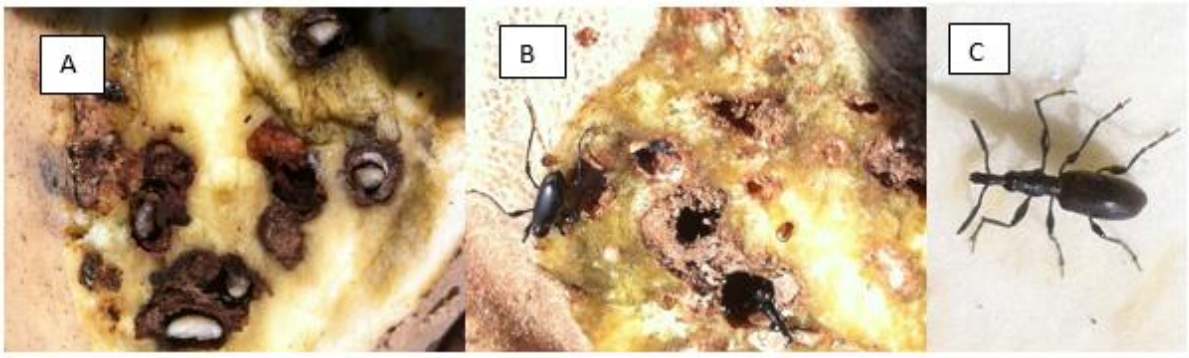

Figure 1.1. Photos of *Cylas Puncticollis* showing: (A) larvae tunneling in sweetpotato storage root, (B) adult insect emerging from storage root after pupa stage, (C) free walking adult insect.

1.2.2 Abiotic constraints

Abiotic constraints to sweetpotato production include drought and low soil fertility (Tairo et al., 2008; Reynolds et al., 2015). Farmers in East Africa considered drought tolerance as the main preferred trait in sweetpotato production (Fuglie, 2007). Drought conditions are associated with high weevil infestation (Anyanga et al., 2013) and shortage of planting material (Mbithe et al., 2016) and reduced yields (Rukundo et al., 2013). Low soil fertility is associated with reduced sweetpotato yields because

small-holder farmers rarely use inorganic fertilizers. Under wetland sweetpotato production systems some farmers incorporate organic residues (Reynolds et al., 2015).

1.2.3 Socio-economic constraints

Socio-economic constraints affecting sweetpotato production include shortage of planting material, limited access to improved varieties with pest and disease resistance, and poor market access (Kapinga and Carey, 2003; Engoru et al., 2005a; Gibson et al., 2008). Kapinga and Carey (2003) reported that poor consumer acceptance of improved cultivars was attributed to low starch content, infestation by pests and diseases and poor taste. This has led to continuous use of landraces by farmers. This can be partly solved by participatory plant breeding involving farmers in selecting their preferred traits in potential varieties (Gibson et al., 2008). There is a lack of processing and storage facilities of sweetpotato harvests which is one of the overriding constraints for wide production and adoption of the crop in SSA (Engoru et al., 2005a).

There is low investment by National Research Programs in sweetpotato research and development in SSA. This is the main cause of the limited breeding efforts in releasing varieties with pest and disease resistance (Kapinga and Carey, 2003). For instance, the sweetpotato breeding programme in Tanzania is in its developmental stage. Thus far there are a limited number of improved sweetpotato cultivars released to farmers in the country. The slow release of cultivars by breeders and poor extension services has led to limited availability and distribution of improved sweetpotato cultivars. Hence farmers still rely on their local landraces which are low yielding and have low dry matter content (Fuglie, 2007).

1.3 Sweetpotato weevils

1.3.1 Types of sweetpotato weevils and their distribution

Sweetpotato weevils belong to genus *Cylas* which includes three species namely: *C. puncticollis, C. brunneus and C. formicarius* (Skoglund and Smit, 1994). Adult stages of *C. puncticollis* and *C. formicarius* are easily distinguishable from each other because *C. puncticollis* is all black in its body and it is larger than the other two species, whereas *C. formicarius* has bluish-black abdomen and reddish-brown thorax. *C. brunneus* has a small body with no uniform colour and it is easily confused with *C. formicarius* (Skoglund and Smit, 1994; Smit, 1997). Weevils of *Cylas* spp. lay shinny round eggs which hatch into white curved legless larvae. The larvae then undergoes white pupation before developing into adults insect (Smit et al., 2001; Reynolds et al., 2015). The male adult are distinguished from female adults by having larger eye facets than females and having thread like cylindrical distal antennae, while females have club like distal antennae and small eye facets

(Skoglund and Smit, 1994; Kumano et al., 2008). *Cylas formicarius* is common in India, USA, south east Asia, Oceania and the Caribbean islands. In Africa *C. formicarius* has been reported only in the KwaZulu-Natal Province of South Africa and the coastal regions of Kenya. *Cylas puncticollis* and *C. brunneus* are widely spread in Africa only (Skoglund and Smit, 1994; Stathers et al., 2003; Anyanga et al., 2013; Anyanga et al., 2017).

1.3.2 Economic significance of weevils

Adult *Cylas spp*. feed on the epidermis of vines and leaves and on the surface of storage roots, while larvae tunnel into the vines and storage roots (Stathers et al., 2003; Kumano et al., 2008; Anyanga et al., 2017). The damage symptoms are the same for all *Cylas spp*. Under serious infestation the leaves may shrivel and die due to adult *Cylas* feeding on them. Feeding on storage root surface by adult *Cyla*s produces round punctures. Storage roots produce toxic terpenes as a response to damage by larvae rendering the roots unpalatable and unmarketable (Stathers et al., 2003). Tunnelling of the larvae into the vines deforms the vines by thickening and cracking leading to reduced translocation of water and minerals. Damages on leaves, vines and roots by weevils results in the rediction of number and size of storage roots (Smit, 1997; Anyanga et al., 2017). The damage on storage roots by weevil larvae, and terpenes accumulation in storage roots as a response to weevil infestation results in yield losses which can reach up to 98% (Anyanga et al., 2017).

1.3.3 Sweetpotato weevil infestation in production fields

Sweetpotato weevil infestation in the fields peaks during the dry season (Stathers et al., 2003). This is associated with dryness of soils forming ground cracks and allowing weevil access to storage roots. The weevils can only reach the roots which are exposed or through soil cracks. Smit (1997) showed that male *C. brunneus* and *C. puncticolis* fly more than females. However it was not known whether flying is the dispersal mechanism or not. Smit (1997) reported that the larvae of *C. brunneus* tunnel deeper in the roots than *C. puncticolis*. Weevil's population grows four fold in roots than vines (Smit, 1997). Therefore, limiting weevil access to roots can keep weevil population and root damage significantly lower.

In determining the level of resistance of sweetpotato to weevils, test genotypes should be evaluated under high pest pressure. This will allow proper infestation and identification of promising genotypes with weevil resistance. Researchers use artificial field infestation using laboratory reared weevil populations for selection (Stathers et al., 2003; Muyinza et al., 2012). However, the natural population of weevils can be used under hotspot fields for effective evaluation and selection of sweetpotato

genotypes for weevil resistance without needing artificial infestation (Stathers et al., 2003). Activity of artificially infested weevils is highly affected by environmental factors such as rainfall and excessively low or high temperature conditions (Stathers et al., 2003).

1.3.4 Control options of sweetpotato weevils

There are several techniques used to control sweetpotato weevils. These include use of cultural methods, resistant and/or tolerant cultivars, chemicals, sex pheromone traps and biological control agents (Skoglund and Smit, 1994; Kumano et al., 2008; Okonya et al., 2014). The use of cultural control methods include field hygiene where by crop residues and volunteer plants are removed from the field; early planting and harvesting to avoid dry periods; soil ridging-up to cover the storage roots and soil cracks, use of clean planting materials, planting in uninfested fields, crop rotation and removal of alternate weevil hosts such as *Ipomoea* weeds (Skoglund and Smit, 1994; Kumano et al., 2008; Anyanga et al., 2017). Early planting is a difficult cultural practice for many farmers due to the shortage of planting materials at the onset of rainfall. Early harvesting is also a challenge since farmers practise sequential and piecemeal harvesting to limit post-harvest losses (Kapinga and Carey, 2003; Lebot and Bradshaw, 2010).

Chemical control options include the use of insecticides. Dipping of the planting material in carbofuran for 30 minutes before planting can control weevils for about 2 months post planting (Skoglund and Smit, 1994; Okonya et al., 2014). However, effectiveness of chemicals is very low for the following reasons: 1) weevils' larvae grow inside the storage roots hence less affected by chemicals, 2) chemicals are expensive therefore unaffordable by most small-holder farmers (Okonya et al., 2014; Hernández-Martínez et al., 2016) and 3) the use of chemicals are environmentally unfriendly.

Use of weevil resistant or tolerant cultivars reduces damage caused by sweetpotato weevils. Some sweetpotato genotypes have escape mechanism to reduce weevil infestation. This mechanism includes deep rooting which keeps roots away from weevils, producing thin storage roots which do not crack the soil and without exposing roots to weevils or by producing much foliage which shield the soil from the sun keeping it moist and reducing cracking thus keeping roots away from weevils (Talekar, 1987; Stathers et al., 2003). Some sweetpotato genotypes express active chemical resistance mechanism. These genotypes have chemicals in their root latex and root surface which are toxic to weevil larvae and repellent to adult weevils (Stevenson et al., 2009; Muyinza et al., 2012; Anyanga et al., 2013; Anyanga et al., 2017).

Biocontrol agents are used to control weevil. The fungus (*Beauveria bassiana)* has been used as a biological control agent by infecting adult weevils. Nematodes (*Heterorhabditid spp.* and *Steinernema spp*.) are used as biological control agents with parasitizing effect against weevil larvae (Skoglund

and Smit, 1994; McQuate, 2014). Pheromones and colour traps are the most widely used control methods in the Americas and Asia. Sex pheromones released by female weevils are used to trap male weevils. Recently it was reported that male *C. furmicarius* are 5 times more attracted to traps baited sex pheromones and a green light provided by a solar-powered light-emitting diode (LED) system (McQuate, 2014).

In other cases, sterile insect techniques (SIT) are used to reduce weevil population. Sterile male weevils are produced using Gama irradiation (Kumano et al., 2008). Weevil production is significantly reduced when these irradiated male weevil mate with wild female (non-mutated) weevils. However, it has been reported that the sexual activity of mutant males was significantly reduced after one week of irradiation (McQuate, 2014).

1.4 Constraints to sweetpotato breeding

Efforts have been made in developing improved sweetpotato cultivars by National Research Institutions and the Consultative Group on International Agricultural Research (CGIAR) organizations (Kapinga and Carey, 2003; Grüneberg et al., 2009; Anyanga et al., 2017; Rukundo et al., 2017). Progress in breeding of sweetpotato can be hindered by the heterozygous nature of sweetpotato, self-incompatibility or cross-incompatibility, reduced flowering ability, and polyploidy nature of sweetpotato (2n=6x=90) (Jones, 1965; Martin, 1988; Grüneberg et al., 2009; Loebenstein and Thottappilly, 2009; Lebot and Bradshaw, 2010; de Nettancourt, 2013).

1.4.1 Flower biology of sweetpotato

Understanding the flower morphology and flowering behaviour of a crop is vital for successful crosses (Acquaah, 2012). Sweetpotato flower is funnel shaped where by sepals and petals are joined at the base. The flowers have five stamens with anthers of varying height attached to the base of the corolla (Lebot and Bradshaw, 2010). Stigma position relative to the height of the stamen is of three types: inserted stigma: this is when the stigma is shorter than the stamen. Same height: this is when the stigma is of the same height with the stamen. Exerted: this is when the stigma is longer than the stamen (Huaman, 1991). Hand pollination is easier with exerted stigma than inserted and same height because with the former the stigma is easily identified.

Flowering in sweetpotato varies depending on sweetpotato genotype and season (day length) (Martin, 1988; Woolfe, 1992; Huaman, 1999; Lebot and Bradshaw, 2010). Most sweetpotato genotypes require short day length to flower, while some flower readily in any day length and some genotypes do not flower at all (Martin, 1988). In temperate countries, sweetpotato genotypes which do not flower easily are induced to flower with increased temperatures, and relative humidity, shortening or

increasing day length (Miller, 1937; Lebot and Bradshaw, 2010; de Nettancourt, 2013). Sweetpotato flowers open early before sunrise and close in the evening. The stigma remains receptive in the morning hours before noon, the best time for pollination (Jones, 1965; Loebenstein and Thottappilly, 2009).

1.4.2 Self- and cross-incompatibility in sweetpotato

Self-incompatibility (SI) is a major mechanism by which hermaphrodite plants under go cross- -fertilization. Self-incompatibility is a condition in plants where by a normal and viable pollen from a flower is not functional on a normal and viable stigma of the same flower thus failing to set a seed (Acquaah, 2012). There are two known types of SI which are heteromorphic SI and homomorphic SI (Acquaah, 2012; de Nettancourt, 2013). Heteromorphic SI is where by a plant bears a flower with a style having different length with stamens, while homomorphic SI is where by a pollen genotype determine fertilization (de Nettancourt, 2013). Homomorphic SI is further divided into two types: Gametophytic SI: in this type the ability of a pollen to function is determined by its own genotype and not by the plant that produces it. The second is Sporophytic SI where by the ability of a pollen to function is determined by the plant that produces it (Acquaah, 2012). SI in sweetpotato is reported to be homomorphic-sporophytic type (Kowyama et al., 2000).

Self- or cross-incompatibility is a major challenge in sweetpotato breeding (Gasura et al., 2010) by limiting the speed and success to sweetpotato improvement. About one third of parental combinations in sweetpotato are cross incompatible (Grüneberg et al., 2009). Some parental combinations exhibiting complementary trait may belong to the same incompatible group thus limiting desirable trait combinations (Gurmu et al., 2013). In order to get a desirable trait combination, compatible parents need to be identified. This can only be done by conducting several controlled crosses rather than allowing open pollination (Vimala and Hariprakash, 2011).

1.4.3 Ploidy level in sweetpotato

Ploidy is defined as the number of complete chromosome sets in the cell nucleus, whereas polyploidy refers to a condition where by an individual possesses one or more sets of homologous chromosome in excess of the normal two sets (Schlegel, 2010). Individuals can be diploid, triploid, tetraploid possessing 2x, 3x, 4x sets of homologous chromosomes, respectively. Polyploidy in sweetpotato is crucial because it affects the performance of genotypes and the relationship between the parent and their offspring (Grüneberg et al., 2009). Sweetpotato is an auto-polyploid (2n = 6x = 90) having six alleles at each locus. This feature results in a remarkable genetic variation due to dominance and epistasis (Vimala and Hariprakash, 2011; Acquaah, 2012). Furthermore, heterosis which to a large extent determines the performance of sweetpotato is due to parental species and inter-gene pool crossing within a species (Cervantes-Flores et al., 2011). Therefore, the ploidy level, heterosis and

heterozygous nature of sweetpotato poses a considerable challenge in genetic studies of sweetpotato and selection of good parents for population improvement (Grüneberg et al., 2009; Cervantes-Flores et al., 2011).

1.5 Genetic diversity in sweetpotato

The centre of origin of sweetpotato is debatable. Tropical America is reported to be the centre of origin for sweetpotato because the crop has been domesticated there for over 5000 years ago (Woolfe, 1992; Austin and Huáman, 1996). Other scholars report Peru as the centre of origin for sweetpotato because archaeological evidence indicate that sweetpotato was domesticated in the Chilca Canyon of Peru over 8000 years ago (Ugent et al., 1982). However, most of the literature accepts Central America both as the primary centre of diversity and centre of origin of the crop especially the region encompassing southern Mexico, Central America and northern South America (Onwueme, 1978; Jones et al., 1986; Loebenstein and Thottappilly, 2009). The use of molecular markers also supported Central America as both as the primary centre of diversity and centre of origin of the crop (Huang and Sun, 2000). About 700 species of Ipomoea are known to exist and more than half of them are concentrated in Central America (Austin and Huáman, 1996). About 8000 cultivars and breeding populations of sweetpotato (*I. batatas*) and about 26000 accessions of other *Ipomoea* species are conserved across 83 gene banks worldwide (Rao et al., 1994).

From Central America, sweetpotato was introduced to Europe by Columbus and then later it was introduced to Asia and Africa by Portuguese and Spanish traders (Vaughan and Geissler, 1997). It is reported that sweetpotato was introduced in Tanzania by Portuguese and British (Kapinga et al., 1995). Over 100 different sweetpotato landraces are reported to exist in Tanzania (Kapinga et al., 1995; Tairo et al., 2008; Kagimbo et al., 2017). Considerable level of diversity exists within these landraces (Elameen et al., 2008; Tairo et al., 2008; Gwandu et al., 2012; Kagimbo et al., 2017). Tairo et al. (2008) using morphological characterization reported a genetic distance of 0.52 among sweetpotato accessions collected from Lake Zone, and Eastern Zone of Tanzania. Using simple sequence repeat markers, Gwandu et al (2012) reported a genetic distance of 0.55 among sweetpotato collections from Eastern, Southern and Lake zone of Tanzania. The collections from Western Tanzania and Lake Zone revealed a genetic distance of 0.54 using morphological descriptors (Kagimbo et al., 2017). In Tanzania there is a lack of well-characterised germplasm of sweetpotato. The genebanks available in the country are scattered among research and tertiary institutions and in most cases the collections are not representative of the national genepool of the crop (Kapinga et al., 1995; Elameen et al., 2008; Tairo et al., 2008).

1.6 Breeding for weevil resistance

Significant efforts have been made to breed for sweetpotato varieties resistant to sweetpotato weevil but with low success rate (Stathers et al., 2003; Grüneberg et al., 2009; Muyinza et al., 2012). The main challenge in weevil resistance breeding was the inconclusiveness of the reported level of resistance due to differences in weevil infestation among trials, locations, seasons and sometimes replications of the same cultivars (Stathers et al., 2003)

Weevil resistance can be classified as escape or active mechanism (Stathers et al., 2003; Muyinza et al., 2012). The following include escape mechanisms: deep rooting of storage roots that increases the distance to which weevils have to burrow to reach the roots thus reducing the weevil damage; high foliage yield protecting the soil from solar radiation and keeping moisture in the soil leading reduced soil crack and limiting weevil damage. Also, narrow storage roots do not cause soil cracks without being exposed to weevil damages than thicker root systems. Root shape, arrangement and time to maturity all contributing to escape mechanism (Talekar, 1987; Stathers et al., 2003).

In recent studies the following sweetpotato cultivars: New Kawogo, Dimbuka, Anamoyoto and Kyebagambire have been identified and reported to express resistance to *Cylas* spp. with active chemical based resistance mechanism (Stevenson et al., 2009; Muyinza et al., 2012; Anyanga et al., 2013). This type of resistance is attributed to high levels of esters of hydroxylcinnamic acid in root latex (Stevenson et al., 2009) and esters of caffeic and coumaric acid in epidermal and root surface of resistant varieties (Anyanga et al., 2013). These chemical compounds conferring resistance to *Cylas* spp. are reported to be toxic to *Cylas* spp. larvae but also repellent to adult *Cylas* spp. thus expressing active and quantifiable resistance which can be explored in breeding programs (Stevenson et al., 2009; Anyanga et al., 2013).

The use of transgenic sweetpotato expressing *Bacillus thuringiensis* proteins (Hernández-Martínez et al., 2016) is a recent approach to controlling weevils. Transgenic sweetpotato have been developed expressing Cry3Aa, Cry3Ca or Cry7Aa proteins which are toxic to *C. puncticollis* (Rukarwa et al., 2014). These Cry-proteins have been tested and reported to be safe to non-targeted organisms and thus ecologically friendly. The effectiveness of this breeding technology against weevils is still under investigation (Hernández-Martínezet al., 2016) and subject to various regulations.

1.7 Gene action and heritability of traits in sweetpotato

Heritability is a measure of the degree to which a phenotype is genetically influenced (Acquaah, 2012). Most economic traits in sweetpotato are quantitatively inherited and are also highly influenced by environmental conditions (Cervantes-Flores et al., 2011). Gene action controlling traits may be

additive or non-additive. Additive gene action upon which narrow sense heritability is based is important because it is transmitted to progeny. Plant breeders are interested in quantifying heritability because breeding gains are ensured with traits of high heritability. Phenotypic based selection and the response to selection are successful and reliable when the traits exhibit higher heritability (Acquaah, 2012).

Several studies have been undertaken to determine the inheritance of various traits in sweetpotato (Komaki et al., 1998; Cervantes-Flores, 2007; Courtney et al., 2008; Chiona, 2010; Balcha, 2015; Ngailo, 2015). Ngailo (2015) reported a narrow sense heritability (h^2) and broad sense heritability (H^2) of 0.1 and 0.98, respectively for total root number per plant. Lower h^2 (34.9%) and higher H^2 (96.9%) for root yield were reported by Chiona (2010). Lower heritability values of 19.0% (h^2) and 20.50% (H^2) were reported for dry matter content (Balcha, 2015). All these authors reported that both additive and non-additive gene actions played significant role in controlling the mentioned traits though additive gene actions played a bigger role than non-additive gene actions.

Heritability of 0.81 for resistance to sweetpotato weevils based on escape mechanism has been reported (Martin, 1988). Additive gene action has been reported to controlling the inheritance of chemical based weevil resistance (Anyanga et al., 2017).

1.8 Mating designs in sweetpotato breeding

A mating design is defined as a scheme used by breeders or geneticists to develop targeted cross combinations for a specific purpose (Acquaah, 2012). Mating designs allows plant breeders to determine the genetic control of various traits of interest and to create base populations for new breeding programmes. The following mating designs are widely used in plant breeding programmes: diallel, North Carolina Designs (NCD) such as NCD I and NCD II, bi-parental and polycross (Chahal and Gosal, 2002; Acquaah, 2012). The following are the most commonly used mating designs in sweetpotato breeding: diallel, NCD II and polycross.

1.8.1 Polycross mating design

A polycross is the natural inter-crossing of a group of plants in an isolated crossing block (Saladaga, 1989; Acquaah, 2012). It is the most suitable mating design for cross pollinated and vegetatively reproducing crops like forage grasses, sweetpotato, sugarcane and legumes. The polycross mating design requires parents which are arranged in a fashion which provides opportunity for each parent to be crossed with every other parent (Olesen, 1976; Morgan, 1988; Saladaga, 1989). In sweetpotato, pollination is performed naturally by insects especially bees. For a successful polycross mating design, it is crucial that all parents flower at the same time. However, this is not guaranteed. To

synchronize flowering, the late flowering genotypes are planted earlier than early flowering ones (Stuber, 1980).

Sweetpotato breeders have used the polycross mating design in their breeding programmes (Jones, 1965; Saladaga, 1989). The polycross mating design is advocated for sweetpotato breeding because it eliminates the need for tedious controlled hand crossing like in diallel and North Carolina mating designs. The polycross also overcomes the problem of poor seed set associated with hand crossing (Saladaga, 1989). However, the polycross mating design poses limitations in the genetic studies due to the following reasons: first the random mating of parents produces progenies which are half-sibs. This reduces the genetic gain by half and allows for only estimation of general combining ability (GCA) effects of female parents (Stuber, 1980; Morgan, 1988; Saladaga, 1989).

1.8.2 Diallel mating design

Diallel mating design is another design that has been successfully used in sweetpotato breeding. It is defined as a crossing scheme whereby all possible combinations among a set of parents are made (Griffing, 1956; Falconer and Mackay, 1996; Gallais, 2003; Acquaah, 2012). It is used to determine the specific combining ability (SCA) effect of crosses, GCA effect of parents, gene action, heterosis and maternal effect. Various studies have used diallel mating design in sweetpotato breeding (Hernandez and Miller, 1962; Martin, 1968; Ngailo, 2015). Diallel mating designs have been used successfully in studying the combining ability and inheritance of SPVD (Mwanga et al., 2002). Chiona (2010) used diallel mating design in studying the combining abilities and inheritances of beta carotene, dry mass content and fresh root yield of sweetpotato. Ngailo (2015) used diallel mating design to study the gene action and inheritance of resistance to SPVD and dry matter content in sweetpotato. The main limitation with diallel mating design is the numerous crosses involved compared to other mating designs especially with large number of parents (Hallauer et al., 2010).

1.8.3 North Carolina mating design II (NCD II)

North Carolina mating design II (NCD II) has been widely used in sweetpotato breeding. In NCD II each member of a group of parents used as male is mated to each member of another group of parents used as females (Acquaah, 2012). NCD II is used to estimate the GCA effect, SCA effect and gene action (additive and dominance) (Bernardo, 1965; Chahal and Gosal, 2002). The main features that distinguish NCD II from diallel designs is that diallel designs test for maternal effects by reciprocal crosses, whereas NCD II does not test for maternal effect by reciprocal crosses (Stuber, 1980; Hill et al., 1998). Using the NCD II the GCA for males and GCA for females can be directly estimated by

mean square for males and mean square for females, respectively. Likewise, the SCA can be directly estimated by male x female interaction (Hallauer et al., 2010). North Carolina Design II has been used in studying the inheritance of alternaria leaf petiole and stem blight, yield traits and combining abilities of sweetpotato genotypes (Sseruwu, 2012).

1.9 Participatory plant breeding

Farmers' involvement in plant breeding programmes is vital for final acceptance and adoption of new cultivars (Grüneberg et al., 2009). Farmers usually have their own traits and criteria which they consider important for selecting sweetpotato varieties. If their criteria and traits of interest for cultivars selection are not considered by the breeding program, they may reject the newly developed cultivars (Kapinga and Carey, 2003; Gibson et al., 2008). For instance, a team of researchers in Uganda listed 11 attributes they considered important in releasing the new sweetpotato cultivars; however, they were surprised by farmers who had 51 attributes for their landraces and released varieties (Gibson et al., 2008).

Good culinary quality traits preferred by most farmers in sub-Saharan Africa are high dry matter content, moderately sweet and with dry mouth feel (Grüneberg et al., 2009; Cervantes-Flores et al., 2011) and low fibre content. Studies conducted in Tanzania showed that the most important traits regarded by farmers in sweetpotato cultivars were: high root yield, culinary quality (low fibre content and high dry matter content), tolerance to pests and diseases and early maturity (Kapinga et al., 2003a). Therefore breeding programmes intending to release new varieties in the country should integrate these traits in their selections.

Farmers in Lake Zone of Tanzania rejected some newly developed sweetpotato varieties which had good agronomic traits like high yielding and tolerance to disease and pests and some were orange fleshed. The reason for rejection was low dry matter content and high fibre content (Kulembeka et al., 2005). Breeding programmes should have a clear understanding of farmer's criteria and trait of interest used to select varieties before developing and releasing new varieties to enhance acceptability and adoption rate. Participatory rural appraisal (PRA) is a multidisciplinary research tool useful to acquiring the information regarding farmer's criteria for cultivar selection (Chambers, 1994).

References

Acquaah, G. 2012. Principles of plant genetics and breeding 2nd ed. Wiley-Blackwell, Oxford USA.

Anyanga, M.O., H. Muyinza, H. Talwana, D.R. Hall, D.I. Farman, G.N. Ssemakula, R.O.M. Mwanga and P.C. Stevenson. 2013. Resistance to the Weevils *Cylas puncticollis* and *Cylas brunneus*

conferred by sweetpotato root surface compounds. Journal of Agricultural and Food Chemistry 61: 8141-8147.

Anyanga, M.O., B. Yada, G.C. Yencho, G.N. Ssemakula, A. Alajo, D.I. Farman, R.O.M. Mwanga and P.C. Stevenson. 2017. Segregation of Hydroxycinnamic Acid Esters Mediating Sweetpotato Weevil Resistance in Storage Roots of Sweetpotato. Frontiers in Plant Science 8. doi:10.3389/fpls.2017.01011.

Austin, D.F. and Z. Huáman. 1996. A synopsis of *Ipomoea* (Convolvulaceae) in the Americas. Taxon: 3-38.

Balcha, F.G. 2015. Breeding of sweetpotato for improvement of root dry matter and β-carotene contents in Ethiopia. PhD Thesis, University of KwaZulu-Natal, Pietermaritzburg.

Bernardo, R.N. 1965.Breeding for quantitative traits in plants. Stemma Press, Woodbury, Minnesota..

Burri, B.J. 2011. Evaluating sweet potato as an intervention food to prevent vitamin A deficiency. Comprehensive Reviews in Food Science and Food Safety 10: 118-130.

Cervantes-Flores, J., B. Sosinski, K. Pecota, R. Mwanga, G. Catignani, V.-D. Truong, R. Watkins, M. Ulmer, and G.C. Yencho. 2011. Identification of quantitative trait loci for dry-matter, starch, and β-carotene content in sweetpotato. Molecular Breeding 28: 201-216.

Cervantes-Flores, J.C. 2007. Development of a genetic linkage map and QTL analysis in sweetpotato. PhD Thesis, North Carolina State University, Raleigh, USA.

Chahal, G.S. and S.S. Gosal. 2002. Principles and procedures of plant breeding biotechnological and conventional approaches. Alpha Science International Ltd, Pangbourne, UK.

Chambers, R. 1994. Participatory rural appraisal (PRA): Challenges, potentials and paradigm. World Development 22: 1437-1454.

Chiona, M. 2010. Towards enhancement of B-carotene content of high dry mass sweetpotato genotypes in Zambia. PhD Thesis, University of KwaZulu Natal, Pietermaritzburg.

Clark, C.A., J.A. Davis, J.A. Abad, W.J. Cuellar, S. Fuentes, J.F. Kreuze, R.W. Gibson, S.B. Mukasa, A.K. Tugume and F.D. Tairo. 2012. Sweetpotato viruses: 15 years of progress on understanding and managing complex diseases. Plant Disease 96: 168-185.

Courtney, M., M. Mcharo, D. La Bonte and W. Gruneberg. 2008. Heritability Estimates for Micronutrient Compositionof Sweetpotato Storage Roots. Horticultural Science 43: 1382-1384.

de Nettancourt, D. 2013. Incompatibility in Angiosperms. Springer, Berlin Heidelberg.

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

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

Engoru, P., J. Mugisha and B. Bashaasha. 2005b. Tuber utilisation options among sweet potato producers in eastern Uganda. *African Crop Science Conference Proceedings*. Kampala, 5-9 December 2005, 7:715-720.

Falconer, D.S. and T.F.C. Mackay. 1996. Introduction to quantitative genetics. Clays Ltd., Great Britain

FAOSTAT. 2017. Food and Agriculture Organisation of the United Nations: Crop production data. FAOSTAT Division, Rome.

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

Gallais, A. 2003. Quantitative genetics and breeding methods in autopolyploid plants. Institut national de la recherche agronomique, Paris.

Gasura, E., A. Mashingaidze and S. 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., E. Byamukama, I. Mpembe, J. Kayongo and R.O. Mwanga. 2008. Working with farmer groups in Uganda to develop new sweet potato cultivars: decentralisation and building on traditional approaches. Euphytica 159: 217-228.

Griffing, B. 1956. A generalized treatment of the use of diallel crosses in quantitative inheritance. Heredity 10: 31-50.

Grüneberg, W., R. Mwanga, M. Andrade, J. Espinoza, S. Ceccarelli, E. Guimarães and E. Weltzien. 2009. Selection methods. Part 5: Breeding clonally propagated crops. Plant breeding and farmer participation. Food and Agriculture Oganization of the United Nations, Rome.p. 275-322.

Gurmu, F., S. Hussein and M. Laing. 2013. Self- and cross-incompatibilities in sweet potato and their implications on breeding. Australian Journal of Crop Science 7: 2074-2078.

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

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

Hallauer, A.R., M.J. Carena and J.D. Miranda Filho. 2010. Quantitative genetics in maize breeding. Springer, New York.

Hernández-Martínez, P., N.M. Vera-Velasco and B. Escriche. 2016. Unshared binding sites for Bacillus thuringiensis Cry3Aa and Cry3Ca proteins in the weevil Cylas puncticollis (Brentidae). Toxicon 122: 50-53.

Hernandez, T.P. and J.C. Miller. 1962. Self-and cross-incompatibilities in the sweet potato. *Proceedings of the American Society for Horticultural Science*, Beltsville.

Hill, J., C. Becker and A. Tigerstedt. 1998. Quantitative and ecological aspects of plant breeding. Chapman & Hall, London.

Huaman, Z. 1991. Descriptors for the characterization and evaluation of sweet potato genetic resources. CIP Lima, Perú. p. 331 - 355.

Huaman, Z. 1999. Botany, origin, evolution and biodiversity of the sweet potato. Sweet potato Germplasm Management. International Potato Center (CIP), Lima, Peru.

Huang, J. 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. Theoretical and Applied Genetics 100: 1050-1060.

Jones, A. 1965. A proposed breeding procedure for sweetpotato. Crop science 5: 191-192.

Jones, A., P. Dukes and J. Schalk. 1986. Sweet potato breeding. Breeding vegetable crops. Eastport: AVI: 1-35.

Kagimbo, F.M., H. Shimelis and J. Sibiya. 2017. Diversity assessment of sweetpotato germplasm collections for yield and yield-related traits in western Tanzania. Acta Agriculturae Scandinavica, Section B — Soil & Plant Science: 1-9. doi:10.1080/09064710.2017.1372516.

Kapinga, R. and E. Carey. 2003. Present status of sweetpotato breeding for eastern and southern Africa. Sweetpotato post-harvest Assessment: Experiences from East Africa. Chatham, United Kingdom. NRI/CPHP/DFID/CIP/Ministry of Agriculture. Natural Resources Institute: The University of Greenwich. ISBN 0 859554: 2.

Kapinga, R., S. Jeremiah, E. Rwiza and D. Rees. 2003a. Farmers criteria for selection of sweetpotato varieties, results from Tanzania. Chatham, United Kingdom.

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.E., P.T. Ewell, S. Jeremiah and R. Kileo. 1995. Sweetpotato in Tanzanian farming and food systems: implications for research. International Potato Center, Tanzanian Ministry of Agriculture, Nairobi and Dar-Es-Salaam.

Kapinga, R.E., S.C. Jeremiah, E.J. Rwiza, D. Rees and D. Rees. 2003b. Sweet potato postharvest assessment: experiences from East Africa. Chatham, United Kingdom.

Komaki, K., K. Katayama and S. Tamiya. 1998. Advancement of sweetpotato breeding for high starch content in Japan. Tropical agriculture 75: 220-223.

Kowyama, Y., T. Tsuchiya and K. Kakeda. 2000. Sporophytic Self-incompatibility in *Ipomoea trifida*, a Close Relative of Sweet Potato. Annals of Botany 85: 191-196.

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.

Kumano, N., D. Haraguchi and T. Kohama. 2008. Effect of irradiation on mating ability in the male sweetpotato weevil (Coleoptera: Curculionidae). Journal of Economic Entomology 101: 1198-1203.

Lebot, V. 2009. Tropical root and tuber crops: cassava, sweet potato, yams and aroids. CABI, Wallingford

Lebot, V. and J.E. Bradshaw. 2010. Root and tuber crops: handbook of plant breeding. Springer., New York.

Loebenstein, G. and G. Thottappilly. 2009. The sweet potato. Springer, Merced, Carlifornia.

Martin, F. 1988. Genetic and physiological basis for breeding and improving the sweet potato. In: L. Degras, editor. *Proceeding of the 7th international symposium on tropical root crops*. Paris, France. p. 749-761.

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

Mbithe, M.J., R. Steven, S. Agili, M.B. Kivuva, W.F. Kioko and E. Kuria. 2016. Morphological Characterisation of Selected Ugandan Sweet potato (*Ipomoea batatas* L) Varieties for Food and Feed. Phylogen Evolution Biology 4. doi:10.4172/2329-9002.1000163.

McQuate, G.T. 2014. Green Light Synergistally Enhances Male Sweetpotato Weevil Response to Sex Pheromone. Scientific Reports 4: 4499. doi:10.1038/srep04499.

Miller, J.C. 1937. Inducing the sweet potato to bloom and set seed. Journal of Heredity 28: 347-349.

Morgan, J.P. 1988. Polycross designs with complete neighbor balance. Euphytica 39: 59-63.

Mukasa, S.B., P.R. Rubaihayo and J.P. Valkonen. 2003. Incidence of viruses and virus like diseases of sweetpotato in Uganda. Plant Disease 87: 329-335.

Muyinza, H., H.L. Talwana, R.O.M. Mwanga and P.C. Stevenson. 2012. Sweetpotato weevil (*Cylas* spp.) resistance in African sweetpotato germplasm. International Journal of Pest Management 58: 73-81.

Mwanga, R., B. Odongo, C. Niringiye, R. Kapinga, S. Tumwegamire, P. Abidin, E. Carey, B. Lemaga, J. Nsumba and D. Zhang. 2007. Sweetpotato selection releases: lessons learnt from Uganda. African Crop Science Journal 15: 11 - 23.

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

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.

Nelles, W. 2009. Sweetpotato Education, Research and Capacity Development through a CIP-Orissa Learning Site. CTCRI, Bhubaneswar, Orissa, India.

Ngailo, S., H. Shimelis, J. Sibiya and K. Mtunda. 2013. Sweet potato breeding for resistance to sweet potato virus disease and improved yield: Progress and challenges. African Journal of Agricultural Research 8: 3202-3215.

Ngailo, S., H.A. Shimelis, J. Sibiya and K. Mtunda. 2016. Assessment of sweetpotato farming systems, production constraints and breeding priorities in eastern Tanzania. South African Journal of Plant and Soil 33: 105-112.

Ngailo, S.E. 2015. Breeding Sweetpotato for Improved Yield and Related Traits and Resistance to Sweetpotato Virus Disease in Eastern Tanzania. PhD Thesis, University of KwaZulu-Natal, Pietermaritzburg.

Okonya, J.S., R.O. Mwanga, K. Syndikus and J. Kroschel. 2014. Insect pests of sweetpotato in Uganda: farmers' perceptions of their importance and control practices. Springer Plus. 3. doi:https://doi.org/10.1186/2193-1801-3-303.

Olesen, K. 1976. A completely balanced polycross design. Euphytica 25: 485-488.

Onwueme, I.C. 1978. The tropical tuber crops: yams, cassava, sweet potato, and cocoyams.Wiley, Sussex.

Rao, V., T. Debouck and M. Iwanga. 1994. The role of international organisations in root and tuber crop conservation. *Japan International Workshop on Genetic Resources* - Root and Tuber Crops,. MAFF, Tsukuba, Japan. p. 7-22.

Reynolds, T.W., S.R. Waddington, C.L. Anderson, A. Chew, Z. True and A. Cullen. 2015. Environmental impacts and constraints associated with the production of major food crops in Sub-Saharan Africa and South Asia. Food Security 7: 795-822.

Rukarwa, R.J., S.B. Mukasa, B. Odongo, G. Ssemakula and M. Ghislain. 2014. Identification of relevant non-target organisms exposed to weevil-resistant Bt sweetpotato in Uganda. Biotechnology 4: 217-226.

Rukundo, P., H. Shimelis, M. Laing and D. Gahakwa. 2013. Storage root formation, dry matter synthesis, accumulation and genetics in sweet potato. Australian Journal of Crop Science 7: 2054-2061.

Rukundo, P., H. Shimelis, M. Laing and D. Gahakwa. 2017. Combining Ability, Maternal Effects, and Heritability of Drought Tolerance, Yield and Yield Components in Sweetpotato. Frontiers in Plant Science 7. doi:10.3389/fpls.2016.01981.

Saladaga, F.A. 1989. The theorotical basis and practice of polycross as used in sweetpotato. In: Mackay K.T., M.K. Palomar and R.T. Sanico, editors. Sweetpotato Research and Development for Small Farmers. 1st ed. SEAMEO-SEARCA College, Laguna, thePhilippines.

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. doi.org/10.1186/1471-2164-11-604.

Schlegel, R.H.J. 2010. Dictionary of plant breeding. CRC Press, Boca Raton London.

Sebastiani, S., 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. *8th African Crop Science Society Conference*, El-Minia, Egypt, 27-31 October 2007.

Skoglund, L.G. and N.E. Smit. 1994. Major diseases and pests of sweetpotato in Eastern Africa. International Potato Center, Lima.

Smit, N. 1997. Integrated pest management for sweetpotato in Eastern Africa. Landbouwuniversiteit, Wageningen.

Smit, N.E.J.M., M.C.A. Downham, P.O. Laboke, D.R. Hall and B. Odongo. 2001. Mass-trapping male *Cylas* spp. with sex pheromones: a potential IPM component in sweetpotato production in Uganda. Crop Protection 20: 643-651.

Sseruwu, G. 2012. Breeding of sweetpotato (*Ipomoea batatas* (L.) Lam.) for storage root yield and resistance to alternaria leaf petiole and stem blight in Uganda. PhD thesis, University of KwaZulu-Natal, Pietermaritzburg.

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

Stathers, T.E., D. Rees, S. Kabi, L. Mbilinyi, N. Smit, 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

Stevenson, P.C., H. Muyinza, D.R. Hall, E.A. Porter, D.I. Farman, H. Talwana and R.O.M. Mwanga. 2009. Chemical basis for resistance in sweetpotato *Ipomoea batata*s to the sweetpotato weevil *Cylas puncticollis*. Pure and Applied Chemistry 81: 141-151.

Stuber, C.W. 1980. Mating designs, field nursery layouts, and breeding records. In: W.R.Fehr and Hadley, H.H., editors, American Publishers, Madisom, Wisconsin. p. 83-104.

Tairo, F., E. Mneney and A. Kullaya. 2008. Morphological and agronomical characterization of sweet potato [*Ipomoea batatas* (L.) Lam.] germplasm collection from Tanzania. African Journal of Plant Science 2: 77-85.

Talekar, N.S. 1987. Feasibility of the use of resistant cultivar in sweetpotato weevil control. International Journal of Tropical Insect Science 8: 815-817.

Ugent, D., S. Pozorski and T. Pozorski. 1982. Archaeological potato tuber remains from the casma valley of Peru. Economic Botany 36: 182-192.

Vaughan, J. and C. Geissler. 1997. The new Oxford book of food plants. Oxford University Press, Oxford, UK.

Vimala, B. and B. Hariprakash. 2011. Variability of morphological characters and dry matter content in the hybrid progenies of sweet potato (*Ipomoea batatas* (L) Lam). Gene Conservation: 65-86.

Woolfe, J.A. 1992. Sweet potato: An untapped food resource. Cambridge University Press, New York.

CHAPTER 2 FARMERS' PERCEPTION ON SWEETPOTATO WEEVIL DAMAGE, PRODUCTION CONSTRAINTS AND VARIETY PREFERENCES IN WESTERN TANZANIA

Abstract

Sweetpotato weevils (*Cylas* spp.) are among the most important constraints to sweetpotato (*Ipomoea batatas* [L.] Lam.) production in most agro-ecological zones of Tanzania. Integration of farmers' perceptions on sweetpotato weevil damage, production constraints and variety preferences is crucial in developing sweetpotato varieties with farmer-preferred traits and weevil resistance. The aim of this study was to identify farmers' perceptions on sweetpotato weevil damage, production constraints, post-harvest storage options and criteria used to select and grow the best sweetpotato varieties in western Tanzania. Surveys were conducted in four selected districts of western Tanzania (Nzega, Sikonge, Kigoma rural and Kasulu) known for sweetpotato production. Data were collected using a structured questionnaire, focus group discussions and transect walk involving 122 sweetpotato farmers. Weevil damage was reported by 84% of the respondents to be the overriding constraint to sweetpotato production. Sweetpotato diseases and drought were the next production constraints, reported by 57% and 54% of respondents, respectively. The main farmers' preferred agronomic traits of sweetpotato included high yield (25% of respondents), drought tolerance (24%), and disease and pest resistance (21%). Farmers' preferred sweetpotato culinary traits in the study areas were high dry matter content (reported by 21% of respondents), followed by reduced cooking time, taste and fiber content (each reported by 19% of respondents). The above-mentioned production constraints and farmers' preferred traits are useful selection criteria for improving sweetpotato with respect to weevil resistance and enhanced storage-root yield and quality.

Keywords: agronomic traits; culinary traits; *Cylas* spp.; resistance breeding; weevil- resistant varieties.

2.1 Introduction

Sweetpotato (*Ipomoea batatas* [L.] Lam.) is an important root crop grown worldwide. It is the fifth most important food crop in developing countries after rice (*Oryza sativa* L.), wheat (*Triticum aestivum* L.), maize (*Zea mays* L.) and cassava (*Manihot esculenta* L.) (Elameen et al., 2008; Nelles, 2009). In sub-Saharan Africa (SSA), it is grown on about 2.1 million ha, providing 9.9 million tons of storage root (Anyanga et al., 2013). Three African countries (Nigeria, Uganda and Tanzania) are among the top 10 largest world producers of sweetpotato. Sweetpotato grows on marginal soils under drought conditions; it has higher production per unit area compared with wheat, rice and cassava (Schafleitner et al., 2010).

Sweetpotato has several nutritional advantages and it is consumed in various forms. Young and succulent sweetpotato leaves, rich in protein and vitamins, are used as a leafy vegetable in SSA. The storage root is rich in carbohydrate and β-carotene, especially in the orange-fleshed sweetpotato (OFSP) varieties. β-carotene is a precursor of vitamin 'A', which is important in combating vitamin A deficiency, cancer and diabetes (Mwanga et al., 2007; Burri, 2011).

In Tanzania, sweetpotato is an important food and cash crop grown in almost all agro-ecological zones (Kapinga et al., 1995). It is a key crop after maize and rice, and is the second most important root crop after cassava (Tairo et al., 2008). The area under sweetpotato cultivation in Tanzania is approximately 560 000 ha, with an average yield of 4.55 t ha^{-1}, which is far below the potentially attainable yield of 12.68 t ha^{-1} (FAOSTAT, 2014). It is widely grown as a mono-crop or is intercropped with cassava, maize, beans, cowpea and groundnut. Most farmers practice sequential harvesting of sweetpotato storage roots to limit postharvest losses of the perishable root (Kapinga et al., 1995; Tairo et al., 2004).

Despite the importance of sweetpotato in food and nutrition security in Tanzania, its production and productivity are constrained by an array of factors. The major constraints contributing to low yields or quality losses include biotic and abiotic stresses, and socio-economic factors (Kapinga et al., 1995; Kulembeka et al., 2005; Ndunguru and Kapinga, 2007; Tairo et al., 2008). Among the major pests, the sweetpotato weevils (*Cylas puncticollis* Boheman and *C. brunneus* Fabricius) are the main constraints affecting sweetpotato production in Tanzania. According to Kapinga et al. (1995), weevils were the most important constraint to sweetpoato production in most zones of Tanzania. However, no recent studies exist on damage and yield loss caused by sweetpotato weevils, farmers' perceptions regarding sweetpotato weevils and farmers' preferred sweetpotato varieties. Early planting and harvesting, crop rotation, ridging, sanitation and flooding are some of the cultural practices used to control weevils in smallholder production systems. Because the success of these control measures

is quite low, there is thus the need for an effective management of the pest through integrated approaches, such as host resistance, crop protection chemicals and cultural practices (Stevenson et al., 2009; Muyinza et al., 2012; Anyanga et al., 2013). Breeding sweetpotato for weevil resistance is considered an economical and most effective control strategy against this pest (Stevenson et al., 2009; Muyinza et al., 2012). This approach is yet to be explored in Tanzania. Further, there is a need to know farmers' preferences regarding sweetpotato varieties before breeding for weevil resistance to be able to incorporate the farmer-preferred traits in elite and weevil-resistant varieties.

Participatory rural appraisal (PRA) is a multidisciplinary research tool to help breeders acquire relevant information regarding farmers' criteria for cultivar selection and adoption (Chambers, 1994). Farmers involvement in plant breeding programs is vital for release, acceptance and adoption of the developed varieties (Grüneberg et al., 2009). Farmers have their own selection criteria for sweetpotato varieties; neglect of which in plant breeding programs can lead to rejection of the developed varieties (Kapinga and Carey, 2003; Gibson et al., 2008). Farmers often use a set of selection criteria for sweetpotato varieties that include resistance to pests and diseases, improved agronomic performance and preferred horticultural attributes for large-scale production, consumption and marketing. In some cases, farmers can reject varieties with the best agronomic performance if their traits of interest, which include good culinary qualities (high dry matter and low fiber content), are not integrated (Kulembeka et al., 2005). In light of the above background, the objectives of this study were to ascertain farmers' perceptions regarding sweetpotato weevil damage, production constraints and criteria used to select and grow the best sweetpotato varieties in western Tanzania. Such information will be useful to establish farmers' selection criteria for breeding of sweetpotato with weevil resistance and enhanced storage root yield and quality in western Tanzania.

2.2 Materials and methods

2.2.1 Description of the study areas and sampling procedure

This study was conducted in western Tanzania (Figure 2.1) and comprised two administrative regions, namely, Tabora and Kigoma, each consisting of six districts. The western zone has an area of 113,260 km^2, which is equivalent to 13% of the total area of Tanzania. Two representative districts were selected in each region: Kigoma rural and Kasulu districts from the Kigoma region and Nzega and Sikonge districts from the Tabora region (Table 2.1). Two villages within each district were selected on the basis of the importance of sweetpotato as a staple food and as a source of income. In each village, 13 to 16 farmers were selected, giving us 122 farmers for the study (Table 2.1).

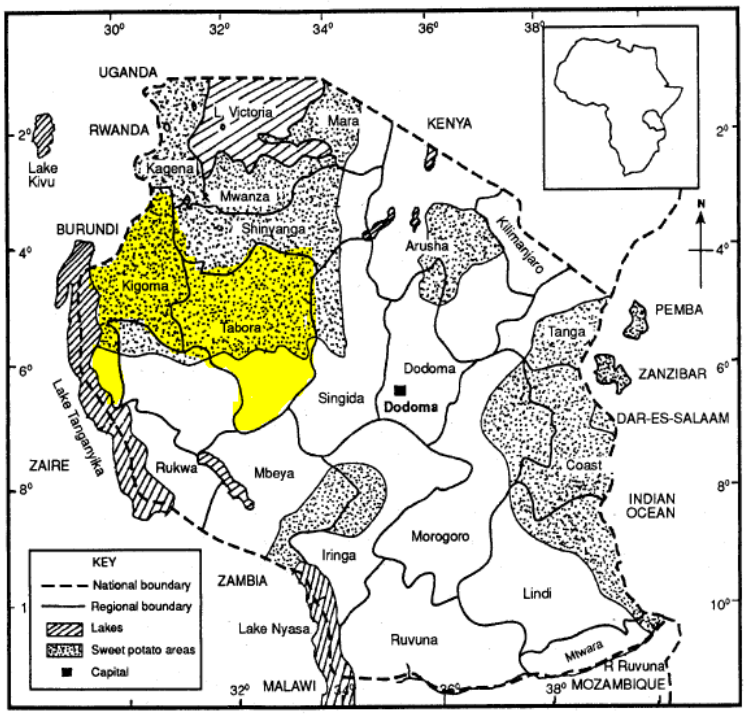

Figure 2.1. Map of Tanzania showing the study locations highlighted in yellow.

Table 2.1. List of study regions, districts and villages and sampled farmers in western Tanzania.

Region	District	Village	Number of respondents	Total
Tabora	Nzega	Kanolo	15	**29**
		Kitangiri	13	
	Sikonge	Tutuo	15	**30**
		Udongo	15	
Kigoma	Kigoma Rural	Mahembe	15	**31**
		Nkungwe	17	
	Kasulu	Rusesa	16	**32**
		Kwaga	16	
		Total	**122**	**122**

2.2.2 Participatory rural appraisal (PRA)

The study was conducted, using PRA tools, from February to March 2015. A semi-structured questionnaire was prepared to collect data through farmer interviews. The interviewees provided responses on the history of sweetpotato production; past and currently grown sweetpotato varieties;

sources of planting materials; biotic, abiotic, and socio-economic constraints to sweetpotato production; postharvest handling; and awareness and perceptions regarding sweetpotato weevils. The other parameters were: sweetpotato cultivar preferences, criteria for cultivar selection, and perceptions regarding quality traits, e.g., dry matter content, taste, and storability. Focus group discussions (FGD) involving 13 to 16 farmers per village including village leaders, were held using a checklist to gather additional data, such as cropping calendar and input application. Furthermore, a transect walk was done across the villages and through field visits to appraise and document the cropping systems, varieties grown and incidence of diseases of sweetpotato in the study areas.

The research team comprised six multidisciplinary members, including one agricultural research officer (agronomist), two research assistants, and one agricultural extension officer from district agricultural office, one ward agricultural extension officer and one village agricultural extension officer. Other participants were farmers and village leaders, who either participated in personal interviews or focus group discussion.

2.2.3 Data collection and analysis

Data analyses were performed using Statistical Package for the Social Sciences (SPSS) version 20 (SPSS, 2009). Frequencies, descriptive statistics and cross tabulation were used to determine pairwise relationships between variables. Pearson Chi-square test procedure was used to draw inferences.

2.3 Results

2.3.1 Demographic profile and socioeconomic characteristics in the study areas

The number of female farmers was significantly higher ($\chi^2 = 14.33$; $P = 0.02$) than number of male farmers (Table 2.2). Crop production was the main source of income in western Tanzania, followed by livestock rearing (Table 2.2). Most households (33.6%) in the surveyed areas owned agricultural land varying from 2.0 to 3.2 hectares. About 23% of respondents owned between 3.6 to 4.8 hectares (Table 2.2). Most households (38.5%) had a family size of 5 to 8 people (Table 2.2). In Kigoma region, 52.4% respondents had 5-8 persons per family, whereas in Tabora region, 40.7% respondents had 5-8 persons per family.

Table 2.2. Demographic profile and sicio-econimic characteristics of interviewed farmers in four districts of western Tanzania.

Variable	Number of respondents	Respondents (%)	Chi-square	df	P-value
Gender					
Male	46	38.0	14.33	3	0.02
Female	76	62.0			
Major source of income					
Crop production	80	65.6	9.68	12	0.64
Livestock rearing	31	25.4			
Carpentry	4	3.3			
Tailoring	2	1.6			
Mini-shops	5	4.1			
Farm size in hectares					
< 0.4	3	2.5	17.94	15	0.27
0.4-1.6	20	16.4			
2-3.2	41	33.6			
3.6-4.8	28	23.0			
5.2-6.4	17	13.9			
>6.4	13	10.7			
Family size in numbers					
1-4	1	0.8	10.87	12	0.54
5-8	47	38.5			
9-12	40	32.8			
13-16	17	13.9			
≥ 16	17	13.9			

2.3.2 Most commonly grown crops in the study area

Farmers in the study area listed the commonly grown crops and ranked them in order of importance. There was a significant difference in the crops grown in different districts of the study areas (χ^2 = 129.716; P = 0.000). Maize, cassava and sweetpotato were ranked as the first, second and third

important crops, respectively (Table 2.3). The main food crops in Kigoma region were maize, cassava and sweetpotato, whereas the main cash crops in this region were oil palm, cassava and sweetpotato. In Tabora region, the main food crops were maize, rice, cassava and sweetpotato, whereas the main cash crops were tobacco, rice and sunflower (Table 2.3).

Table 2.3. List of commonly important crops grown in the study area and ranks.

Commonly grown crops	Rank	Chi-square	df	P-value
Maize	1			
Cassava	2			
Sweetpotato	3			
Rice	4			
Groundnuts	5	129.716	24	0.000
Beans	6			
Tobacco	6			
Oil palm	6			
Horticultural crops (tomatoes, onions, water melons, vegetables, okra and cucumbers)	7			

2.3.3 Importance of sweetpotato in the study area

Results (frequency of consumption and production objectives) regarding the importance of sweetpotato in the study area, assessed through structured interviews are shown in Table 2.4. Most of the respondents (61.5%) consumed sweetpotato daily during harvesting season and 65.6% of the respondents produce sweetpotato primarily for home consumption. All respondents (100%) indicated that they grew sweetpotato for home consumption, of which 78% grew sweetpotato also for marketing. Other indicated uses were: as leaf vegetable (61%) and livestock feed (4%).

Table 2.4. Indicators of the importance of sweetpotato in the study area.

Indicator	Number of respondents	Respondents (%)	Chi-square	df	Probability
Frequency of sweetpotato consumption during harvesting season					
Daily	75	61.5			
More than 3 times a week	36	29.5	15.83	9	0.07
At least 2 times a week	10	8.2			
Once in a week	1	0.8			
Sweetpotato production objective					
Home consumption	122	100			
Marketing	95	78	18.48	9	0.03
Vegetable	74	61			
Livestock feed	5	4			

2.3.4 Sweetpotato production constraints in the study area

The list of sweetpotato production constraints (ranked in order of importance) described by farmers in western Tanzania is presented in Table 2.5. A total of 13 main sweetpotato-production constraints were reported by respondents. There was a significant difference in sweetpotato-production constraints in the study areas (χ^2 = 72.982; p = 0.00). Sweetpotato weevil was the most significant yield- and quality-limiting factor in sweetpotato production in western Tanzania, followed by drought and limited access to credit. Farmers had limited access to cash, which limited their ability to hire labor; to purchase planting material, and to rent land for sweetpotato production or conservation of planting materials, which is often practised in swampy lands in the study areas.

Table 2.5. Sweetpotato production constraints and rank in the study area.

Production constraints	Rank	Chi-square	Df	P-value
Weevils	1			
Drought	2			
Lack of capital	3			
Shortage of market	4			
Diseases	5			
Shortage of planting material	6			
Low yield	7	72.98	36	0.00
Damage by livestock	8			
Labor shortage	9			
Poor storage facilities	10			
Shortage of land	10			
Shortage of improved varieties	11			
Weeds	11			

2.3.5 Damages caused by sweetpotato weevils in western Tanzania

2.3.5.1 Farmers awareness on sweetpotato weevils in the study area

All respondents (100%) were aware of damage caused by the sweetpotato weevils. About 69% of the respondents did not know the local names of sweetpotato weevils (Figure 2.2). About one-third of the respondents (31%) knew the local names but did not have mutual agreements on the common names of weevils. The local names used for sweetpotato weevil in the study included: '*minyoo*', '*funza*', '*ngenya*', '*magino*', '*nyongoli*' and '*uhinu*'.

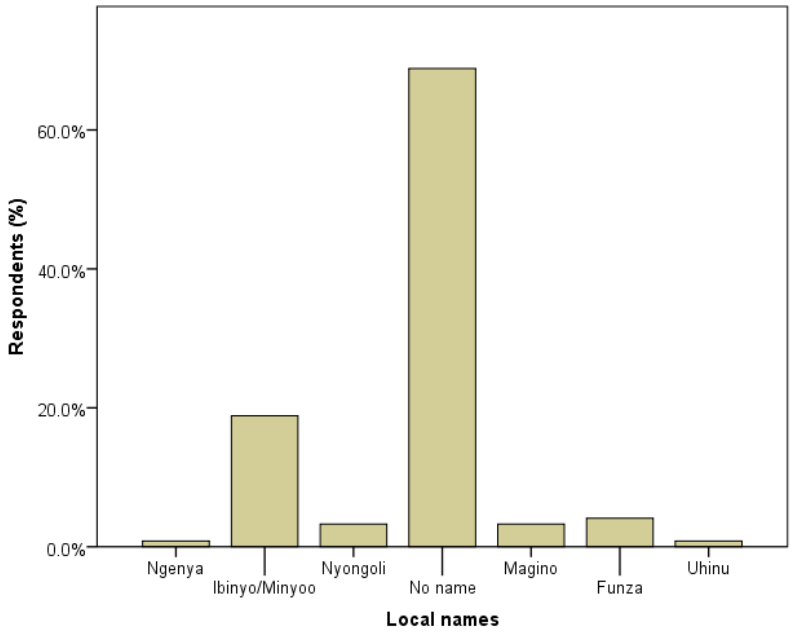

Figure 2.2. Local names used for sweetpotato weevil in western Tanzania.

2.3.5.2 Sweetpotato weevil infestation

Respondents identified the impact of sweetpotato weevil infestation as follows: causing yield loss (100% respondents), poor marketability of storage roots (98.4%), and poor palatability of storage roots (49.2%) (Table 2.6). In the study areas, weevils caused extensive damage to storage roots of sweetpotato, which is illustrated in Figure 2.3.

Table 2.6. Losses caused by sweetpotato weevil infestation reported by respondent farmers in western Tanzania.

Losses	Number of respondents	Percent of respondents	Chi-square	df	P-value
Yield loss	122	100			
Market loss	120	98.4	9.12	6	0.17
Palatability loss	60	49.2			

Figure 2.3. Damaged sweetpotato storage roots caused by weevils: A and B show internal damages while C and D show external damages.

2.3.5.3 Sweetpotato weevils control options

Respondent farmers used various control options to manage sweetpotato weevils in western Tanzania (Table 2.7). Many respondents (88.4%) mentioned early harvesting as their main weevil control option. Hilling up was used by 16.5% of the respondents, crop rotation by 4.1% of respondents, while 10.7% of the respondents did not control weevils at all.

Table 2.7. Sweetpotato weevil management options in western Tanzania.

Control option	Number of respondents	Percent of respondents	Chi-square	df	P-value
Early harvesting	107	88.4			
Crop rotation	5	4.1	6.767	9	0.661
Ridging	20	16.5			
No control	13	10.7			

2.3.6 Availability of improved sweetpotato varieties

Respondents from the study areas reported different sources of improved sweetpotato varieties, such

as white-fleshed varieties and orange-fleshed sweetpotato varieties (OFSPs) (Table 2.8). Most of the respondents (77%) had no access to improved white-fleshed varieties, whereas 14.8% accessed them from neighbouring farmers and 8.2% from non-governmental organizations (NGOs). Most of the respondents (92.8%) accessed improved OFSP from neighbouring farmers, whereas 5.8% accessed them from NGOs and 1.4% from district agricultural offices.

Table 2.8. Source of improved orange-fleshed and white-fleshed sweetpotato varieties in western Tanzania.

Respondents	**Source of improved varieties**					
	Orange-fleshed sweet potato varieties			**White-fleshed varieties**		
	Agricultural office	Neighboring farmers	NGOs	Neighboring farmers	NGOs	No access
Number of respondents	1	64	4	18	10	94
% of respondents	1.4%	92.8%	5.8%	14.8%	8.2%	77%

NGO = Non-governmental organization

2.3.7 Sources of sweetpotato planting materials, cropping calendar and crop husbandry

Most of the respondents (84.6%) conserved their own planting materials from previous crop, whereas the remainder 16.4% of respondents bought planting materials from neighbors. Sweetpotato planting in the study areas was practiced from December through February. Very few farmers (those with enough planting material) planted in December. Most of the farmers started multiplying sweetpotato vines in December and planted them in the field in February. About 69% of respondents used hoeing only once to control weeds, whereas 31% of farmers hoed twice. Not all interviewed farmers in the study areas applied fertilizer in sweetpotato fields. Most of them (79.5%) grew sweetpotato as a sole crop, whereas 20.5% intercropped it with cassava, maize, cowpeas, pigeonpeas and groundnuts because of shortages of land and manpower. Farmers reported that they did not get good yield returns of sweetpotato when they intercropped.

Harvesting of storage roots and succulent leaves of sweetpotato in western Tanzania started at the end of February when the crop was planted in December. Mostly farmers practiced piecemeal harvesting of their crop to preserve the crop in their fields and to limit postharvest losses. Therefore, sweetpotato harvesting continued through August, depending on cultivar chosen and the extent of weevil infestation. In August, most of the farmers harvested the entire crop and kept vines in conservation areas for sequential planting. Farmers in western Tanzania conserved sweetpotato planting materials in swampy areas or near water sources. Some farmers, especially in Tabora region, who had no access to swampy areas or water sources, conserved their planting materials on old termite mounds that had no termite activity. Conservation of planting materials on termite mounds was done in early May when the mounds were still moist and soft. Farmers partially covered sweetpotato vines in a termite mound, and the vines sprouted when it started raining. Farmers claimed that the termite mounds either kept moist or they were capable of sucking moisture from below the ground. This traditional practice enabled them to conserve sweetpotato vines during the entire dry season.

2.3.8 Farmers' preferences of sweetpotato varieties for production, marketing and consumption

The criteria used by farmers to identify good sweetpotato varieties, organized into agronomic criteria and quality criteria, are listed in Table 2.9. The results showed that the first three agronomic and farmer-preferred traits in order of importance were high yield (reported by 25% of respondents), drought tolerance (24%) and resistance to diseases and pests (21%). Farmers used seven traits to identify good quality sweetpotato roots for marketing and consumption (Table 2.9). The most important farmer-preferred quality traits of sweetpotato were dry matter content (reported by 21% respondents), followed by reduced cooking time, taste and low fiber content (each reported by 19% of respondents).

Table 2.9. Agronomic and root quality traits preferred by farmers in sweetpotato varieties in the study area.

Agronomic criteria	Percent of respondents	Quality criteria	Percent of respondents
High yield	25	Dry matter content	21
Drought tolerance	24	Taste	19
Disease and pest resistance	21	Reduced cooking time	19
Early maturity	15	Low fiber content	19
Medium root size	12	Flavor	13
		Flesh colour	5
Above ground biomass	3	Skin color	4

2.3.9 Post-harvest storage of sweetpotato

In Kigoma region, not all interviewed farmers stored sweetpotato after harvesting. They practiced piecemeal harvesting for consumption and marketing. However, under severe sweetpotato weevil infestation, farmers were forced to harvest the entire crop at once and consume or sell the produce at any market price. This often led to poor market demand and reduced market price of produce.

Conversely, all interviewed farmers in Tabora region stored sweetpotato after harvesting. However, piecemeal harvesting was also practiced in Tabora. Under increased sweetpotato weevil infestation, farmers harvested the entire crop for processing and storage. Sweetpotato storage roots in Tabora region were processed into two main products for long-term storage (Figure 2.4): The first product was locally referred to as '*makewe'* in Nyamwezi language or '*mapalage/michembe'* in Sukuma language. In this paper, the local name *'makewe'* is adopted where necessary. The second product was locally known as '*matoborwa'* in Nyamwezi language. Procedure for preparing *matoborwa* was similar to that of preparing *makewe*, except that the sweetpotato roots were boiled in preparing *matoborwa*. *Matoborwa* could be stored for up to 12 months, whereas *makewe* could be stored for up to 7 months. The procedures of preparing the two products are briefly outlined below:

Procedure for processing of makewe for storage:

- Harvest sweetpotato storage roots and clean them with water.

- Slightly dry the roots. Roots are spread on the ground under the sun and covered with a thin layer of grass and left to wither for two days.
- Peel the roots and chop into small pieces.
- Dry the chopped roots under the sun. Chopped pieces are spread on mats and dried under the sun for 5 to 10 days depending on the weather.
- Pack dried roots in containers and transfer to storage rooms under room temperature.

Procedure for processing of matoborwa for storage:

- Harvest sweetpotato storage roots and clean them with water.
- Slightly dry the roots. Roots are spread on the ground under the sun and covered with a thin layer of grass and left to wither for two days.
- Boiling of the roots. The withered roots are boiled in water for 50 to 60 minutes
- Peeling the roots and chopping into round pieces.
- Drying under the sun. Chopped pieces are spread on mats and dried under the sun for 7 to 14 days depending on weather.
- Pack dried roots in containers and transfer to storage rooms under room temperature

Figure 2.4. Two widely known processed sweetpotato products (A = *Makewe* and B = *Matoborwa*) developed by farmers in western Tanzania to minimize postharvest deterioration of storage root.

2.3.10 Postharvest storage constraints of sweetpotato in western Tanzania

The list of postharvest storage constraints of sweetpotato storage roots in western Tanzania is shown in Table 2.10. Pests (reported by 54.2% of the respondents), rodents (by 25.4%) and fungi (by 16.9%) were the main limiting factors for post-harvest storage of sweetpotato in western Tanzania.

Table 2.10. Constraints to in-situ postharvest storage of sweetpotato in western Tanzania.

Postharvest constraints	Respondents (%)	Chi-square	Df	P-value
Pests	54.2			
Rodents	25.4	2.58	3	0.46
Fungus	16.9			
Rain	3.4			

2.4 Discussion

2.4.1 Potential of sweetpotato in western Tanzania

The present study established sweetpotato to be an important crop in western Tanzania. It was ranked as the third most important crop after maize and cassava in the study areas. This ranking slightly differed from that of Kapinga et al. (1995), who reported sweetpotato to be the 4th most important crop in Tanzania, next to maize, rice and cassava. The crop served as food and as a source of income in the study areas. The significant role of sweetpotato in the study area was indicated by 61.5% of respondents, who consumed sweetpotato daily during harvesting (Table 2.4), and 29.5% of respondents reported consuming sweetpotato at least three times a week during the harvest season. Sweetpotato leaves served as a leafy vegetable in the study areas (Table 2.4). About 61% of respondents used sweetpotato as leafy vegetable for home consumption and marketing. The present study concurs with reports from East African countries, including Tanzania, where sweetpotato farmers consumed about 80% of their produce and sell the rest in local markets (Andrade et al., 2009).

Early maturity and prolonged piecemeal harvesting makes sweetpotato an important food security crop in western Tanzania. Sweetpotato cropping calendar showed that planting occurred from December through February. Farmers who planted in December started harvesting in February and were food secure early in the season when most of the staple crops were not ready to be harvested. Flexibility of planting time for sweetpotato and piecemeal harvesting practiced by farmers prolonged the availability of sweetpotato. The cropping calendar of sweetpotato in western Tanzania slightly differed from that of other areas of Tanzania. For instance, in eastern and Lake zone of Tanzania, the crop was planted from August to October because of bimodal rainfall pattern (Kulembeka et al., 2005; Ngailo et al., 2016). In Tabora region, sweetpotato roots were processed into various products, such as *makewe* and *matoborwa*, allowing for long-term storage of the produce and availability, and providing sustainable food and income.

The importance of sweetpotato as a food crop in western Tanzania was complemented by low production cost, making it the best crop for poor rural farmers. Most of the respondents (69%) did weeding in sweetpotato fields only once, whereas 31% did it twice (data not shown). The spreading growth habit of most of the sweetpotato varieties provides ground cover and supresse weeds. Weeds in sweetpotato fields affected shoot growth but had minor effects on root growth (Harrison and Jackson, 2011). All respondents in the study area did not use fertilizer or chemical for pest control in sweetpotato field. Potential of increasing sweetpotato yields in western Tanzania existed if inputs like fertilizer and pest control measures were applied in sweetpotato fields and the frequency of weeding increased.

2.4.2 Production constraints

A range of sweetpotato production constraints prevailed in western Tanzania including biotic, abiotic and social economic constraints. Although famers listed 13 production constraints; weevils, drought, lack of capital, poor market access, diseases and shortage of planting materials were regarded as the main constraints (Table 2.5). Interestingly, the same production constraints to sweetpotato were reported by farmers in eastern Tanzania (Ngailo et al., 2016). Pests, predominantly weevils, were the main production constraint reported in the study area. Similar results were found in the highlands of Papua New Guinea, where weevils were reportedly the most damaging root pests (Gurr et al., 2016) and in Kenya where weevils were reported to be the main pests affecting sweetpotato production (Kivuva et al., 2014). About 36.9% of the respondents ranked weevils as the most important production constraint in the present study. Sweetpotato roots were reportedly severely infested by weevils mainly when the roots started bulking and when the soil became dry (Stathers et al., 2003). Bulky roots and dry soil enhanced soil cracking, giving weevils the entry points to access roots in the soil. The dry season coincides with roots maturity. Shortage of weevil control options makes this pest a great challenge for farmers in western Tanzania. Most of the farmers in the study area used early harvesting as a weevil-management option (Table 2.7). However, because of the perishability of sweetpotato roots after harvesting, farmers practiced piecemeal harvesting, which made this control option relatively ineffective.

The impact of weevil infestation was felt more in Kigoma region than in Tabora region because farmers in the former region did not have any postharvest processing and storage for sweetpotato roots. In times of severe weevil infestation, farmers in Kigoma region had only two choices: the first being to harvest the entire crop and consume it all or sell it at any price available in the market. The second choice was to continue with their normal piecemeal harvesting, which could result up to 100%

loss of the roots left in the field for long. The need for small-enterprise development for sweetpotato processing to boost sweetpotato production has been indicated in SSA (Fuglie, 2007). During severe infestation, farmers in Tabora region could harvest the entire crop or store roots processed into *makewe* or *matoborwa* (Figure 2.4). Farmers in Kigoma region reported that it was not part of their tradition to process and store sweetpotato roots as was done in Tabora region. Therefore, it would be necessary to sensitize farmers in Kigoma region to adopt the storage techniques used in Tabora to reduce losses. Farmers in different areas used dried products of sweetpotato roots, though the names of the products and the way of processing differed. For instance, Ugandan farmers stored sweetpotato roots as two different dried products (*Inginyo* and *Amukeke*), which were prepared differently from the way it was done in western Tanzania (Engoru et al., 2005).

In this study, all the interviewed farmers were aware of the damage caused by sweetpotato weevils. However, few farmers had knowledge about the pest. About 69% of the interviewed farmers did not know the local name of the pest (Figure 2.2); few respondents in the same village, who knew the local names, did not have mutual agreements on the common names of the pest. Gurr et al. (2016) also reported that most of the farmers in Papua New Guinea reported damage of sweetpotato roots by weevils but had little knowledge about the pest. This posed a challenge to farmers in controlling the pest.

Drought and diseases were also mentioned among the main constraints to sweetpotato production in western Tanzania. The main disease described, especially in Kigoma region, was the sweetpotato virus disease (SPVD). Sweetpotato virus disease has also been reported in many sweetpotato-growing areas in southern Tanzania, where it has been shown to cause about 36-98% yield loss (Ndunguru and Kapinga, 2007). Shortage of improved varieties was ranked 11th in order of importance as a constraint to sweetpotato production in this study. However, the availability of sweetpotato varieties, which are resistant or tolerant to drought and diseases can be an economic and cost-effective solution for enhancing productivity in the surveyed areas. In the study areas, 77% of the respondents had no access to planting materials of improved varieties, suggesting the need to develop sweetpotato varieties with weevil resistance and enhanced storage root yield and quality. Access to sweetpotato planting material was considered an important production factor in SSA to improve sweetpotato productivity (Fuglie, 2007). Lack of capital in the study area was ranked as the 3rd constraint to sweetpotato production. Therefore, farmers in western Tanzania should have access to capital to boost sweetpotato production.

Shortage of planting material was another constraint to sweetpotato production, which was ranked 6th. This was the main reason for extended planting time in the study areas. Because of shortage of planting material, few farmers with enough vines planted sweetpotato in December, whereas the

majority of farmers started multiplying planting material in December, followed by field establishment in February. Most of the farmers in western Tanzania kept their own planting material from previous fields in swampy areas or near water sources and on an old termite mounds. Unimodal rainfall pattern caused longer dry seasons, especially in Tabora region, which was the main cause for shortage of sweetpotato planting material in western Tanzania. Farmers used local conservation methods to preserve their planting material. However, rapid vine multiplication techniques should be introduced to farmers to facilitate rapid availability of planting material during the onset of rainfall.

2.4.3 Farmers' preferences for sweetpotato varieties

In the study areas, farmers mentioned high yield, drought tolerance, pest and disease resistance and root size as the main agronomic traits they used for selecting good sweetpotato varieties. The main quality traits mentioned by most of the respondents were: high dry matter content, low fiber content, taste, flavor and reduced cooking time. In previous surveys conducted in Tanzania (Kapinga et al., 1995; Ngailo et al., 2016), farmers favored the same traits as their main criteria in selecting sweetpotato varieties. In a study conducted in Uganda, farmers considered agronomic traits, such as resistance to pests and diseases, drought resistance and high yield, as the main criteria for selecting good sweetpotato varieties for production (Gibson et al., 2008). These authors indicated that farmers in Uganda preferred these traits because they favored sequential harvesting, which was widely practiced. In the present study, farmers preferred sweetpotato that remained intact after cooking and was not watery; this quality is related to high dry matter content. In earlier studies conducted in Lake Zone, Eastern Zone, Southern Zone and Southern Highlands of Tanzania, famers described traits such as high dry matter content, flavor, taste and low fiber content as important attributes of sweetpotato varieties (Kapinga and Carey, 2003). In Uganda, farmers also used high yield, high dry matter content, disease and pest resistance and root size as preferred traits in selecting good sweetpotato varieties for production (Gibson et al., 2008). Sweetpotato breeding programs should select for agronomic and quality traits in accordance with farmers' preferences for easy adoption of released varieties by farmers. In some cases, farmers could reject varieties with the best agronomic performance if their traits of interest were not integrated, which included good culinary qualities, such as high dry matter and low fiber content (Kulembeka et al., 2005).

2.5 Conclusions

In the study areas, weevils were reported to be the main production constraint affecting storage root, yield and quality. Other main constraints reported were diseases and drought. Adoption of sweetpotato roots processing and storage techniques by farmers in Kigoma region can be useful in reducing sweetpotato yield loss in western Tanzania. The main farmers' preferred agronomic traits of sweetpotato included high yield, drought tolerance and disease and pest resistance. High dry matter content, reduced cooking time, taste and low fiber content were the main farmer-preferred sweetpotato quality traits. This information will be valuable for use as selection criteria for breeding of sweetpotato with weevil resistance and enhanced agronomic and horticultural attributes in western Tanzania.

Reference

Andrade, M., I. Barker, D. Cole, S. Fuentes, W. Gruneberg, R. Kapinga, J. Kroschel, R. Labarta, B. Lemaga and C. Loechl. 2009. Unleashing the potential of sweetpotato in Sub-Saharan Africa.: Current challenges and way forward International Potato Center, Lima.

Anyanga, M.O., H. Muyinza, H. Talwana, D.R. Hall, D.I. Farman, G.N. Ssemakula, R.O.M. Mwanga, and P.C. Stevenson. 2013. Resistance to the Weevils *Cylas puncticollis* and *Cylas brunneus* conferred by sweetpotato root surface compounds. Journal of Agricultural and Food Chemistry 61:8141-8147.

Burri, B.J. 2011. Evaluating sweet potato as an intervention food to prevent vitamin A deficiency. Comprehensive Reviews in Food Science and Food Safety 10:118-130.

Chambers, R. 1994. Participatory rural appraisal (PRA): Challenges, potentials and paradigm. World Development 22:1437-1454.

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

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

FAOSTAT. 2014. Food and Agriculture Organisation of the United Nations : Crop production data. FAOSTAT Division, Rome.

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

Gibson, R.W., E. Byamukama, I. Mpembe, J. Kayongo, and R.O. Mwanga. 2008. Working with farmer groups in Uganda to develop new sweet potato cultivars: decentralisation and building on traditional approaches. Euphytica 159:217-228.

Grüneberg, W., R. Mwanga, M. Andrade, J. Espinoza, S. Ceccarelli, E. Guimarães, and E. Weltzien. 2009. Selection methods. Part 5: Breeding clonally propagated crops. *Plant Breeding and Farmer Participation*. Food and Agriculture Oganization of the United Nations, Rome. p. 275-322.

Gurr, G.M., J. Liu, A.C. Johnson, D.N. Woruba, G. Kirchhof, R. Fujinuma, W. Sirabis, Y. Jeffery, and R. Akkinapally. 2016. Pests, diseases and crop protection practices in the smallholder sweetpotato production system of the highlands of Papua New Guinea. PeerJ 4: e2703. DOI 10.7717/peerj.2703

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

Kapinga, R., and E. Carey. 2003. Present status of sweetpotato breeding for eastern and southern Africa. Sweetpotato post-harvest Assessment.: Experiences from East Africa. Chatham, United Kingdom. NRI/CPHP/DFID/CIP/Ministry of Agriculture. Natural Resources Institute: The University of Greenwich. ISBN 0 859554:2.

Kapinga, R.E., P.T. Ewell, S. Jeremiah, and R. Kileo. 1995. Sweetpotato in Tanzanian farming and food systems: implications for research. International Potato Center, Tanzanian Ministry of Agriculture, Nairobi and Dar-Es-Salaam.

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.

Muyinza, H., H.L. Talwana, R.O.M. Mwanga, and P.C. Stevenson. 2012. Sweetpotato weevil (*Cylas* spp.) resistance in African sweetpotato germplasm. International Journal Of Pest Management 58:73-81.

Mwanga, R., B. Odongo, C. Niringiye, R. Kapinga, S. Tumwegamire, P. Abidin, E. Carey, B. Lemaga, J. Nsumba and D. Zhang. 2007. Sweetpotato selection releases: lessons learnt from Uganda. African Crop Science Journal 15: 11-23

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.

Nelles, W. 2009. Sweetpotato Education, Research and Capacity Development through a CIP-Orissa Learning Site. CTCRI, Bhubaneswar, Orissa, India.

Ngailo, S., H.A. Shimelis, J. Sibiya, and K. Mtunda. 2016. Assessment of sweetpotato farming systems, production constraints and breeding priorities in eastern Tanzania. South African Journal of Plant and Soil 33:105-112.

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. doi.org/10.1186/1471-2164-11-604.

SPSS. 2009. Statistical Package for Social Scientists. SPSS for Windows Release 18.0, Chicago, IL.

Stathers, T.E., D. Rees, A. Nyango, H. Kiozya, L. Mbilinyi, S. Jeremiah, S. Kab, and N. Smit. 2003. Sweetpotato infestation by *Cylas* spp. in East Africa: II. Investigating the role of root characteristics. International Journal of Pest Management 49:141-146..

Stevenson, P.C., H. Muyinza, D.R. Hall, E.A. Porter, D.I. Farman, H. Talwana, and R.O.M. Mwanga. 2009. Chemical basis for resistance in sweetpotato *Ipomoea batata*s to the sweetpotato weevil *Cylas puncticollis*. Pure and Applied Chemistry 81:141-151.

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

Tairo, F., E. Mneney, and A. Kullaya. 2008. Morphological and agronomical characterization of sweet potato [*Ipomoea batatas* (L.) Lam.] germplasm collection from Tanzania. African Journal of Plant Science 2:77-85.

CHAPTER 3 VARIATIONS OF SWEETPOTATO GERMPLASM COLLECTIONS FOR YIELD AND YIELD-RELATED TRAITS IN WESTERN TANZANIA

Abstract

Sweetpotato (*Ipomoea batatas* [L.] Lam.) is an important food crop widely grown under low input production systems and harsh growing environments. It is a relatively drought tolerant crop attaining higher biomass production per unit area. Genetic diversity present in breeding populations is a raw material for selection of parental genotypes with desirable and complementary traits. The objective of this study was to determine the genetic diversity present among Tanzania grown sweetpotato germplasm for yield and yield-related traits and dry matter content. Seventy six sweetpotato accessions collected from Tanzania and 20 sweetpotato accessions received from International Potato Centre (CIP) in Lima/Peru were characterized in two seasons. The study was conducted using a 16 x 6 triple lattice design. The data collected included 16 morphological traits using CIPs standard descriptors. Data were analysed using multivariate procedure including cluster analysis and principle component analysis. The tested sweetpotato collections differed significantly for storage root yield ($P< 0.001$), dry matter content (DMC) ($P< 0.001$) and number of roots per plot ($P< 0.001$). Genotypes New Kawogo, Kiti cha Nyerere and Kisu cha Masai had the highest root yields of 10.14, 9.85 and 9.67 tha^{-1} whereas genotypes Ngw'anangusa, Rugomoka and Secondary had significantly higher mean DMC of 43.45, 43.3 and 43.3% respectively . Traits considered in the study revealed positive and significant correlations. The first four principal components accounted for 69.33% of the variations present in the tested sweetpotato genotypes. Cluster analysis grouped the studied genotypes into two major classes with genetic diversity of 0.54. The selected genotypes can be recommended for future breeding programs to bolster yield and dry matter content of sweetpotato under western Tanzania conditions.

Keywords: dry matter content, genetic diversity, morphological traits, sweetpotato, western Tanzania.

3.1 Introduction

Sweetpotato (*Ipomoea batatas* [L.] Lam.) is the world's seventh most important food crop (Elameen et al., 2008; Nelles, 2009). In sub-Saharan African (SSA) countries sweetpotato is cultivated as a food security crop. It is a highly preferred crop by smallholder farmers owing to its ability to grow under marginal soil and dryland environmental conditions yet attaining higher yield per unit area compared to wheat, rice and cassava (Schafleitner et al., 2010). The crop is early maturing (3 to 4 months) hence able to escape drought under short rainfall conditions.

The storage root of sweetpotato is consumed as fried chips, boiled root or as baked products (Engoru et al., 2005). Also the root is an industrial raw material to extract starch, alcohol, biofuel or for animal feed (Schafleitner et al., 2010; Clark et al., 2012). Young and succulent leaves of the crop are used as leaf vegetable as well as fodder crop. The orange fleshed sweetpotato (OFSP) varieties are rich in carbohydrate and β-carotene content that is a precursor of vitamin 'A' useful in combating vitamin A deficiency (Mwanga et al., 2007; Burri, 2011).

Tanzania is amongst the top 5 leading world producers of sweetpotato (FAOSTAT, 2014). In the country sweetpotato is cultivated on 560 000 ha of agricultural lands with a mean national yield of 4.55 t ha^{-1} (FAOSTAT, 2014). This yield level is far below the potential productivity of the crop varying from 15 to 23 t ha^{-1} reached under 30 kg N ha^{-1} and 60 kg P ha^{-1} level of fertilization (Sebastiani et al., 2007). Moreover there is limited progress in sweetpotato breeding in Tanzania due to several constraints that include lack of knowledge on the genetic diversity of the crop among locally grown genotypes (Kapinga and Carey, 2003; Tairo et al., 2008). Often locally grown genotypes bear different names despite their considerable genetic similarity. A report by Kapinga et al. (1995) revealed that there were more than 100 local names for sweetpotato varieties grown in the Maswa district in Tanzania. In some cases, the same variety bear different names in different locations and/or different varieties may bear the same name. Therefore, there is need to systematically characterise and select genotypes with high yields and high dry matter content for effective breeding of the crop.

Genetic diversity analysis of germplasm collections can be undertaken using agro-morphological traits and molecular markers. Some of the molecular markers used in genetic analysis of sweetpotato included simple sequence repeat (SSR), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), restriction fragment length polymorphism (RFLP), allozyme and single nucleotide polymorphism (SNP) (Acquaah, 2012). Morphological markers have been

widely and successively used in studying the diversity of sweetpotato genotypes (Tairo et al., 2008; Vimala and Hariprakash, 2011; Mbithe et al., 2016; Shumbusha et al., 2017).

Genetic diversity present in a breeding population is vital for selecting promising genotypes with desirable and complementary traits. Different studies reported the availability of a considerable level of genetic diversity of the crop in Tanzania. Elameen et al. (2008) used amplified fragment length polymorphism (AFLP) and studied the genetic diversity of 97 accessions of the crop from Eastern Tanzania and reported an average genetic similarity of 0.71. Tairo et al. (2008) examined genetic diversity of the crop using 136 landraces collected from Lake Zone, eastern and southern Tanzania and reported a genetic diversity of 0.52. Gwandu et al. (2012) used 57 sweetpotato genotypes collected from eastern and southern Tanzania and subjected for simple sequence repeat (SSR) analysis to investigate the genetic diversity of the crop for sweetpotato virus disease (SPVD) resistance and dry mass content. The authors reported a mean pair-wise genetic distance of 0.55. Ngailo et al. (2016) used SSR markers and characterised 48 sweetpotato genotypes collected from Lake and eastern zones of Tanzania. This study reported a mean number of alleles amplified per locus at 9.78. The above studies indicated the presence of a considerably higher level of genetic diversity among Tanzanian sweetpotato genotypes. Previous studies used sweetpotato germplasm collections from eastern, southern and lake zones of Tanzania. Thus far there is no report on the genetic diversity of the crop using germplasm collections from western Tanzania. The objective of this study was to determine the genetic diversity present among sweetpotato germplasm widely grown in western Tanzania using morphological markers to select promising parents with enhanced yield and yield-related traits and dry matter content.

3.2 Materials and methods

3.2.1 Description of the study site

The study was conducted at Tumbi Agricultural Research Institute (ARI-Tumbi) situated at 5˚ 4’11’’S, 32˚ 40’1’’E in western Tanzania. The area is characterized by a unimodal rainfall pattern with a mean annual rainfall of 920 mm. The main rainfall season is between November and April followed by 6 months dry season. The rainfall distribution at the study site during the two seasons of the study is presented in Figure 3.1. The climate is generally dry and warm with a mean daily temperature of 23˚C. The soils are slightly acidic predominantly with 67% sand, 24% clay and 9% silt (Bagarama et al., 2012).

3.2.2 Germplasm collection and trial establishment

A total of 82 sweetpotato genotypes were collected during October and November 2014 from seven districts of western Tanzania and Lake Zone while 20 sweetpotato genotypes were received from CIP-Peru. The collected genotypes were multiplied at ARI-Tumbi. During multiplication, some duplicate genotypes from western Tanzania and Lake Zone were excluded based on their morphological similarities leaving 96 germplasm genotypes (Table 3.1). Among the 96 genotypes, 57 were local varieties or landraces collected from western Tanzania; 19 were collected from Lake Zone and Maruku and Ukiriguru Research Institutes. Twenty genotypes were kindly supplied by International Potato Centre (CIP)–Lima/Peru. The CIP collections were originally obtained from India. Trials were conducted at ARI-Tumbi from February to June 2015 (season I) and January to May 2016 (season II). The experiment was designed using a 16 x 6 lattice with 3 replications. The plot size was 1.3 m^2 (1m x 1.3m) composed of two ridges. Five plants were established on each ridge making a total of 10 plants per plot. The spacing used was 1m inter-row and 0.3m intra-row. Weeding was done twice using hand hoe. Fertilizers applied were nitrogen, phosphorus and potassium (23:10:5) at the rate of 233 kg/ha a month after planting. This fertilization rate was used to boost vegetative growth because the soils at trial site (ARI Tumbi) are dominated by sand (Bagarama et al., 2012).

3.2.3 Data collection

Test genotypes were phenotyped using 16 morphological traits including 11 quantitative traits and 5 qualitative traits (Table 3.2). Characterization was done using CIP's standard descriptors (Huaman, 1991). Data were averaged from measurements made on five plants of each accession. The colour and pigmentations on leaves and vines were recorded as the average expression of the character observed in a section of the main stem located in the middle portion of 5 main stems. Dry matter content was determined by taking a sample of 100-200 g fresh storage root mass from five randomly selected healthy roots of each genotype followed by chopping roots into smaller sections. Each sliced root sample was oven dried at 70˚C for 72 hours to constant mass. The dry matter content was determined as the proportion of dry matter relative to fresh mass expressed as a percentage.

Table 3.1. List, origin and description of sweetpotato genotypes used in the study.

Tanzania collection (Western Zone)			
SN	**Name**	**Origin**	**Description**
1	Kibandule	Western Zone	Landrace
2	Chrolophenical	Western Zone	Landrace
3	Mvumbagu	Western Zone	Landrace
4	Kimburu	Western Zone	Landrace
5	Ntegakatebo	Western Zone	Landrace
6	Kajiji	Western Zone	Landrace
7	UN 7 Kabelele	Western Zone	Landrace
8	Wangeni	Western Zone	Landrace
9	Pananzala	Western Zone	Landrace
10	Polista	Western Zone	Landrace
11	Shitoli	Western Zone	Landrace
12	Ngw'anakurwa	Western Zone	Landrace
13	Ngw'anangusa	Western Zone	Landrace
14	UN 1	Western Zone	Landrace
15	Kalamu	Western Zone	Landrace
16	Ngw'ananzugi	Western Zone	Landrace
17	Mulozi-Mahembe	Western Zone	Landrace
18	Chuchu ya nesi	Western Zone	Landrace
19	Magunhwa	Western Zone	Landrace
20	Sengi	Western Zone	Landrace
21	Ngw'alu	Western Zone	Landrace
22	Tumauma	Western Zone	Landrace
23	Masinia M.W.N	Western Zone	Landrace
24	UN 2	Western Zone	Landrace
25	UN 6	Western Zone	Landrace
26	Rugomoka	Western Zone	Landrace
27	Madebe	Western Zone	Landrace
28	Kafu	Western Zone	Landrace
29	Awilo	Western Zone	Landrace
31	Kabelele	Western Zone	Landrace
32	Kasinia	Western Zone	Landrace
33	Kisu cha Masai	Western Zone	Landrace
34	Kabakuli	Western Zone	Landrace
35	Ukimwi	Western Zone	Landrace
36	Nkima atina siri	Western Zone	Landrace
37	Malulumba	Western Zone	Landrace
38	Masinia njano	Western Zone	Landrace
39	burenda	Western Zone	Landrace
40	Ntulawima	Western Zone	Landrace
41	Ndezu ya ntemi	Western Zone	Landrace
42	Nyamvuva	Western Zone	Landrace
43	Lusafisha	Western Zone	Landrace
44	Ngeni	Western Zone	Landrace
45	Utitiri-Udongo	Western Zone	Landrace
46	Ngw'anakasenga	Western Zone	Landrace
47	Haraka	Western Zone	Landrace
48	UN 4	Western Zone	Landrace
49	China	Western Zone	Landrace
50	Uchungu wa mbwa	Western Zone	Landrace
51	Magazi	Western Zone	Landrace
52	Mabangili	Western Zone	Landrace
53	Ndovadoe	Western Zone	Landrace

Western Zone continued			
SN	**Name**	**Origin**	**Description**
54	Chuga	Western Zone	Landrace
55	Un 3	Western Zone	Landrace
56	Kiti cha Nyerere	Western Zone	Landrace
57	Masinia nyeupe	Western Zone	Landrace
	Tanzania collection (Lake Zone)		
58	Komando	Lake Zone	Landrace
59	Ukerewe	Lake Zone	Landrace
60	Jewel	Lake Zone	Improved variety
61	Ejumla	Lake Zone	Improved variety
62	Kabode	Lake Zone	Improved variety
63	Simama	Lake Zone	Improved
64	Vitaa U	Lake Zone	Improved variety
65	Mugandi	Lake Zone	Landrace
66	Carot Dar	Lake Zone	Improved variety
67	Carot C	Lake Zone	Improved variety
68	New kiwoso	Lake Zone	Improved variety
69	Secondary	Lake Zone	Improved variety
70	Naspot 1	Lake Zone	Improved variety
71	Kakamega	Lake Zone	Improved variety
72	New Kawogo	Lake Zone	Improved variety
73	New Dimbuka	Lake Zone	Improved variety
74	Vitaa K	Lake Zone	Landrace
75	Mwana tata	Lake Zone	Landrace
76	SPKBH/03/03	Lake Zone	Improved variety
	CIP Introduced germplasm		
77	9-CIP	CIP-Lima	Introduction, CIP
78	18-CIP	CIP-Lima	Introduction, CIP
79	8-CIP	CIP-Lima	Introduction, CIP
80	5-CIP	CIP-Lima	Introduction, CIP
81	6-CIP	CIP-Lima	Introduction, CIP
82	10-CIP	CIP-Lima	Introduction, CIP
83	24-CIP	CIP-Lima	Introduction, CIP
84	22-CIP	CIP-Lima	Introduction, CIP
85	25-CIP	CIP-Lima	Introduction, CIP
86	21-CIP	CIP-Lima	Introduction, CIP
87	3-CIP	CIP-Lima	Introduction, CIP
88	13-CIP	CIP-Lima	Introduction, CIP
89	2-CIP	CIP-Lima	Introduction, CIP
90	12-CIP	CIP-Lima	Introduction, CIP
91	7-CIP	CIP-Lima	Introduction, CIP
92	17-CIP	CIP-Lima	Introduction, CIP
93	20-CIP	CIP-Lima	Introduction, CIP
94	4-CIP	CIP-Lima	Introduction, CIP
95	11-CIP	CIP-Lima	Introduction, CIP
96	14-CIP	CIP-Lima	Introduction, CIP

SN = Serial Number, CIP = International Potato Centre

Table 3.2. List of Agro-morphological traits used to characterize 96 sweetpotato genotypes in the study.

S/N	Traits	Data description	Unit
		Quantitative traits	
1.	Root number	Number of storage roots	Number per plot
2.	Leaf lobe number	Number of leaf lobes	Number
3.	leaf size	Length from the basal lobes to the tip of the leaf Small <8 cm (3), Medium 8 – 15 cm (5), Large 16 – 25 cm (7), Very large >25 cm (9)	cm
4.	Petiole length	Length of the petiole	cm
5.	Dry matter content	Dry matter content of storage roots as a proportion of dry matter weight relative to fresh weight expressed as a percentage	%
6.	Storage root stalk	Sessile or absent (0), Very short <2 cm (1), Short 2-5 cm (3), Intermediate 6-8 cm (5), Long 9-12 cm (7), Very long >12 cm (9)	cm
7.	Internode diameter	Very thin <4 mm (1), Thin 4-6 mm (3), Intermediate 7-9 mm (5), Thick 10-12 mm (7), Very thick >12 mm (9)	mm
8.	Internode length	Very short 3 cm (1), Short 3-5 cm (3), Intermediate 6-9cm (5), Long 10-12 cm (7), Very long > 12 cm (9)	cm
9.	Root yield	Total storage root weight	Kg per plot
10.	Plant type	Length of the main vine: Erect <75cm (1), semi-erect 75-150cm (2), spreading 151-250cm (3), extremely spreading >250cm (4)	cm
11.	Ground cover	Low <50% (1), medium 50-74% (2), high 75-90% (3), total >90% (4)	%
		Qualitative traits	
12.	Leaf lobe type	no lobe (1), slight (2), very slight (3), moderate (4), deep (5) or very deep (6)	Code number
13.	Root flesh colour	white (1), cream (2), yellow (3), orange (4), purple (5).	Code number
14.	Root skin colour	white (1), cream (2), yellow (3), orange (4), brown (5), pink (6), red (7), or purple (8)	Code number
15.	Storage root shape	Round (1), Round elliptic (2), Elliptic (3), Ovate (4), Obovate (5), Oblong (6), Long-oblong (7), Long-elliptic (8), Long irregular or curved (9)	Code number
16.	General outline of the leaf	rounded (1), reniform/kidney-shaped (2), cordate (3), triangular (4), hastate (5), lobed (6) or divided (7)	Code number

S/N = Serial Numbre

3.2.4 Data analysis

Restricted maximum likelihood (REML) procedure (Payne et al., 2015) was used to analyse the variations of genotypes for yield and yield components. Genotypes were treated as fixed effects whereas season and genotype by season interaction, replication and block were treated as random effects. The model for REML analysis was as follows:

$Yijkl = \mu + Gi + Sj + GSij + Rk + Bl + \varepsilon ijkl$

Where: μ is the general mean, G is the genotype effects, S is the season effects, GS is the interaction effects of genotype and season, R is replication effects, B is the block effects and ε is the random term. The mean separation was done using Fisher's unprotected least significant difference (LSD) at $P \leq 0.05$.

Pearson's correlation coefficients were calculated using SPSS 20 program (SPSS, 2009) to assess the relationship between traits. Cluster analysis by Ward's method was done using the squared Euclidean distance to classify the genotypes into main groups and sub-groups.

Principal component analysis (PCA) was conducted using GENSTAT 14th edition program (Payne et al., 2015) to detect which descriptor variables contributed more to the variations among sweetpotato genotypes. The latent vectors were used to select the principal components which explained most of the variations among the tested sweetpotato genotypes. The vector loadings were used to ascertain which descriptor variables highly correlated with principal components which explain most of the variations among sweetpotato genotypes. Hierarchical cluster analysis based on complete linkage method was used to classify genotypes into main groups and sub-groups and genetic similarity matrix using 16 key morphological descriptors.

3.3 Results

3.3.1 Storage root number, root yield and dry matter content

There was a significant difference ($P < 0.001$) among genotypes for number of roots per plot, root yield and dry matter content (Table 3.3). Season had a significant effect ($P < 0.001$) on root number per plot and yield t ha^{-1}. There was also a significant effect of variety by season interaction for these traits. The mean root number per plot (1.3 m^2) ranged from 4.50 to 36.20. The genotypes Jewel, 18-CIP and Kisu cha Masai had significantly higher mean root number of 36.20, 32.20 and 31.20, in that order (Table 3.4). The storage root yield ranged from 1.72 to 10.14 t ha^{-1}. Genotype New Kawogo

collected from Lake Zone had the highest yield of 10.14 t ha^{-1} followed by Kiti cha Nyerere and Kisu cha Masai all collected from western Tanzania and yielding 9.85 and 9.67 t ha^{-1} respectively. The following genotypes: Kibandule, Madebe and Kabelele had significantly lower mean root yields of 1.72, 2.65 and 2.85 t ha^{-1} respectively. Genotypes expressed high yields during season I than season II. This could be attributed to a relatively better rainfall distribution in season I (Figure 3.1). DMC varied from 27.40% to 43.50% (Table 3.4). The following genotypes: Ngw'anangusa and Rugomoka collected from Western Zone and genotype Secondary collected from Lake Zone had significantly higher dry matter content of 43.50%, 43.30% and 43.30% respectively (Table 3.3). Genotypes 20-CIP, Chuga and Awilo had significantly lower DMC of 27.40%, 31.40% and 31.50%, respectively.

Table 3.3. Wald statistic showing significant tests for root yield, dry matter content and number of roots per plant.

Source of variation	DF	Wald statistic		
		Number of roots per plot	Yield	Dry matter content
Replication	2			
Genotype	95	448.02***	200.38***	928.50***
Season	1	20.97***	464.86***	1.37
Genotype * Season	95	282.01***	215.89***	361.26***
Error	192			

DF = degree of freedom, *** = significant at P< 0.001

Table 3.4. Mean root number, root yield and dry matter content of sweetpotato genotypes assessed in two seasons in western Tanzania.

SN	Genotype	Root number/plot	Root yield (t ha^{-1})	Dry matter content (%)
1	New Kawogo	21.67 $^{l-B}$	10.136 ^{x}	39.96 $^{t-H}$
2	Kiti cha Nyerere	19.33 $^{f-y}$	9.847 $^{w-x}$	41.33 $^{z-K}$
3	Kisu cha Masai	31.17 $^{D-F}$	9.672 $^{v-x}$	36.12 $^{f-m}$
4	18-CIP	32.17 $^{E-F}$	9.590 $^{u-x}$	39.13 $^{n-B}$
5	Tumauma	22.83 $^{q-B}$	9.535 $^{u-x}$	41.37 $^{z-K}$
6	New dimbuka	20.83 $^{j-A}$	9.321 $^{t-x}$	37.37 $^{i-u}$
7	8-CIP	21.67 $^{l-B}$	9.289 $^{t-x}$	36.05 $^{f-m}$
8	Ngw,ananzugi	20.50 $^{j-A}$	9.213 $^{s-x}$	37.^{16} $^{h-t}$
9	Masinia njano	30.50 $^{C-F}$	9.205 $^{s-x}$	43.00 $^{J-K}$
10	Secondary	22.17 $^{o-B}$	9.173 $^{r-x}$	43.30 $^{J-K}$
11	3-CIP	21.83 $^{m-B}$	9.000 $^{q-x}$	32.50 $^{b-c}$
12	Haraka	19.00 $^{f-x}$	8.849 $^{p-x}$	38.46 $^{l-y}$
13	UN 6	26.50 $^{y-E}$	8.795 $^{p-x}$	40.13 $^{u-I}$
14	Kimburu	25.00 $^{u-E}$	8.682 $^{o-x}$	42.26 $^{E-K}$
15	Mabangili	25.67 $^{v-E}$	8.581 $^{o-x}$	35.40 $^{d-j}$
16	Ntulawima	18.50 $^{e-v}$	8.549 $^{o-x}$	34.05 $^{b-g}$
17	UN 2	22.50 $^{p-B}$	8.541 $^{o-x}$	38.13 $^{j-x}$
18	Mwanatata	21.67 $^{l-B}$	8.455 $^{n-x}$	42.87 $^{I-K}$
19	Komando	23.00 $^{q-B}$	8.407 $^{m-x}$	42.96 $^{I-K}$
20	6-CIP	25.67 $^{v-E}$	8.260 $^{l-x}$	35.47^{d-k}
21	Shitoli	24.33 $^{t-D}$	8.199 $^{k-x}$	38.24 $^{j-y}$
22	Ngeni	20.83 $^{j-A}$	8.164 $^{j-x}$	37.39 $^{i-u}$
23	Wangeni	28.50 $^{B-E}$	8.164 $^{j-x}$	32.97 $^{b-d}$
24	Mugandi	24.00 $^{s-D}$	8.058 $^{j-x}$	34.37 $^{c-h}$
25	Kabakuli	17.33 $^{c-t}$	8.008 $^{j-x}$	36.31 $^{f-n}$
26	Magunhwa	20.17 $^{h-z}$	8.005 $^{j-x}$	35.99 $^{e-m}$
27	UN 1	19.83 $^{g-z}$	7.961 $^{i-x}$	35.48 $^{d-k}$
28	UN 4	22.17 $^{o-B}$	7.913 $^{h-x}$	39.34 $^{p-D}$
29	Kajiji	26.33 $^{y-E}$	7.629 $^{g-x}$	38.63 $^{m-A}$
30	Nkima atina siri	22.00 $^{n-B}$	7.608 $^{g-x}$	38.69 $^{m-A}$
31	Mwalu	22.83 $^{q-B}$	7.555 $^{g-x}$	34.48 $^{c-h}$
32	Naspot 1	22.33 $^{o-B}$	7.540 $^{g-x}$	39.11 $^{n-B}$
33	17-CIP	27.50 $^{A-E}$	7.509 $^{g-x}$	35.99 $^{e-m}$
34	Chuchu ya nesi	26.00 $^{x-E}$	7.460 $^{g-x}$	37.67 $^{j-v}$
35	Masinia M.W. N	19.50 $^{g-y}$	7.431 $^{g-x}$	39.12 $^{n-B}$
36	China	15.50 $^{b-p}$	7.428 $^{g-x}$	36.66 $^{f-q}$
37	12-CIP	20.33 $^{i-A}$	7.402 $^{g-x}$	41.4 $^{z-K}$
38	Nyaisome	16.67 $^{b-r}$	7.272 $^{g-x}$	39.77 $^{s-G}$
39	Malulumba	24.17 $^{s-D}$	7.254 $^{g-x}$	38.3 $^{k-y}$
40	SPKBH/03/03	14.00 $^{b-j}$	7.248 $^{g-x}$	37.51 $^{j-u}$
41	Kalamu	18.50 $^{e-v}$	7.219 $^{f-x}$	39.67 $^{s-F}$
42	Kabode	17.67 $^{d-t}$	7.196 $^{f-x}$	33.82 $^{b-f}$
43	Uchungu wa mbwa	25.33 $^{v-E}$	7.140 $^{f-x}$	36.46 $^{f-o}$
44	Lusafisha	20.50 $^{j-A}$	7.060 $^{f-x}$	39.71 $^{s-G}$
45	Kakamega	16.83 $^{b-r}$	7.057 $^{f-x}$	39.68 $^{s-G}$
46	UN 7 Kabelele	18.83 $^{f-x}$	6.790 $^{e-x}$	39.08 $^{n-B}$
47	14-CIP	23.00 $^{q-B}$	6.765 $^{e-x}$	43.00 $^{J-K}$
48	Masinia nyeupe	20.67 $^{j-A}$	6.742 $^{e-x}$	39.^{56} $^{r-E}$
49	Chrolophenical	14.67 $^{b-m}$	6.694 $^{e-x}$	41.57 $^{B-K}$
50	Kasinia	20.00 $^{h-z}$	6.555 $^{d-w}$	42.53 $^{G-K}$
51	Sengi	13.00 $^{b-h}$	6.544 $^{d-w}$	35.99 $^{e-m}$
52	Carot Dar	25.83 $^{w-E}$	6.533 $^{d-w}$	35.63 $^{d-I}$
53	Awilo	23.67 $^{r-C}$	6.520 $^{d-w}$	31.46 ^{b}
54	Ejumla	22.67 $^{p-B}$	6.480 $^{d-w}$	38.29 $^{k-y}$
55	21-CIP	22.50 $^{p-B}$	6.356 $^{d-v}$	36.93 $^{h-s}$
56	2-CIP	17.50 $^{d-t}$	6.329 $^{d-v}$	36.81 $^{g-r}$
57	Mulozi	27.00 $^{z-E}$	6.301 $^{d-v}$	37.60 $^{j-u}$
58	Mvumbagu	12.67 $^{b-g}$	6.300 $^{d-v}$	40.51 $^{v-J}$
59	Ukimwi	22.00 $^{n-B}$	6.283 $^{d-v}$	40.70 $^{x-K}$
60	24-CIP	18.17 $^{d-u}$	6.220 $^{c-u}$	37.42 $^{j-u}$
61	Magazi	17.50 $^{d-t}$	6.219 $^{c-u}$	41.02 $^{y-K}$
62	Chuga	12.17 $^{b-f}$	6.187 $^{c-u}$	31.35 ^{b}
63	Ndezu ya ntemi	18.67 $^{e-w}$	6.178 $^{c-u}$	42.97 $^{I-K}$
64	UN 3	14.50 $^{b-l}$	6.017 $^{b-t}$	42.95 $^{I-K}$
65	Rugomaka	16.50 $^{b-r}$	5.979 $^{b-t}$	43.30 $^{J-K}$
66	Ndovadoe	23.67 $^{r-C}$	5.934 $^{b-t}$	39.29 $^{o-D}$

Table 3.4 continued

SN	Genotype	Root number/plot	Root yield (t ha^{-1})	Dry matter content (%)
67	Ngw'anakurwa	13.17 $^{b-i}$	5.919 $^{b-t}$	42.49 $^{F-K}$
68	Ngw'anangusa	15.17 $^{b-o}$	5.919 $^{b-t}$	43.45 ^{K}
69	Polista	14.83 $^{b-n}$	5.826 $^{b-s}$	42.70 $^{H-K}$
70	Jewel	36.17 ^{F}	5.785 $^{b-s}$	31.87 $^{b-c}$
71	4-CIP	9.67 $^{a-b}$	5.757 $^{b-r}$	42.80 $^{H-K}$
72	Tegakatebo	16.33 $^{b-q}$	5.689 $^{b-q}$	42.01 $^{C-K}$
73	Simama	16.67 $^{b-r}$	5.680 $_{b-q}$	37.99 $^{j-x}$
74	11-CIP	16.67 $^{b-r}$	5.568 $^{b-p}$	34.56 $^{c-i}$
75	Pananzala	10.17 $^{a-c}$	5.546 $^{b-p}$	39.23 $^{o-C}$
76	Vitaa K	25.17 $^{u-E}$	5.427 $^{b-p}$	39.38 $^{q-D}$
77	Nyamvuva	11.50 $^{a-e}$	5.292 $^{b-o}$	42.14 $^{D-K}$
78	9-CIP	16.33 $^{b-q}$	5.291 $^{b-o}$	40.76 $^{x-K}$
79	5-CIP	9.67 $^{a-b}$	5.044 $^{a-n}$	36.33 $^{f-n}$
80	Kafu	14.17 $^{b-k}$	5.027 $^{a-n}$	38.60 $^{m-z}$
81	7-CIP	20.50 $^{j-A}$	4.998 $^{a-m}$	36.^{73} $^{g-r}$
82	10-CIP	25.67 $^{v-E}$	4.942 $^{a-l}$	40.65 $^{w-K}$
83	Utitiri	21.17 $^{k-A}$	4.936 $^{a-l}$	37.48 $^{j-u}$
84	Ukerewe	12.67 $^{b-g}$	4.911 $^{a-l}$	37.93 $^{j-x}$
85	Burenda	17.00 $^{c-s}$	4.775 $^{a-k}$	37.97 $^{j-x}$
86	UN 5	11.50 $^{a-e}$	4.737 $^{a-j}$	35.53 $^{d-k}$
87	Ngw,anakasenga	23.67 $^{r-C}$	4.550 $^{a-i}$	33.19 $^{b-e}$
88	25-CIP	14.33 $^{b-k}$	4.492 $^{a-h}$	37.80 $^{j-w}$
89	22-CIP	27.50 $^{A-E}$	4.270 $^{a-g}$	41.46 $^{A-K}$
90	Vitaa U	16.67 $^{b-r}$	3.561 $^{a-e}$	36.52 $^{f-p}$
91	20-CIP	13.83 $^{b-j}$	3.530 $^{a-e}$	27.40 ^{a}
92	Carot C	20.83 $^{j-A}$	3.501 $^{a-e}$	38.39 $^{l-y}$
93	13-CIP	10.17 $^{a-c}$	3.185 $^{a-d}$	41.48 $^{A-K}$
94	Kabelele	13.17 $^{b-i}$	2.848 $^{a-c}$	41.43 $^{z-K}$
95	Madebe	11.17 $^{a-d}$	2.652 $^{a-b}$	38.11 $^{j-x}$
96	Kibandule	4.50 ^{a}	1.718 ^{a}	39.72 $^{s-G}$
	Mean	**19.81**	**6.684**	**38.42**
	LSD (5%)	**7.386**	**3.473**	**2.937**
	Sed	**3.64**	**1.7**	**1.4**

SN= Serial number; Means in a column followed by the same letter are not significantly different at P=0.05; LSD = Least significant difference; Sed = Standard error of difference

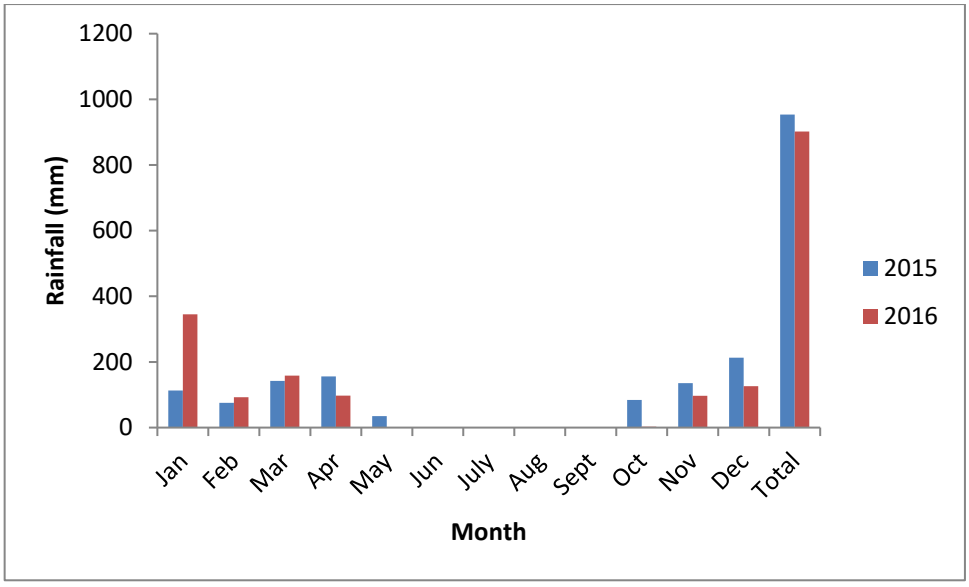

Figure 3.1. Rainfall distribution of the study site during 2015 and 2016.

3.3.2 Correlation among traits

The correlations among quantitative traits are presented in (Table 3.5). There was a significant positive correlation ($P < 0.01$) between root yield and root number per plot ($r = 0.736$), dry matter content and ground cover ($r = 0.475$), root yield and ground cover ($r = 0.320$), (Table 3.4). A significant negative correlation ($r = -0.21$) was revealed between root number and dry matter content.

3.3.3 Principal component analysis (PCA)

The results of the principal component analysis are presented in Table 3.6. The first four principal components with latent roots value >1 accounted for 69.33% of the variations among sweetpotato genotypes. PC1 was highly and positively correlated (0.90) with the root number per plot, and root yield (0.20) but highly and negatively correlated with root dry matter content (0.14). PC2 was highly and positively correlated (0.56) with root dry matter content, while PC3 was highly and positively correlated (0.47) with root dry matter content and root number per plot (0.20). PC4 was highly and positively correlated (0.56) with root dry matter content.

Table 3.5. Pearson correlation coefficients showing pair-wise association of 9 quantitative traits among 96 sweetpotato genotypes evaluated in western Tanzania.

Traits	Root number	Dry mass content	Root yield	Ground cover	Leaf lobe number	Leaf size	Petiole length	Internode diameter	Internode length
Root number		-0.209*	0.736**	0.119	0.246*	-0.073	0.144	-0.093	-0.017
Dry matter content			-0.118	0.475**	0.156	0.363**	0.122	0.123	-0.008
Root yield				0.32**	0.182	-0.06	0.211*	-0.097	0.07
Groundcover					0.092	0.323**	0.306**	0.258*	-0.27
Leaf lobe number						0.336**	-0.148	0.089	0.051
Leaf size							0.189	0.273**	0.059
Petiole length								0.328**	0.011
Internode diameter									-0.204*
Internode length									

** = Significant correlation at P < 0.01 probability level, * = Significant correlation at P < 0.05 probability lev

Table 3.6. Principal component analysis showing the latent roots, % variation and vector loadings of the first four PCs based on 16 agro-morphological traits used in the study.

Parameters/descriptors	PC1	PC2	PC3	PC4
Latent roots	7.8710	2.5401	1.4461	1.0732
% variation	42.21	13.62	7.75	5.75
Cumulative % variation	42.21	55.83	63.58	69.33
		Vector loadings		
General outline of the leaf	0.03616	0.19390	-0.26159	0.04852
Ground cover	0.01398	0.15765	0.14199	0.00978
Leaf lobe number	0.03921	0.22274	-0.22954	-0.00232
Leaf lobe type	0.08489	0.42130	-0.56144	0.08938
leaf size	-0.01289	0.10024	0.00751	0.01046
Petiole length	0.00778	0.00905	0.03320	0.00017
Plant type	-0.00839	0.01040	-0.00870	-0.00546
Root flesh colour	0.04472	-0.03925	0.03802	-0.08238
Root skin colour	-0.07591	0.31700	0.18084	-0.30565
Dry matter content	-0.14168	0.56830	0.47299	0.55939
Storage root shape	-0.00371	-0.03043	0.05979	0.02392
Storage root stalk	-0.11385	0.06415	0.02199	0.02624
Root number	0.91458	0.12906	0.19489	-0.11895
Internode diameter	-0.01208	0.03971	0.01762	-0.03496
Internode length	0.00109	0.00432	-0.03616	0.03709
Root yield	0.19882	0.07946	0.07363	-0.04308

PC1 = Principal component 1, PC2 = Principal component 2, PC3 = Principal component 3, PC4 = Principal component 4.

3.3.4 Clustering of sweetpotato genotypes based on phenotypic traits

The cluster analysis resulted in two major groups: Group A and Group B (Table 3.7). Group A had 11 sub-groups consisting of 66 genotypes whereas Group B had 5 sub-groups with 30 genotypes. The analysis showed a genetic diversity of 0.54 among test genotypes. Clustering of sweetpotato genotypes in groups showed a lack of association between origin of collection and genotypes. However most of the test genotypes from all the three geographical areas were clustered in Group A. Sub-group B3 had 4 genotypes all obtained from CIP/Peru (Table 3.7).

Genetic similarities among and within groups and sub-groups of characterized sweetpotato genotypes ranged from 0.66 to 0.91 with the mean similarity value of 0.85. The highest similarity of 0.91 was expressed within sub-group A2 consisting of 4 genotypes collected from Lake Zone, 3 from CIP and 4 from western Tanzania. The lowest similarity of 0.66 was expressed within sub-group B5 (consisting of 2 genotypes from Lake Zone and 1 from western Tanzania) and sub-group A10 (with 3 genotypes from western Tanzania and 1 from CIP.

Table 3.7. Main genetic groups, sub-groups and name of genotypes based on cluster analysis using complete linkage method.

Group	Sub-group	Name of genotype
A	A1	Malulumba, Uchungu wa mbwa, Ukerewe, Kabakuli, 7-CIP, 6-CIP, 3-CIP, Lusafisha, Awilo, UN 1, Haraka
	A2	Kakamega, 10-CIP, Simama, Kimburu, Kabelele, 5-CIP, Naspot 1, Vitaa K, Kisu cha Masai, New Kawogo, 22-CIP
	A3	Komando, Mwanakurwa, New Dimbuka , Secondary
	A4	Mvumbago, Masinia M.W. N, Polista
	A5	4-CIP, UN 5, 13-CIP
	A6	Utitiri, UN 6, Ndovadoe, UN 7, Kabelele, 2-CIP
	A7	Wangeni, Mwalu, Mabangili, Ejumla
	A8	UN 4, Kafu Carot C, Kalamu vitaa U, 12-CIP, Kabode, Masinia njano, 17-CIP
	A9	18-CIP, Mwana tata, Jewel
	A10	Ndezu ya ntemi, Ukimwi, 21CIP, Chrolophenical
	A11	Mwanangusa, Nyaisome, Rugomoka, Tegakatebo, Kasinia, Tumauma, Masinia nyeupe, burenda, Kajiji, Magazi
B	B1	Nyamvuva, 11-CIP, UN 3, Chuga, Kiti cha Nyerere, UN 2,Ntulawima
	B2	SPKBH/03/03, China, 14-CIP
	B3	24-CIP, 9-CIP, 25-CIP, 20-CIP
	B4	Nkima anina siri, Ngeni, Chuchu ya nesi, Pananzala, Mwanakasenga, Mwananzugi, 8-CIP, Sengi, Mulozi, Kibandule, Madebe, Shitoli
	B5	Carot Dar, Mugandi, Magunhwa

3.4 Discussion

3.4.1 Storage root yield

Sweetpotato genotypes used in this study were collected from different agro-ecological areas (Table 3.1) hence had differences in adaptability to the trial site leading to significant difference in root yield (Table 3.4). Sweetpotato varieties differ in their interaction with the environment in which they are growing. Varieties tend to have high yield in the environment in which they are well-adapted (Acquaah, 2012). The variation in root yield among tested sweetpotato genotypes also might be attributed to genetic differences among test entries (Kapinga et al., 2003; Lebot, 2009; Acquaah, 2012; Rukundo et al., 2013). Sweetpotato varieties differ in their genetic make-ups controlling accumulation of dry matter, growth and development of storage roots (Rukundo et al., 2013). Lebot (2009) suggested that root yield is the function of growing time. The more the time a crop takes to grow under field conditions the more the dry matter it accumulates and thus more yield. Therefore the difference in time to maturity among sweetpotato varieties also might have contributed to their differences in root yield. Significant difference in root yield has

been found among sweetpotato varieties in other studies (Tairo et al., 2008; Ngailo et al., 2016). Season one had higher root yield than season two due to difference in rainfall distribution among the two seasons (Figure 3.1). In this study, genotypes New Kawogo, Kiti cha Nyerere and Kisu cha Masai had significantly higher yield potential (Table 3.4). These genotypes are promising parents to be used in sweetpotato breeding programs to enhance yield and yield related traits.

3.4.2 Dry matter content and root number

Dry matter content is an important criterion for sweetpotato variety selection. For instance, in sub-Saharan Africa farmers prefer sweetpotato genotypes with high dry matter content (>28%), moderate sweetness and with dry mouth feel, while in the continental America farmers prefer sweetpotato varieties with low dry matter content, moist mouth feel and very sweet (Grüneberg et al., 2009; Cervantes-Flores et al., 2011). Dry matter content also is a crucial quality trait for sweetpotato cultivar adoption (Grüneberg et al., 2009; Cervantes-Flores et al., 2011).

Gasura et al. (2010) observed marked differences among genotypes in dry matter content and root number per plot. The significant difference in dry matter content and root number may be attributed to genotypic variations. For instance the expression of storage root formation and dry matter accumulation are controlled by different genes which differ among varieties (Rukundo et al., 2013). Dry matter accumulation in storage root also depends on the ability of the plant to translocate the photosynthetic assimilates from shoots to underground roots. Dry matter content decreases as the number of storage roots increases because it becomes difficult for a plant to supply enough photosynthetic assimilates to all the roots (Gasura et al., 2010). The presently tested genotypes Ngw'anangusa, Rugomoka and Secondary were found to have the highest dry matter content (Table 3.4). These are selected as the best parents for breeding to enhance high dry matter content.

3.4.3 Correlation among traits

Most traits considered in this study revealed a significant positive correlation (Tables 3.5). For instance a significant correlation (0.74) was revealed between root yield and root number. Other studies have also reported a significant positive correlation between root number and root yield (Gasura et al., 2010; Ngailo et al., 2016). Also, significant correlations were

calculated between dry matter content and ground cover (0.48), root yield and ground cover (0.32). Selection of correlated traits influences each other thus allowing simultaneous selection in plant breeding programs (Acquaah, 2012; Rukundo et al., 2013). In the current study a negative correlation (-0.21) was also revealed between root number and dry matter content (Table 3.5). This implies that selection for high dry matter content reduces the number of roots per plant. This result conforms to the previous findings that dry matter content decreases as the number of storage roots increases because it becomes difficult for a plant to supply enough photosynthetic assimilates to all the roots (Gasura et al., 2010).

3.4.4 Genetic diversity

The current study anticipated higher genetic diversity among test genotypes given the inclusion of some germplasm from CIP. However, minimal genetic diversity was detected. The CIP genotypes used in this study, though introduced from Peru, had their origins from India. Both Tanzania and India are neither the centre of diversity nor centre of origin of sweetpotato. The present study found a genetic diversity of 0.54 when using CIP standard morphological descriptors of sweetpotato geneotypes. This value is at par with the value of 0.52 found among sweetpotato genotypes collections and evaluations made from 3 different agro-ecological zones of Tanzania (Tairo et al., 2008). Genetic diversity of 0.55 was reported using simple sequence repeat markers (Gwandu et al., 2012). Therefore, the observed low genetic diversity among the characterized germplasm in this study might be due to the fact that both geographical areas received sweetpotato variety introductions from the same genetic pool.

The current results showed higher genetic similarity of 0.85 when genotypes were evaluated using agro-morphological traits. This value is higher than the value of 0.71 found in Tanzania sweetpotato germplasm using the amplified fragment length polymorphism (AFLP) (Elameen et al., 2008). Sub-group A2 expressed the highest genetic similarity of 0.91 due to varied sources of genotypes from all geographical sources (i.e. 4 from Lake Zone, 3 from CIP and 4 from Western Tanzania). The lowest genetic similarity was expressed in sub-group B5 and sub-group A10. Sub group B5 had 2 genotypes from Lake Zone and 1 from western Tanzania, while sub-group A10 had 3 genotypes from western Tanzania and 1 from CIP. This result suggests that there are more variations within the region than between regions. The high genetic similarity revealed in this study among genotypes of different geographical sources is in agreement with the result reported by Elameen et al (2008) and it is attributed to common genetic pool of the genotypes characterized. The current results also conform to earlier findings that sweetpotato germplasm express more variations within the geographic region

than between geographical regions (Gichuki et al., 2003). The authors proposed that this may be due to natural mutational events, inbreeding and some introductions of new genotypes.

3.4.5 Clustering of sweetpotato genotypes

Cluster analysis grouped the tested sweetpotato genotypes into two main groups, group A and group B (Table 3.7). The same trend of grouping was reported by other researchers characterising Tanzanian sweetpotato genotypes (Elameen et al., 2008; Tairo et al., 2008; Gwandu et al., 2012).These reports indicated that the two main grouping of sweetpotato could have been a result of introductions of sweetpotato to Tanzania. It is believed that the crop was introduced into the country firstly by Portuguese and secondly by British (Kapinga et al., 1995). Elameen et al. (2008) suggested that the two main introductions of sweetpotato to Tanzania might have come from two different genetic pools. The two main groups formed by cluster analysis in this study (Table 3.7) can serve as important genetic clusters for breeding.

Two main groups of genotypes presented in Table 3.7 by cluster analysis, were formed in a random manner irrespective of their geographical origin. Proper naming of sweetpotato varieties is the first and easiest criteria in distinguishing sweetpotato varieties. However, farmers in Tanzania use non-standardized system of naming leading to the same variety bearing different names in different areas (Kapinga et al., 1995; Tairo et al., 2008). For instance in the current study, *Simama* is an improved variety which is slightly orange fleshed, the same variety is called *Mayai* in Nzega district and *Kayai* in Sikonge district. This way the same variety can be considered bearing three different varieties. However, the present study could not detect any phenotypic difference in shoot and root morphology confirming these entries as duplicates. In some cases different varieties bear the same name but are basically different though the difference can be less conspicuous. For instance in Kigoma region three different varieties bear the same name of *Masinia.* In this situation one variety can be sampled, while excluding the other two. However, some farmers cautioned and suggested that though the varieties bear the same name they are different. Therefore the present study named the three genotypes as *Masinia Mguu wa kware*, *Masinia njano* and *Masinia nyeupe*. These collections had phenotypic resemblance in their shoot morphology and skin colour. However, they had some slight differences in flesh colour and root latex production.

3.5 Conclusions

The present study detected a genetic diversity of 0.54 in the sampled sweetpotato germplasm. The cluster analysis also grouped the sweetpotato germplasm into two main groups. The genetic diversity detected in the study and the two main genetic groups of germplasm can be exploited by sweetpotato breeders to breed new varieties. Genotypes Ngw'anangusa, Rugomoka and Secondary were selected with the highest dry matter content, while genotypes New Kawogo, Kiti cha Nyerere and Kisu cha Masai had the highest storage root yield. These genotypes are recommended as the best parents for sweetpotato breeding to enhance yield and dry matter content in western Tanzania or similar agro-ecologies.

Reference

Acquaah, G. 2012. Principles of plant genetics and breeding 2nd ed. Wiley-Blackwell, Oxford USA.

Bagarama, F.M., E.M. Shenkalwa, and Z.P. Matata. 2012. The effect of gypsum and NPK fertiliser on groundnut performance in Western Tanzania. *Third RUFORUM Biennial Meeting*. Entebbe, Uganda, 24-28 September 2012.

Burri, B.J. 2011. Evaluating sweet potato as an intervention food to prevent vitamin A deficiency. Comprehensive Reviews in Food Science and Food Safety 10: 118-130.

Cervantes-Flores, J., B. Sosinski, K. Pecota, R. Mwanga, G. Catignani, V.-D. Truong, R. Watkins, M. Ulmer and G.C. Yencho. 2011. Identification of quantitative trait loci for dry-matter, starch, and β-carotene content in sweetpotato. Molecular Breeding 28: 201-216.

Clark, C.A., J.A. Davis, J.A. Abad, W.J. Cuellar, S. Fuentes, J.F. Kreuze, R.W. Gibson, S.B. Mukasa, A.K. Tugume and F.D. Tairo. 2012. Sweetpotato viruses: 15 years of progress on understanding and managing complex diseases. Plant Disease 96: 168-185.

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

Engoru, P., J. Mugisha and B. Bashaasha. 2005. Tuber utilisation options among sweet potato producers in eastern Uganda. African Crop Scince Journal 7: 715.

FAOSTAT. 2014. Food and Agriculture Organisation of the United Nations: Crop production data. FAOSTAT Division, Rome.

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

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.

Gruneberg, W., R. Mwanga, M. Andrade and J. Espinoza. 2009. Breeding clonally propagated crops *In*: Ceccarelli, S., E.P. Guimarães and E. Weltzien, editors, *Plant breeding and farmer participation.* Food and Agriculture Oganization of the United Nations, Rome. p. 275-323.

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

Huaman, Z. 1991. Descriptors for the characterization and evaluation of sweet potato genetic resources. CIP Lima, Perú. p. 331 - 355.

Kapinga, R., and E. Carey. 2003. Present status of sweetpotato breeding for eastern and southern Africa. Sweetpotato post-harvest Assessment. Experiences from East Africa. Chatham, United Kingdom. NRI/CPHP/DFID/CIP/Ministry of Agriculture. Natural Resources Institute: The University of Greenwich. ISBN 0 859554: 2.

Kapinga, R., S. Jeremiah, E. Rwiza, and D. Rees. 2003. Farmers criteria for selection of sweetpotato varieties, results from Tanzania. Chatham, United Kingdom.

Kapinga, R.E., P.T. Ewell, S. Jeremiah, and R. Kileo. 1995. Sweetpotato in Tanzanian farming and food systems: implications for research. International Potato Center, Tanzanian Ministry of Agriculture, Nairobi and Dar-Es-Salaam.

Lebot, V. 2009. Tropical root and tuber crops: cassava, sweet potato, yams and aroids. CABI, Wallingford.

Mbithe, M.J., R. Steven, S. Agili, M.B. Kivuva, W.F. Kioko, and E. Kuria. 2016. Morphological Characterisation of Selected Ugandan Sweet potato (*Ipomoea batatas* L) Varieties for food and feed. Phylogen Evolution Biology 4. doi:10.4172/2329-9002.1000163.

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.

Nelles, W. 2009. Sweetpotato Education, Research and Capacity Development through a CIP-Orissa Learning Site. CTCRI, Bhubaneswar, Orissa, India.

Ngailo, S., H. Shimelis, J. Sibiya, and K. Mtunda. 2016. Screening of Tanzanian sweet potato germplasm for yield and related traits and resistance to sweet potato virus disease. Acta Agriculturae Scandinavica, Section B — Soil & Plant Science 66: 52-66.

Payne, R., S. Welham, and S. Harding. 2015. A Guide to REML in Genstat. VSN International, 2 Amberside, Wood Lane, Hemel Hempstead, Hertfordshire HP2 4TP, UK.

Rukundo, P., H. Shimelis, M. Laing, and D. Gahakwa. 2013. Storage root formation, dry matter synthesis, accumulation and genetics in sweet potato. Australian Journal of Crop Science 7: 2054-2061.

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. doi.org/10.1186/1471-2164-11-604.

Sebastiani, S., 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. *8th African Crop Science Society Conference*, El-Minia, Egypt, 27-31 October 2007.

Shumbusha, D., H. Shimelis, M. Laing, and T. Asiimwe. 2017. Phenotypic diversity analysis of sweetpotato for breeding dual-purpose varieties. Acta Agriculturae Scandinavica, Section B—Soil & Plant Science 67: 340-351.

SPSS. 2009. Statistical Package for Social Scientists. SPSS for Windows Release 18.0, Chicago, IL.

Tairo, F., E. Mneney, and A. Kullaya. 2008. Morphological and agronomical characterization of sweet potato [*Ipomoea batatas* (L.) Lam.] germplasm collection from Tanzania. African Journal of Plant Science 2: 77-85.

Vimala, B., and B. Hariprakash. 2011. Variability of morphological characters and dry matter content in the hybrid progenies of sweet potato (*Ipomoea batatas* (L) Lam). Gene Conserve 10: 65-86.

CHAPTER 4 SCREENING OF SWEETPOTATO GERMPLASM FOR SWEETPOTATO WEEVIL (*CYLAS* SPP.) RESISTANCE IN TANZANIA

Abstract

Sweetpotato in Tanzania is cultivated almost in all agro-ecological zones under subsistence farming systems as a source of food and cash income. It is preferred by most rural and smallholder farmers due to its high productivity per unit area, drought tolerance, early maturity and relatively good performance under the low input production systems. However, weevil infestation caused by the sweetpotato weevil (*Cylas* spp.) is a major constraint to sweetpotato production in the country as there are no improved varieties with reasonable resistance to the pest. The objective of this study was to screen sweetpotato germplasm collections for weevil resistance and to select the best parents to be used in resistance breeding. Field studies involving a total of 96 sweetpotato genotypes were conducted at two weevil hotspot sites in western Tanzania using a 12 x 8 lattice design with three replications at each site. Data collected included yield and yield related traits, weevil reaction and weevil damage score. The tested genotypes differed significantly ($P < 0.01$) for sweetpotato storage root number, root weight, root infestation and root damage score. Weevil infestation on storage roots was significantly ($P < 0.05$) correlated with total root number and weevil damage score ($r = 0.38$ and 0.79 respectively). Marketable root weight and total root weight were significantly correlated with infested root weight ($r = 0.45$ and 0.45 respectively). Nine sweetpotato genotypes expressing resistance and 10 genotypes expressing moderate resistance to weevils were identified. Five genotypes which included Magunhwa, Chuchu ya Nesi, Rugomoka, Tumauma and New Kawogo were selected as they expressed both weevil resistance and desirable yield and yield-related traits. These genotypes will be used in future weevil resistance breeding programs of sweetpotato in western Tanzania or related agro-ecologies.

Keywords: *Cylas* spp.*,* resistance breeding, screening, weevils, western Tanzania

4.1 Introduction

Sweetpotato (*Ipomoea batatas* [L.] Lam.) is an important root crop grown in more than 110 countries worldwide on an estimated area of 8.21 million hectare (ha), with an annual production of 104.02 million tonnes (FAOSTAT, 2014). As a food crop, sweetpotato ranks seventh globally and fifth in developing countries after rice (*Oryza sativa* L.), wheat (*Triticum aestivum* L.), maize (*Zea mays* L.) and cassava (*Manihot esculenta* L.) (Elameen et al., 2008; Nelles, 2009). In sub-Saharan Africa (SSA), sweetpotato is the most important staple food crop grown on about 2.1 million ha and producing about 9.9 million tonnes fresh storage roots per annum (Anyanga et al., 2013).

In addition to food, sweetpotato is also used as a source of cash income and feed in many countries in SSA (Fuglie, 2007). The storage roots are used in various forms such as fried chips, boiled roots or as baked products (Engoru et al., 2005). The young leaves of the crop are used as leaf vegetable. In some instances the entire canopy of the crop can be used as fodder for livestock. Sweetpotato roots are rich in carbohydrates and the orange-fleshed sweetpotato varieties (OFSPs) contain high β-carotene that is a precursor of vitamin 'A' useful in combating vitamin A deficiency in humans (Mwanga et al., 2007; Burri, 2011). Sweetpotato roots are also used as industrial raw material for biofuel, starch and alcohol extraction (Schafleitner et al., 2010; Clark et al., 2012).

Tanzania is the second largest producer of sweetpotato in SSA after Nigeria (FAOSTAT, 2014), where the crop is grown on an estimated area of 0.56 million ha of agricultural lands with a mean national yield of 4.55 t ha^{-1}. In Tanzania, sweetpotato is cultivated in almost all agro-ecological zones under subsistence farming systems (Kulembeka et al., 2005; Masumba et al., 2005; Kagimbo et al., 2017). Sweetpotato is preferred by most rural farmers due to its high productivity per unit area, drought tolerance, early maturity and relatively good performance in marginal and poor soils (Kapinga et al., 1995). In most growing zones of Tanzania, farmers practice flexible planting and harvesting schedules of the crop. Further, sweetpotato fits into different cropping systems where it can be cultivated as a monocrop or intercropped with cassava, maize, beans, cowpea or groundnut (Ngailo et al., 2016a).

Sweetpotato production in Tanzania is faced with a range of constraints including biotic, abiotic and socio-economic factors which have contributed to the existing low yields of 4.62 t ha^{-1}compared to the potential productivity of the crop varying from 15 to 23 t ha^{-1} (Sebastiani et al., 2007). Amongst these constraints, sweetpotato weevil infestation caused by sweetpotato weevil (*Cylas* spp.) poses a major threat to sweetpotato production in Tanzania. To control the weevils, agronomic practices such as field sanitation, early planting and early harvesting, and chemical treatment have been used by farmers. However, chemical control is too expensive and unaffordable to farmers and it is less effective because the juvenile weevils develop in roots and vines (Lebot and Bradshaw, 2010). Cultural practices such as early planting are a difficult management practice for many farmers due to

the shortage of planting materials at the onset of rainfall. Early harvesting is also a challenge since farmers practice sequential and piecemeal harvesting to minimise post-harvest losses. In SSA sweetpotato growers experience a range of challenges from a lack of; well-designed storage facilities, postharvest handling facilities during packaging and transport, knowledge on processing, processing equipment and a problem of transporting bulky products (Masumba et al., 2005). Therefore, field maintained storage roots of the crop are vulnerable to several pests and diseases. Among these, sweetpotato weevils are reported to be serious insect pests damaging the crop in the field.

Breeding sweetpotato varieties with durable resistance to weevils is advocated as the best strategy to control weevils (Muyinza et al., 2012; Anyanga et al., 2013). However, weevil resistance varieties are yet to be developed and released in Tanzania. It is thus important to identify weevil resistant germplasm through effective screening involving adequate weevil infestation among trials, locations and seasons (Stathers et al., 2003). A study conducted in Tanzania and Uganda by Stathers et al. (2003) reported the existence of sweetpotato varieties exhibiting different levels of resistance to weevils, which was partly attributed to escape mechanism (Stathers et al., 2003; Muyinza et al., 2012).

In determining the level of resistance of sweetpotato varieties to weevils, test genotypes need to be subjected to the required level of pest pressure. This will ensure high levels of infestation to screen for resistance. Researchers practice artificial inoculation of laboratory reared weevils for field inoculation with a small population of the weevils for effective infestation and screening (Stathers et al., 2003; Muyinza et al., 2012). In weevil hotspot areas including western Tanzania where large population of natural weevil infestation occurs, artificial inoculation of the pest is not required (Stathers et al., 2003). The activity of artificially inoculated weevils is reported to be highly affected by environmental factors such as rainfall, and excessively low or high temperature conditions (Stathers et al., 2003).

Recently, the existence of sweetpotato varieties with reasonable levels of resistance to weevils has been reported. For instance the following varieties: New Kawogo, Dimbuka, Anamoyoto and Kyebagambire have been identified and reported to express resistance to *Cylas* spp. with active chemical based resistance mechanism (Stevenson et al., 2009; Muyinza et al., 2012; Anyanga et al., 2013). This type of resistance is attributed to higher levels of esters of hydroxylcinnamic acid in root latex (Stevenson et al., 2009) and esters of caffeic and coumaric acid in epidermal and root surface of resistant varieties (Anyanga et al., 2013). These chemical compounds conferring resistance to *Cylas* spp. are reported to be toxic to juvenile *Cylas* spp. but also repellent to adult *Cylas* spp. This indicates that more resistant varieties can possibly be selected among the local landraces. To date sweetpotato germplasm collections in Tanzania have not been effectively screened for weevil resistance breeding. Therefore, the objective of this study was to screen sweetpotato germplasm

collections for sweetpotato weevil (*Cylas* spp) resistance in Tanzania and to select best parents to be used in breeding for weevil resistance.

4.2 Material and methods

4.2.1 Description of the study sites

This study was conducted under field experiments established at two sites. The first site was situated at Tumbi Agricultural Research Institute (ARI-Tumbi) located at 5˚4'11''S, 32˚ 40'1''E and the second location was a farm situated at Ndorobo village located at 5˚5'12''S, 32˚1'26''E both in western Tanzania. ARI-Tumbi is characterized by a unimodal rainfall pattern receiving a mean annual rainfall of 920 mm. The main rainfall season is between November and April. The climate is generally dry and warm with a mean daily temperature of 23˚C. These conditions favour sweetpotato weevil activity (Muyinza et al., 2012). Ndorobo village has a unimodal rainfall pattern receiving a mean annual rainfall of 960 mm. It is generally dry and warm with a mean daily temperature of 22˚C. The two sites were identified as hotspots for sweetpotato weevils in western Tanzania. The soil physio-chemical characteristics of both sites selected for the study are presented inTable 4.1 whereas the the rainfall distribution of the sites during the study season is presented in Figure 4.1.

Table 4.1. Physio-chemical characteristics of soils of the study sites.

	Soil characteristics										
	pH	**Total N (%)**	**OC (%)**	**Available P (ppm)**	**Exchangeable bases (meq/100g)**		**EC (mS/cm)**	**Texture (%)**			**Textural class**
Study site					Mg	Ca		Sand	Silt	Clay	
Ndorobo	6.2	0.13	0.63	17.5	1.22	0.22	0.06	71	9	20	SL
ARI-Tumbi	6.1	0.04	0.270	16.1	0.04	0.23	1.62	75	9	16	SL

OC = organic carbon, EC = electrical conductivity, SL = Sandy loam,

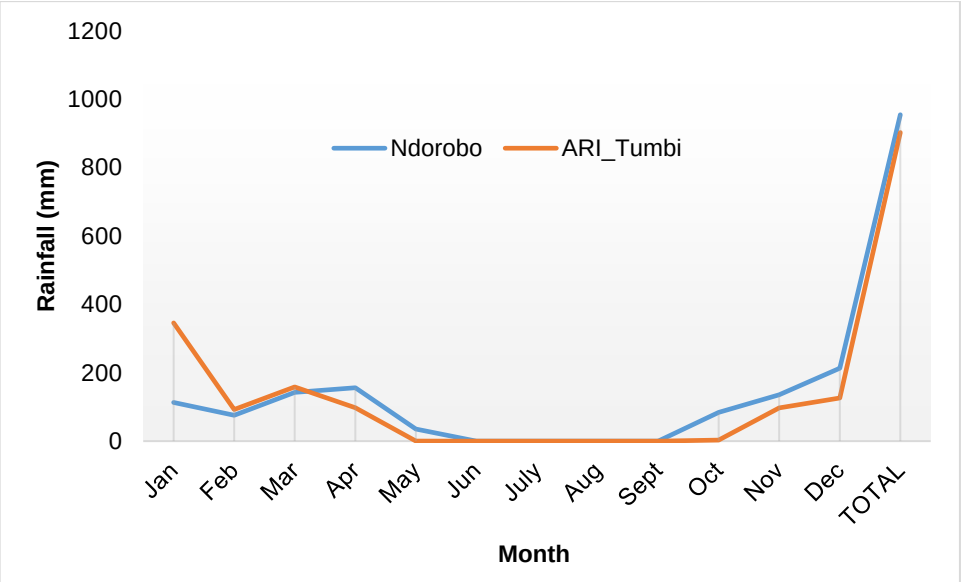

Figure 4.1 Rainfall distribution at the sites during the study season.

4.2.2 Germplasm and trial establishment

The list of sweetpotato genotypes used in this study are presented in Table 3.1. A collection of 96 sweetpotato genotypes were used in this study. Among the 96 genotypes, 57 were local varieties or landraces collected from western Tanzania; 19 were collected from Lake Zone and 20 genotypes were introductions from International Potato Centre (CIP)–Lima/Peru. The CIP collections were originally obtained from India. The genotype Simama was used as a susceptible check, while genotype New Kawogo was used as a resistant check. Genotypes were screened for weevil resistance under natural infestation at the selected hotspot areas. Trials were established in late January 2015 and harvested in late June 2015 to ensure high level of weevil infestation for selection. Experiments were conducted using a 12 x 8 lattice design with three replications at each site. The spacing used was 1m inter-row and 0.3m intra-row. The plot size was 3 m x 2.1 m consisting of 3 ridges each with 7 plants making a total of 21 plants per plot. Fertilizers were applied using Nitrogen, Phosphorus and Potassium (15:9:20) at the rate of 233 kg/ha a month after planting. Weeding was done three times at 30, 70 and 110 days after planting.

4.2.3 Data collection

Six months after planting (MAP), the number of surviving plants in the middle row were recorded and the storage roots dug. The total weight of storage root per plot and the number of marketable and unmarketable storage roots per plot were recorded. Then the storage roots were separated into

infested and non-infested roots and weighed separately. Infested roots were counted to get the infested root number (IRN) per plot. Weevil damage score (WDS) of roots was scored based on the proportion (percentage) of the root area damaged on the outer surface and inner parts of the root. WDS was assessed using a scale of 0 to 10 where 0 = no damage, 1 = 1-10% of the root damaged, 2 = 11- 20%, 3 = 21- 30%, 4= 31- 40%, 5 = 41- 50%, 6 = 51- 60%, 7 = 61- 70%, 8 = 71- 80%, 9 = 81-90% and 10 = 91-100%.

4.2.4 Data analysis

Data collected were organised in excel and analysed using GENSTAT PROGRAM 14th edition (Payne et al., 2015). Marketable root number (MRN), total root number (TRN), marketable root weight (MRW), total root weight (TRW), IRN, infested root weight (IRW) and WDS were analysed using the restricted maximum likelihood (REML) procedure (Payne et al., 2015). Genotype was set as fixed effect, whereas season and genotype by season interaction, replication and block were treated as random effects. The model used was:

$$Yijkl = \mu + Gi + Lj + GLij + Rk + Bl + \varepsilon ijkl$$

Where: μ is the general mean, G, L, GL, R, and B denote the effects of genotype, location, the interaction effects of genotype and location, replication, the incomplete block, in that order. Ɛ is the random term. Following significant tests, treatment means were separated using the least significant difference (LSD) procedure at $p \leq 0.05$. The relationship between traits were assessed by computing the Pearson's correlation coefficients using SPSS 24 program (SPSS, 2009).

4.3 Results

4.3.1 Storage root number, root weight and weevil damage score

There was a significant difference ($P < 0.001$) among genotypes on all the studied traits (Table 4.2). Location had significant effect on MRN, MRW, IRN and WDS (Table 4.2).

Table 4.2. Restricted maximum likelihood analysis of root number, root weight and root damage score of 96 sweetpotato genotypes evaluated across two sites.

Source of variation	DF	Wald statistic						
		MRN	TRN	MRW	TRW	IRN	IRW	WDS
Replication	2							
Genotype	95	272.04***	275.01***	197.94***	192.23***	156.54***	141.94***	134.75**
Location	1	15.81***	0.19	7.29**	1.75	5.67*	3.05	4.35*
Genotype * Location	95	74.22	54.51	54.35	57.83	42.94	41.43	32.41
Error	192							

DF = degree of freedom, *** = significant at P < 0.001, ** = significant at P < 0.01, *significant at P < 0.05, MRN = Marketable root number per plot, TRN = Total root number per plot, MRW = Marketable root weight per plot (kg/plot), TRW = Total root weight per lot (kg/plot), IRN = Infested root number per plot, IRW = Infested root weight per plot (kg/plot), WDS = Weevil damage score.

4.3.2 Mean response of genotypes for storage roots: root number, root weight, weevil infestation and damage

The mean TRN, TRW, IRN and WDS differed significantly among the tested sweetpotato genotypes (Table 4.2 and 4.3). MRN per plot ranged from 1.69 to 19.52 with a mean of 12.12 (Table 3). The following genotypes: Kiti cha Nyerere Shitoli, Tumauma and New Kawogo had the highest MRN per plot. TRN per plot ranged from 3.20 to 36.15 with a mean of 21.06 (Table 4.3). Genotypes Mugandi, 7-CIP, Ukimwi and Ngw'anakasenga had the highest TRN per plot of 36.15, 34.07, 33.10 and 32.37, in a decreasing order.

MRW per plot ranged from 0.15kg to 6.77kg with a mean of 3.73kg. Genotypes Ngw'ananzugi, Kiti cha Nyerere, Magunhwa and Shitoli had the highest MRW per plot of 6.77kg, 6.55kg, 5.87kg and 5.70kg, in that order. The TRW per plot ranged from 0.28kg to 7.40kg with a mean of 4.31kg (Table 4.3). Genotypes Ngw'ananzugi, Kiti cha Nyerere, Ukimwi and Shitoli had the highest TRW per plot of 7.40kg, 6.93kg, 6.43kg and 6.28kg, respectively.

IRW per plot ranged from 1.85% to 71.97% with a mean of 34.74%. Genotypes Madebe, Kibandule, Malulumba and Utitiri had the lowest IRW per plot of 1.85%, 4.14%, 6.27% and 7.33%, in that order. IRN per plot ranged from 2.01% to 59.84% with a mean of 27.84 (Table 4.3). Genotypes Malulumba, Kibandule, 4-CIP and Madebe had the lowest IRN of 2.01%, 2.40%, 4.87% and 5.59%, in that order.

WDS ranged from 3.42% to 62.76% with a mean of 32.12% (Table 4.3). Genotypes with WDS between 0% and 14.9% were categorised as resistant to the weevil. Therefore, the following genotypes were selected for weevil resistance: Kibandule, Malulumba, Utitiri, 3-CIP, Madebe,

Magunhwa, 5-CIP, Kafu and Chuchu ya nesi. Genotypes with WDS between 15% and 20% were categorized as moderately resistant. This group included: Nyamvuva, Sengi, 22-CIP, Rugomoka, Tumauma, Ejumla, Carot C, New Kawogo 2, Haraka and 4-CIP. Genotypes with WDS between 20.1% and 24.9 were categorised as moderately susceptible. This group included Chuga, Ukerewe, UN 6, New Kawogo, 25-CIP, Kimburu, Nyaisome, Masinia M.W.N and Mulozi. Genotypes with WDS > 25% were categorized as susceptible. Some of the tested genotypes categorised as resistant or moderately resistant lacked good agronomic traits such as yield and yield-related traits (Table 4.3). Only five genotypes with weevil resistance and desirable yield were identified with data summary presented inTable 4.4. These genotypes included: Magunhwa, Chuchu ya nesi, Rugomoka, Tumauma and New kawogo.

In general the Ndorobo Village site had the higher percentage of MRN, IRN and WDS (Table 4.3). ARI site had higher values of MRW.

Table 4.3. Mean values of seven traits of 96 sweetpotato genotypes evaluated at two sites in western Tanzania.

SN	Genotype	MRN	TRN	MRW	TRW	IRN	IRW	WDS
1	Komando	12.86 e-y	21.70 f-A	5.099 u-C	5.892 y-I	8.573 g-v	3.395 r-x	45.25m-z
2	Vitaa K	14.69 p-E	30.44 A-G	4.334 l-A	5.026 l-H	7.837 e-u	2.028 d-w	30.06b-w
3	Mvumbagu	11.38 b-u	14.72 b-k	3.870 f-z	4.181 c-B	7.486 d-t	2.796 o-x	42.74 k-z
4	Kimburu	16.05 t-E	25.05 m-F	5.311 w-C	5.977 z-I	5.68 a-s	1.728 b-r	23.44 a-q
5	Ntegakatebo	12.74 e-y	21.73 g-A	3.503 b-x	4.205 c-D	8.325 g-v	1.191 a-o	28.05 a-u
6	8-CIP	12.65 d-y	21.47 f-A	4.623 q-A	5.279 o-H	6.322 a-s	2.317 h-x	36.92 d-z
7	18-CIP	15.92 s-E	28.32 w-G	4.281 k-A	4.985 l-H	10.049 l-x	2.642 l-x	44.16 m-z
8	Ukerewe	8.40 b-h	10.89 a-c	3.598 c-x	3.888 b-x	4.59 a-o	1.015 a-l	20.47 a-n
9	Ngw'anangusa	9.57 b-n	19.28 c-w	2.625 b-o	3.407 b-p	3.533 a-j	0.681 a-h	25.81 a-t
10	17-CIP	7.10 b-c	15.10 b-k	1.620 a-b	2.001 a-b	3.707 a-l	0.913 a-j	31.30 c-x
11	Kalamu	10.76 b-r	17.34 c-o	4.237 j-A	4.625 f-G	4.84 a-q	1.707 b-q	25.78 a-s
12	13-CIP	7.70 b-d	10.66 a-c	2.364 b-k	2.503 b-d	5.512 a-r	1.767 c-s	29.67 a-w
13	25-CIP	9.70 b-p	19.50 c-w	2.159 b-g	2.605 b-e	3.30 a-i	0.837 a-i	23.27 a-q
14	Chuchu ya nesi	15.70 r-E	31.70 C-G	4.984 s-C	5.759 u-I	2.753 a-g	0.982 a-l	14.32 a-h
15	Magunhwa	12.76 e-y	17.94 c-t	5.868 A-C	6.282 F-I	3.613 a-k	1.506 a-p	12.80 a-e
16	Sengi	12.63 d-y	17.47 c-p	4.033 g-A	4.566 e-G	1.229 a-d	0.332 a-c	15.31 a-i
17	Jewel	9.65 b-o	31.31 C-G	1.871 a-d	2.650 b-f	11.331 rx	1.199 a-o	51.06 r-z
18	Ejumla	10.69 b-q	21.77 g-A	3.099 b-t	3.751 b-u	2.353 a-g	0.822 a-i	18.99 a-m
19	Masinia M.W.N	10.18 b-p	14.01 b-i	3.611 c-x	3.800 b-u	5.27 a-r	1.655 a-q	24.24 a-q
20	UN 2	13.70 j-B	24.54 l-E	4.561 p-A	5.244 n-H	14.302v-x	3.424 s-x	48.26 p-z
21	UN 6	13.14 g-A	21.19 e-z	4.976 t-C	5.617 t-I	3.40 a-i	0.940 a-k	21.47 a-o
22	Rugomoka	18.04 A-E	28.78 x-G	5.118 u-C	5.863 v-I	3.30 a-i	0.974 a-l	16.28 a-k
23	5-CIP	7.66 b-d	15.15 b-k	3.012 b-r	3.567 b-s	2.73 a-g	1.113 a-n	13.50 a-f
24	Kafu	12.38 d-y	19.34 c-w	3.962 f-A	4.572 e-G	1.49 a-e	0.685 a-h	13.65 a-g
25	Awilo	12.00 c-x	22.75 i-C	3.588 c-x	4.128 c-A	8.000 fv	2.065 e-w	40.51 h-z
26	Kabelele	9.14 b-l	15.41 b-l	2.353 b-j	3.728 b-t	6.461 a-s	1.817 c-v	41.53 i-z
27	Kasinia	14.24 m-D	21.78 g-A	4.210 j-A	4.765 h-G	10.753 p-x	2.910 p-x	54.41 u-z
28	Kakamega	11.28 b-u	18.85 c-v	4.137 i-A	4.823 j-G	5.421 a-r	1.597 a-q	35.41 d-y
29	10-CIP	11.55 b-v	27.31 u-G	2.355 b-j	3.360 b-p	7.097 c-s	1.106 a-m	31.12 b-x
30	Ukimwi	16.39 v-E	33.10 E-G	5.186 v-C	6.430 G-I	7.125c-s	1.972 c-w	28.41 a-v
31	Nkima ati na siri	15.34 q-E	23.46 j-D	5.101 u-C	5.614 t-I	4.233 a-m	1.177 a-o	27.80 a-t
32	Malulumba	12.98 f-z	22.20 h-B	3.501 b-x	4.154 c-A	0.541 a	0.326 a-c	04.68 a-b
33	Masinia njano	11.91 c-x	21.79 g-A	3.447 b-x	4.111 c-A	7.446 d-t	1.519 a-p	34.66 d-y
34	Burenda	7.86 b-e	16.34 b-m	2.555 b-m	3.116 b-l	5.731 a-s	1.461 a-p	28.40 a-v
35	Ntulawima	10.71 b-r	17.45 c-p	3.381 b-v	3.875 b-w	7.008 b-s	1.553 a-p	40.02 f-z
36	Ndezu ya ntemi	10.65 b-q	19.43 c-w	3.207 b-u	3.823 b-u	3.645a-k	1.139 a-o	26.29 a-t
37	Nyamvuva	12.83 e-y	18.23 c-u	3.627 c-x	3.946 b-y	3.658 a-k	0.974 a-l	15.27 a-i
38	Lusafisha	13.58 i-B	20.12 d-x	4.533 n-A	5.063 l-H	2.93 a-g	0.769 a-i	26.54 a-t
39	Vitaa U	10.09 b-p	18.76 c-v	2.496 b-l	2.987 b-k	3.267 a-i	0.694 a-h	37.27 d-z
40	Utitiri	8.14 b-f	11.56 a-d	3.079 b-s	3.341 b-p	0.982 a-c	0.445 a-e	7.86 a-c
41	Ngw'anakasenga	12.13 d-x	32.37 D-G	2.434 b-l	3.442 b-p	9.562 i-x	1.416 a-p	35.54 d-y
42	Haraka	10.94 b-s	20.22 d-x	2.681 b-p	4.580 e-G	3.014 a-h	0.503 a-f	19.84 a-m
43	UN 4	11.70 b-v	18.62 c-v	3.796 e-z	4.449 d-G	3.97 a-l	1.097 a-m	31.48 c-x
44	China	13.98 k-C	19.51 c-w	4.149 i-A	4.621 f-G	10.346 m-x	2.713 m-x	41.23 i-z
45	Carot C	11.10 b-t	25.60 n-F	2.060 a-f	2.913 b-j	2.498 a-g	0.360 a-d	19.38 a-m
46	Magazi	11.76 b-w	21.50 f-A	4.079 h-A	4.676 g-G	4.750 a-p	1.731 b-r	37.97 d-z
47	Mabangili	14.61 o-E	23.33 j-D	5.611 y-C	6.230 E-I	3.23 a-i	1.197 a-o	30.47 b-w
48	3-CIP	10.47 b-q	21.76 g-A	3.965 g-A	4.593 e-G	2.576 a-g	0.358 a-d	11.63 a-d
49	2-CIP	10.45 b-q	21.39 f-A	2.609 b-m	3.231 b-n	5.413 a-r	0.956 a-k	28.04 a-u
50	12-CIP	9.02 b-k	15.95 b-m	2.969 b-r	3.533 b-r	3.235 a-i	0.919 a-j	25.21 a-r
51	Secondary	10.11 b-p	13.24 b-g	3.523 b-x	4.075 c-A	6.843 e-s	1.771 c-t	45.78 p-z
52	Masinia nyeupe	15.33 q-E	26.43 o-F	4.623 q-A	5.328 p-H	6.022 a-s	1.433 a-p	30.90 b-x
53	11-CIP	11.45 b-v	17.97 c-t	3.769 e-y	4.022 c-z	5.279 a-r	1.641 a-q	32.14 c-x
54	Kabode	14.04 l-C	21.66 f-A	4.503 n-A	4.905 j-G	5.027 a-r	1.351 a-p	27.02 a-t
55	20-CIP	9.48 b-n	16.23 b-m	2.292 b-i	2.726 b-g	1.699 a-f	0.580 a-g	33.01 c-x
56	4-CIP	10.12 b-p	13.87 b-i	3.371 b-v	3.726 b-t	0.71 a-b	0.330 a-c	19.88 a-m
57	New Kawogo	18.32 B-E	28.36 w-G	4.953 s-C	5.581 s-I	4.220 a-m	1.164 a-o	21.47 a-o
58	Pananzala14-CIP	6.83 b	12.23 a-e	3.395 b-w	3.835 b-u	4.984 a-r	2.247 g-x	35.50 d-y
59	14-CIP	8.80 b-j	19.48 c-w	2.199 b-h	2.753 b-h	6.588 a-s	1.555 a-p	44.59 m-z
60	Simama	9.86 b-p	17.86 c-s	3.251 b-u	3.737 b-t	5.65 a-r	1.638 a-q	38.47 e-z
61	Wangeni	13.02 f-z	25.97 o-F	3.286 b-v	3.973 b-y	14.226 v-x	2.790 n-x	62.76 z
62	7-CIP	15.23 q-E	34.07 F-G	3.219 b-u	4.195 c-C	14.019 u-x	2.063 e-w	54.79 v-z
63	Carot Dar	15.39 q-E	27.45 v-G	4.228 j-A	4.940 k-H	8.415 g-v	2.160 f-w	37.37 d-z
64	24-CIP	11.04 b-s	29.42 y-G	2.617 b-n	3.293 b-o	8.594 h-w	2.033 e-w	40.47 m-z
65	Kibandule	1.69 a	3.20 a	0.146 a	0.283 a	0.41 a	0.015 a	3.42 a
66	Chrolophenical	8.24 b-g	14.35 b-j	2.342 b-j	2.773 b-i	7.049 b-s	2.191 g-w	47.63 o-z
67	UN 7	8.18 b-g	12.56 b-f	3.003 b-r	3.255 b-n	4.237 a-m	1.705 b-q	37.56 d-z
68	Kajiji	16.79 x-E	27.52 v-G	4.941 s-C	5.687 t-I	13.715 t-x	3.495 v-x	47.46 o-z

Table 4.3 continued

SN	Genotype	MRN	TRN	MRW	TRW	IRN	IRW	WDS
69	UN 3	11.46 b-v	19.47 c-w	3.625 c-x	4.053 c-A	5.356 a-r	1.276 a-p	40.13 g-z
70	Ngeni	11.90 c-x	17.57 c-q	3.778 d-y	4.051 c-z	9.886 j-x	3.270 q-x	49.74 q-z
71	Nyaisome	13.29 h-A	21.92 g-A	5.629 y-C	6.180 B-I	3.844 a-l	2.155 f-w	23.59 a-q
72	Madebe	7.10 b-c	7.88 a-b	2.939 b-r	3.054 b-l	0.50 a	0.076 a-b	12.31 a-e
73	Kabakuli	10.22 b-p	13.36 b-h	4.033 g-A	4.215 c-E	6.647 a-s	2.570 j-x	40.91 i-z
74	9-CIP	10.22 b-q	20.78 e-y	2.731 b-q	3.216 b-m	10.642 n-x	2.410 i-x	60.99 y-z
75	Polista	11.94 c-x	19.11 c-v	2.950 b-r	3.593 b-s	5.805 a-s	1.343 a-p	40.13 g-z
76	Shitoli	19.20 D-E	29.99 z-G	5.704 z-C	6.283 F-I	14.004 u-x	3.632 w-x	42.20 j-z
77	Ngw'alu	17.22 y-E	27.38 v-G	4.784 r-B	5.510 r-I	9.903 k-x	2.758 m-x	55.49 w-z
78	6-CIP	16.39 w-E	31.09 B-G	4.836 r-B	5.483 q-I	6.700 a-s	2.598 k-x	42.50 k-z
79	Tumauma	18.74 C-E	26.24 o-F	5.617 y-C	6.046 A-I	2.341 a-g	0.785 a-i	16.84 a-l
80	Kisu cha Masai	14.35 M-D	24.99 m-F	4.755 r-B	5.291 o-H	6.560 a-s	1.541 a-p	34.08 c-x
81	22-CIP	8.33 b-h	26.50 p-F	1.779 a-c	2.651 b-f	2.450 a-g	0.441 a-e	15.83 a-j
82	Ndovadoe	9.39 b-m	17.60 c-r	1.930 a-e	2.358 b-c	5.236 a-r	0.844 a-i	29.35 a-w
83	Ngw'anakurwa	8.62 b-i	12.11 a-e	3.114 b-t	3.477 b-q	4.67 a-p	1.634 a-q	43.01 l-z
84	Mwanatata	13.41 i-B	23.52 k-D	4.441 m-A	5.136 m-H	4.833a-p	1.741 b-r	29.25 a-w
85	Mulozi	13.91 k-C	26.41 o-F	4.164 i-A	4.775 i-G	5.137 a-r	1.492 a-p	24.91 a-r
86	Ngw'ananzugi	17.98 z-E	26.72 q-F	6.771 C	7.395 I	6.430 a-s	2.158 f-w	33.64 c-x
87	Chuga	11.59 b-v	13.72 b-i	3.977 g-A	4.132 c-A	2.96 a-g	1.228 a-o	20.19 a-m
88	Naspot 1	9.91 b-p	15.94 b-m	3.406 b-x	3.852 b-v	9.856 j-x	1.855 c-v	34.98 d-y
89	Kiti cha Nyerere	19.52 E	27.52 v-G	6.552 B-C	6.934 H-I	14.082u-x	3.894 x	54.79 v-z
90	UN 1	13.10 f-A	21.41 f-A	4.131 i-A	4.544 e-G	7.322 c-s	1.489 a-p	38.48 e-z
91	New Dimbuka	10.58 b-q	17.34 c-o	3.753 d-y	4.272 c-F	6.755 a-s	1.720 b-r	43.32 l-z
92	SPKBH/03/03	14.34 m-D	17.78 c-s	5.301 x-C	5.540 r-I	4.355 a-n	1.758 c-s	27.46 a-t
93	21-CIP	15.42 q-E	27.05 t-G	3.748 d-y	4.388 d-F	8.313 g-v	1.808 c-u	30.20 b-w
94	Mugandi	16.28 u-E	36.15 G	3.989 g-A	5.287 o-H	10.748 p-x	2.124 f-w	44.25 m-z
95	Uchungu wa mbwa	14.43 n-D	24.81 m-E	3.201 b-u	3.786 b-u	12.045 s-x	2.446 i-x	57.46 x-z
96	New Kawogo 2	9.19 b-l	17.50 c-p	3.218 b-u	3.800 b-u	4.233 a-m	1.427 a-p	1.979 a-m
	Grand mean	12.12	21.06	3.733	4.314	5.977	1.584	3.212
	LSD (5%)	5.005	9.152	1.918	2.017	6.360	1.668	2.657
	Sed	2.542	4.635	0.9726	1.022	3.201	0.8515	1.337
	Location Means							
	ARI Tumbi	37.61	21.21	88.65	4.407	25.61	33.47	30.00
	Ndorobo	47.31	20.91	82.50	4.217	31.12	40.22	34.27

SN= Serial number; Means in a column followed by the same letter are not significantly different at P=0.05; LSD = Least significant difference; Sed = Standard error of difference, MRN = Marketable root number per plot, TRN = Total root number per plot, MRW = Marketable root weight per plot (kg/plot), TRW = Total root weight per lot (kg/plot), IRN = Infested root number per plot, IRW = Infested root weight per plot (kg/plot), WDS = Weevil damage score.

Table 4.4. Sweetpotato genotypes selected for weevil resistance and desirable yield and yield-related traits.

No.	Name	Weevil resistance	Agronomic or market traits
1	Magunhwa	Resistant	Higher marketable root weight and total root weight per plot
2	Chuchu ya Nesi	Resistant	Higher total root number and lower infested root weight percent per plot
3	Rugomoka	Moderately resistant	Higher marketable root number per plot
4	Tumauma	Moderately resistant	Higher marketable root number and root weight per plot
5	New Kawogo	Moderately resistant	Higher marketable root number per plot

4.3.3 Correlation between root number, root weight and weevil infestation

Table 4.5 presents the degree of association of storage root number and root weight with root infestation and damage by weevils. Results showed that TRN was significantly ($P < 0.05$) correlated with IRN ($r = 0.38$). MRW and TRW were significantly ($P < 0.05$) correlated with IRW ($r = 0.45$). Further, significant correlations ($P < 0.01$) were recorded between IRN and IRW with WDS with correlation values of $r = 0.79$ and 0.72, respectively (Table 4.5).

Table 4.5. Pearson correlation coefficients showing the association between root number and root weight with weevil damage and damage score.

Traits	MRN	TRN	MRW	TRW	IRN	IRW	WDS
MRN		0.73**	0.76**	0.77**	0.37*	0.38*	0.20
TRN			0.42*	0.54*	0.38*	0.25	0.02
MRW				0.96**	0.22	0.45*	0.10
TRW					0.26	0.45*	0.12
IRN						0.84**	0.79**
IRW							0.72**
WDS							

** = Significant correlation at $P<0.01$ probability level; * = Significant correlation at $P< 0.05$ probability level, MRN = Marketable root number per plot, TRN = Total root number per plot, MRW = Marketable root weight per plot (kg/plot), TRW = Total root weight per lot (kg/plot), IRN = Infested root number per plot, IRW = Infested root weight per plot (kg/plot), WDS = Weevil damage score.

4.4 Discussion

4.4.1 Storage root number and root yield

The tested genotypes showed significant differences in total storage root number per plot (Table 4.3). This result is attributed to genotypic variation. Storage root formation is controlled by multiple independent genes which differ among sweetpotato varieties (Rukundo et al., 2013). The variation might also have been caused by the difference in their ability to translocate photosynthetic material from leaves to the roots. Genotypes with higher translocation ability produces more roots per unit area. Significant difference in root production among sweetpotato genotypes were reported in earlier studies (Tairo et al., 2008; Ngailo et al., 2016a).

There were significant differences in root yield per plot among the tested sweetpotato genotypes across tested locations. Genotypes with good adaptation to the test environments yield better (Masumba et al., 2005; Rukundo et al., 2013; Kagimbo et al,. 2017). Differences in maturity time is another attribute for variable root yield in sweetpotato genotypes (Lebot, 2009). Dry matter accumulation leads to high storage yield which is associated with long maturity.

Higher MRN, MRW and IRN were recorded at Ndorobo village site (Table 4.3). This observation is attributed to the high fertility status of the soils at Ndorobo village (Table 4.1). The soils at Ndorobo village had the higher levels of total nitrogen and organic carbon which might have favoured good growth and yield at that location. It is not surprising that higher levels of IRN and WDS were also recorded at Ndorobo village site (Table 4.3). This is due to the fact that increased storage root size and root number per plot were recorded at the site that led to soil cracks exposing storage roots to weevils hence increased infestation and damage. Stathers et al. (2003) reported that increased sweetpotato yield is associated with high level of weevil infestation.

The levels of weevil infestation recorded across the two testing locations were lower but relatively the same (Table 4.3). This was related to the challenges in controlling the weevils in field. The level of weevil infestation on roots increases with time when roots remain in the field after maturity. Before sweetpotato matures, weevils (*Cylas spp*.) in their adult stage feed on the epidermis of vines and leaves, while larvae tunnel into the vines. When the roots enlarge and mature, they get exposed to weevil damage. At this stage the adult weevils can also feed on the surface of the roots, while larvae tunnel inside the storage roots (Skoglund and Smit, 1994). Multiplication of weevils is four times higher in storage roots than in vines (Smit et al., 2001). This implies that more weevil pressure is built after storage root maturity. Likewise, weevil infestation increases after storage root maturity.

4.4.2 Genotypes response to weevil infestation and damage

The present study revealed that the tested sweetpotato genotypes were significantly different regarding IRN and WDS (Table 4.2). Differences in the genetic constitution, environmental conditions and storage root morphology could attribute to the observed differences in response to sweetpotato weevil infestation and damage (Stathers et al., 2003; Muyinza et al., 2012). Deep root systems of some genotypes increased the distance to which weevils have to burrow to reach the roots hence reducing the weevil infestation and damage (Stathers et al., 2003). High foliage production by some genotypes protect soils from being exposed to intense solar radiation keeping moisture in the soil. This was found to reduce soil cracks and hence limit weevil infestation and damage. Production of thicker storage roots by some genotypes cause soil cracks and exposure to weevil damage (Talekar,

1987; Stathers et al., 2003). Differential response of sweetpotato varieties to weevil damage is also attributed to variation in chemical composition of storage roots (Stevenson et al., 2009; Anyanga et al., 2013). In the studies conducted in Uganda, some weevil resistant sweetpotato varieties had high levels of esters of hydroxylcinnamic acid in root latex (Stevenson et al., 2009) and esters of caffeic and coumaric acid in epidermal and root surface (Anyanga et al., 2013).

The present study identified weevil resistant genotypes which included Kibandule, Mulumba, Utitiri, 3-CIP, Madebe, Magunhwa, 5-CIP, Kafu and Chuchu ya nesi. The genotypes Nyamvuva, Sengi, 22-CIP, Rugomoka, Tumauma, Ejumla, Carot C, New Kawogo 2, Haraka and 4-CIP were categorized as moderately weevil resistant collections (Table 4.3). The selected genotypes with resistance and moderate resistance reactions are ideal sweetpotao parents for weevil resistance breeding programs. Genotypes: Magunhwa, Chuchu ya Nesi, Rugomoka, Tumauma and New Kawogo were also identified to be promising parents having both weevil resistance and desired yield and yield component traits.

4.4.3 Association of yield and yield components with weevil infestation and damage

The present study found a significant but weak correlation between TRN and IRN (Table 4.5). In addition, there were significant moderate correlations between MRW and TRW with IRW (Table 4.5). This suggests that sweetpotato varieties with numerous and bigger sized roots get more weevil infestations than those with few and small sized roots. The same observations were reported by Stathers et al. (2003) who indicated that sweetpotato genotypes which produced higher numbers and thicker sized roots per plot, had higher field weevil infestation and damage. Genotypes with thicker sized roots and high number of roots per plot tend to crack the soil creating access to storage roots by weevils resulting in heavy weevil infestation and damage (Skoglund and Smit, 1994; Stathers et al., 2003).

The significant correlation of both IRN and IRW with WDS revealed by this study indicates that high IRN reflects the level of susceptibility of a genotype to weevils. The main challenge encountered when assessing WDS is the occurrence of some sweetpotato genotypes expressing low levels of IRN but with high WDS. If both IRN and WDS are high (positively correlated) then it implies a high susceptibility to weevils. Sweetpotato genotypes expressing high levels of IRN but low WDS and vice versa can be attributed to having resistance to weevils or escape mechanism from weevils.

4.5 Conclusions

This study successfully identified weevil resistant genotypes which included: Kibandule, Malulumba, Utitiri, 3-CIP, Madebe, Magunhwa, 5-CIP, Kafu and Chuchu ya nesi. The genotypes Nyamvuva, sengi, 22-CIP, Rugomoka, Tumauma, Ejumla, Carot C, New Kawogo 2, Haraka and 4-CIP expressed

moderate resistance to weevils. These genotypes were selected as the best parents to be used in breeding of sweetpotato varieties with enhanced weevil resistance. Furthermore, this study identified genotypes Magunhwa, Chuchu ya Nesi, Rugomoka, Tumauma and New Kawogo with weevil resistance and desired yield and yield-related traits such as high marketable root number, increased total root number per plot, high marketable root weight per plot and low infested root weight per plot. The study demonstrated that weevil infestation on storage roots was associated with sweetpotato root number per plot and large sized storage root. The study also indicated that the level of weevil infestation was associated with the level of damage on roots. The selected genotypes are recommended for weevil resistance breeding programs of sweetpotato in western Tanzania or similar agro-ecologies.

References

Acquaah, G. 2012. Principles of plant genetics and breeding 2nd ed. Wiley-Blackwell, Oxford USA.

Anyanga, M.O., H. Muyinza, H. Talwana, D.R. Hall, D.I. Farman, G.N. Ssemakula, R.O.M. Mwanga, and P.C. Stevenson. 2013. Resistance to the Weevils *Cylas puncticollis* and *Cylas brunneus* conferred by sweetpotato root surface compounds. Journal of Agricultural and Food Chemistry 61:8141-8147.

Burri, B.J. 2011. Evaluating sweet potato as an intervention food to prevent vitamin A deficiency. Comprehensive Reviews in Food Science and Food Safety 10:118-130.

Clark, C.A., J.A. Davis, J.A. Abad, W.J. Cuellar, S. Fuentes, J.F. Kreuze, R.W. Gibson, S.B. Mukasa, A.K. Tugume and F.D. Tairo. 2012. Sweetpotato viruses: 15 years of progress on understanding and managing complex diseases. Plant Disease 96: 168-185.

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

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

FAOSTAT. 2014. Food and Agriculture Organisation of the United Nations : Crop production data. FAOSTAT Division, Rome.

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

Kagimbo, F.M., H. Shimelis, and J. Sibiya. 2017. Diversity assessment of sweetpotato germplasm collections for yield and yield-related traits in western Tanzania. Acta Agriculturae Scandinavica, Section B — Soil & Plant Science:1-9. doi:10.1080/09064710.2017.1372516.

Kapinga, R.E., P.T. Ewell, S. Jeremiah, and R. Kileo. 1995. Sweetpotato in Tanzanian farming and food systems: implications for research. International Potato Center, Tanzanian Ministry of Agriculture, Nairobi and Dar-Es-Salaam.

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.

Lebot, V. 2009. Tropical root and tuber crops : cassava, sweet potato, yams and aroids. CABI, Wallingford

Lebot, V. 2009. Sweetpotato. *In*: Bradshaw, J.E., editor, *Root and tuber crops: Handbook of plant breeding.* Springer Sciences and Business Media, New York, NY 10013, USA. p. 97-125.

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.

Muyinza, H., H.L. Talwana, R.O.M. Mwanga, and P.C. Stevenson. 2012. Sweetpotato weevil (*Cylas* spp.) resistance in African sweetpotato germplasm. International Journal of Pest Management 58:73-81.

Mwanga, R., B. Odongo, C. Niringiye, R. Kapinga, S. Tumwegamire, P. Abidin, E. Carey, B. Lemaga, J. Nsumba and D. Zhang. 2007. Sweetpotato selection releases: lessons learnt from Uganda. African Crop Science Journal 15: 11 - 23.

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.

Nelles, W. 2009. Sweetpotato Education, Research and Capacity Development through a CIP-Orissa Learning Site. CTCRI, Bhubaneswar, Orissa, India.

Ngailo, S., H. Shimelis, J. Sibiya, and K. Mtunda. 2016a. Screening of Tanzanian sweet potato germplasm for yield and related traits and resistance to sweet potato virus disease. Acta Agriculturae Scandinavica, Section B — Soil & Plant Science 66:52-66.

Ngailo, S., H.A. Shimelis, J. Sibiya, and K. Mtunda. 2016b. Assessment of sweetpotato farming systems, production constraints and breeding priorities in eastern Tanzania. South African Journal of Plant and Soil 33:105-112.

Payne, R., S. Welham, and S. Harding. 2015. A Guide to REML in Genstat. VSN International, 2 Amberside, Wood Lane, Hemel Hempstead, Hertfordshire HP2 4TP, UK.

Rukundo, P., H. Shimelis, M. Laing, and D. Gahakwa. 2013. Storage root formation, dry matter synthesis, accumulation and genetics in sweet potato. Australian Journal of Crop Science 7:2054-2061.

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. doi.org/10.1186/1471-2164-11-604.

Skoglund, L.G., and N.E. Smit. 1994. Major diseases and pests of sweetpotato in Eastern Africa. International Potato Center (CIP).Nairobi, Kenya.

Smit, N.E.J.M., M.C.A. Downham, P.O. Laboke, D.R. Hall, and B. Odongo. 2001. Mass-trapping male Cylas spp. with sex pheromones: a potential IPM component in sweetpotato production in Uganda. Crop Protection 20:643-651.

SPSS. 2009. Statistical Package for Social Scientists. SPSS for Windows Release 18.0, Chicago, IL.

Stathers, T.E., D. Rees, S. Kabi, L. Mbilinyi, N. Smit, 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.

Stevenson, P.C., H. Muyinza, D.R. Hall, E.A. Porter, D.I. Farman, H. Talwana, and R.O.M. Mwanga. 2009. Chemical basis for resistance in sweetpotato *Ipomoea batata*s to the sweetpotato weevil *Cylas puncticollis*. Pure and Applied Chemistry 81:141-151.

Tairo, F., E. Mneney, and A. Kullaya. 2008. Morphological and agronomical characterization of sweet potato [*Ipomoea batatas* (L.) Lam.] germplasm collection from Tanzania. African Journal of Plant Science 2:77-85.

Talekar, N.S. 1987. Feasibility of the use of resistant cultivar in sweetpotato weevil control. International Journal of Tropical Insect Science 8:815-817.

CHAPTER 5 COMBINING ABILITY, GENE ACTION AND HERITABILITY OF WEEVIL RESISTANCE, STORAGE ROOT YIELD AND YIELD RELATED-TRAITS IN SWEETPOTATO

Abstract

Knowledge of gene action and trait inheritance helps in selecting suitable parents and crosses to advance in a breeding programme and to subsequently determine the selection procedure that leads to optimal genetic gain. The objective of this study was to determine general combining ability (GCA), specific combining ability (SCA), gene action and heritability of weevil (*Cylass* spp.) resistance, dry matter content (DMC), yield and yield components of newly developed sweetpotato clones. Six weevil resistant and six susceptible parents were selected based on high storage root yield or DMC. The 12 parents were crossed using a 6 x 6 North Carolina Design II mating scheme. The resultant 36 families were evaluated at three locations using a 3 x 12 lattice design with two replications for weevil resistance and yield and related traits in western Tanzania. Families differed significantly ($P<0.05$) for all measured traits. Total root number (TRN) per plot ranged from 16.00 to 61.42 with a mean of 32.48. The range and mean responses of the families for root yield (RY) was 11.26 to 35.42 tha^{-1} and 22.49 tha^{-1}, DMC (28.36 to 45.01% and 38.95%), percentage infested root number (PIRN) (0.74 to 27.08%, 10.59%), and weevil damage sore (WDS) (5.00 to 42.92%, and 21.64%), in that order. The GCA effects of females differed significantly for the studied traits except for percentage marketable root number (PMRN) and percentage marketable root yield (PMRY). Significant GCA effect of males were detected for all traits except PMRY. The SCA effects of families were significantly different for all traits. Additive gene action showing a >0.5 general predicted ratio (GPR) was more influential for TRN, RY, DMC, PIRN, percentage infested root yield (PIRY) and WDS, whereas non-additive gene action was more influential for PMRN and PMRY with a <0.5 GPR. The narrow sense heritability for TRN, RY, DMC, PIRN and WDS were 0.24, 0.56, 0.84, 0.62 and 0.62, while the broad sense heritability for these traits were 0.58, 0.72, 0.93, 0.78 and 0.77, in that order. Based on the GCA effects, Ukerewe, Jewel, 2-CIP, 18-CIP and 17-CIP were selected as the best parents for TRN, while Simama, 2-CIP, 8-CIP and 17-CIP were the best parents for RY. Burenda, Kasinia, and Masinia were the best parents for DMC, PIRN, PIRY and WDS, while 8-CIP was the best for DMC. The male parents 4-CIP and 5-CIP were good combiners for WDS, whereas 17-CIP, 18-CIP and 4-CIP were good male combiners for PIRN. The following families: Jewel x 4-CIP, Simama x 2-CIP, and Ukerewe x 2-CIP had the best SCA effects for enhanced TRN, while families selected for improved RY were Kasinia x 8-CIP, Simama x 2-CIP, Jewel x 5-CIP and Masinia x 18. The following families: Burenda x 2-CIP, Kasinia x 8-CIP, Masinia x 17-CIP and Simama x 17-CIP were superior for high DMC. The families Jewel x 18-CIP, Simama x 4-CIP, Masinia x 2-CIP and Kasinia x 5-CIP were selected for improved

PIRN and WDS. High heritability values and both additive and non-additive gene action were detected for the studied traits. This suggests that breeding gain can be realized through hybridization and clonal selection in breeding programs. The above parents and families will be useful genetic resources for development of sweetpotato varieties resistant to weevils and enhanced root yield, yield components and dry matter content.

Keywords: additive gene action, combining ability, heritability, general combining ability, non-additive gene action, selection, specific combining ability, sweetpotato.

5.1 Introduction

Sweetpotato *(Ipomoea batatas* [L.] Lam; 2n=6x=90) is an important root crop worldwide. It is cultivated on an estimated area of 8.21 million hectares in more than 110 countries (FAOSTAT, 2017). In sub-Saharan Africa (SSA), sweetpotato is widely used for food, source of cash income, and livestock feed (Fuglie, 2007). Further, sweetpotato storage roots are valuable sources of industrial raw material for biofuel, starch and alcohol extraction (Schafleitner et al., 2010; Clark et al., 2012). Sweetpotato grows under marginal soils and dryland environmental conditions relatively attaining higher yield levels per unit area making it the most preferred crop of smallholder farmers in SSA (Schafleitner et al., 2010).

Tanzania is amongst the top five leading world producers of sweetpotato (FAOSTAT, 2014). In the country, the crop is cultivated in almost all agro-ecological zones under both monocrop and intercrop systems (Kulembeka et al., 2005; Ngailo et al., 2016; Kagimbo et al., 2017). It is a fourth important food crop after maize, rice, and cassava (Tairo et al., 2008). Farmers practice flexible planting and harvesting schedules of the crop in most growing zones of Tanzania. Sweetpotato production and productivity in Tanzania is affected by multifaceted constraints including biotic, abiotic and socio-economic factors (Tairo et al., 2008; Ngailo et al., 2016). Sweetpotato weevils (*Cylas puncticollis* Boheman and *C. brunneus* Fabricius) are among the main biotic constraints.

Weevils have been reported to be a problem in all sweetpotato growing zones in the country causing up to 95% yield loss in susceptible varieties (Kapinga et al., 1995). Early planting, early harvesting, field sanitation and chemical treatment are some of the main control measures against weevils. However, these control measures are less effective or costly under small-holder farming systems due to a number of farmer practices. For instance, farmers plant late in the growing season due to shortage of planting material at the start of the rainfall season. Furthermore, farmers practice sequential harvesting to limit the root decay after harvest making early harvesting technique impractical (Kapinga et al., 2003). Weevil larvae which is the most destructive stage to sweetpotato roots, are difficult to control using chemical treatments because they grow inside the roots or vines (Lebot, 2009). Therefore, the use of sweetpotato varieties with weevil resistance and enhanced yield and yield components is the most economic approach to boost sweetpotato productivity (Muyinza et al., 2012; Anyanga et al., 2013).

In the past, lack of sources of resistance against weevils has been the main bottleneck to breeding sweetpotato for weevil resistance (Stathers et al., 1999; Stathers et al., 2003). Recent reports suggests the existence of sources of resistance to weevils among east African sweetpotato germplasm collections. These genotypes can be explored for effective resistance breeding against weevils (Muyinza et al., 2012; Anyanga et al., 2013). Sweetpotato genotypes expressing high root yield, dry matter content (Kagimbo et al., 2017) and weevil resistance have been recently identified in western Tanzania (Kagimbo, unpublished data). These selections can be useful genetic resources

for breeding sweetpotato varieties resistant to weevils and with enhanced root yield and dry matter content. However, the combining ability of the identified sweetpotato genotypes and families and inheritance of associated traits should be established for successful breeding.

Knowledge of gene action and trait inheritance helps in selecting suitable parents and crosses to advance in a breeding program and to determine the subsequent selection procedure leading to optimal genetic gain (Acquaah, 2012). General combining ability (GCA) effect is the average performance of a genotype in a series of cross combinations, while specific combining ability (SCA) effect is the deviation in performance of a cross combination from that predicted on the basis of the general combining abilities of the parents involved in the cross (Schlegel, 2010). The GCA effect is attributed to additive gene action, whereas SCA is due to non-additive gene action which can be dominance or epistasis (Acquaah, 2012).

Heritability, on the other hand, is a measure of the degree to which a phenotype is genetically influenced (Acquaah, 2012). Most economic traits in sweetpotato are quantitatively inherited, thus are affected by environmental conditions (Cervantes-Flores et al., 2011). Gene action controlling traits can be additive, non-additive (Acquaah, 2012). Additive gene action which is based on narrow sense heritability is the important component of genetic variance because it is transmitted to progeny. It therefore influences selection based on the phenotype. Therefore, plant breeders are interested in quantifying heritability because breeding programs are more successful with traits of high heritability because phenotypic based selection and the response to selection are successful and reliable when the traits exhibit higher heritability (Acquaah, 2012).

Various mating designs can be used in crossing sweetpotato genotypes to create genetic variability. These include polycross, diallel and North Carolina Design II (NCD II) (Komaki et al., 1998; Chiona, 2010; Balcha, 2015; Ngailo, 2015). The choice of a mating design depends on the objective(s) of a breeding program. North Carolina mating design II is one of the widely used designs in sweetpotato breeding programs. This design involves crossing of genotypes consisting of two groups of parents, one group serves as male parents and the other group as female parents. The two groups can be selected based on priory grounds, e.g., weevil resistance and desirable agronomic attributes. The NCD II is used to estimate the GCA and SCA effects and type of gene action (additive and non-additive) (Bernardo, 1965; Chahal and Gosal, 2002). In this design, the GCA effects of males and GCA effects of females can be estimated using the mean square values for males and females, respectively. Likewise the SCA effects of families can be directly estimated by male x female interaction (Hallauer et al., 2010). Therefore, the objective of this study was to determine the general combining ability, specific combining ability, gene action and heritability of weevil (*Cylass* spp.) resistance, dry matter content, yield and yield-related traits of newly developed sweetpotato clones in western Tanzania.

5.2 Material and methods

5.2.1 Parental materials

The study used six weevil resistant sweetpotato genotypes acquired from the International Potato Centre (CIP)-Lima, and six susceptible genotypes collected in Tanzania. The details of the sweetpotato genotypes is presented in Table 5.1. The 12 selected sweetpotato genotypes were used as parents and were crossed to develop recombinant individuals for family selection. Parental genotypes were selected based on their high dry matter content, weevil resistance, flowering ability and high storage root yields (Kagimbo et al., 2017).

Table 5.1. Description of sweetpotato parents crossed in this study.

No	Genotype name	Origin	Reaction to weevil infestation	Agronomic attributes	Role in a cross
1	Burenda	Landrace	Susceptible	High DMC	Female
2	Masinia M.W.N.	Landrace	Susceptible	High DMC	Female
3	Simama	ARI Ukiriguru	Susceptible	High yielding	Female
4	Ukerewe	ARI-Ukiriguru	Susceptible	High yielding	Female
5	Jewel	ARI-Ukiriguru	Susceptible	High yielding	Female
6	Kasinia	Land race	Susceptible	High DMC	Female
7	8-CIP	CIP-Lima	Resistant	High DMC	Male
8	4-CIP	CIP-Lima	Resistant	High DMC	Male
9	18-CIP	CIP-Lima	Resistant	High yielding	Male
10	2-CIP	CIP-Lima	Resistant	High yielding	Male
11	5-CIP	CIP-Lima	Resistant	High yielding	Male
12	17-CIP	CIP-Lima	Resistant	High yielding	Male

CIP = International Potato Centre, ARI = Agricultural Research Institute, DMC = dry matter content

5.2.2 Mating design, crosses and seedling preparation

The 12 parents were crossed using a 6 x 6 North Carolina Design II (NCD II). The six parents used as females were: three landrace collections and three released varieties from Tanzania, whereas the other six parents used as males were supplied by CIP-Lima. A crossing block was established in January 2016 at Tumbi Agricultural Research Institute (ARI-Tumbi) situated at 5˚ 4’11’’S, 32˚ 40’1’’E in western Tanzania. Plants were grown in plastic pots of 20 litre capacity under screen house conditions. Irrigation was done four times a week and fertilizer was applied using Nitrogen, Phosphorus and Potassium (23:10:5) at a rate of 233 kg/ha a month after planting. Weeding was done regularly. Plants were inclined to grow twining on either wooden or sisal trellises (Figure 5.1A). Flowers were hand pollinated between 6:00am to 10:00am, labelled and tagged (Figure 5.1B). The

dried seeds from successful crosses were harvested regularly, threshed and kept in labelled paper envelopes (Figure 5.1C).

Cross combinations provided 36 F1 families. Seeds from each family were harvested separately. The seeds were scarified by soaking in concentrated sulphuric acid (98% H_2SO_4) for 40 minutes. The acid was discarded and the seeds rinsed with running tap water for 1 minute and then soaked in a saturated sodium bicarbonate solution for 1 minute while stirring. The seeds were again rinsed with running tape water for 1 minute. The seeds were spread on a Whatman® filter paper to dry at room temperature (Figure 5.1D). After 24 hours of drying, each seed was sown in a 750 ml plastic pot to raise healthy and vigorous seedlings (Figure 5.1E). After 3 weeks the F1 seedlings were field transplanted and grown on ridges to provide vines for Clone I evaluation.

5.2.3 Study sites and clonal evaluations

Clonal generation I evaluations were conducted at two stages. At stage I, 36 Clone I families from 36 crosses were planted in August 2016 at ARI-Tumbi using a 3 x 12 lattice design with three replications. Each family was represented by 30 genotypes. Weeding, fertilizer application and irrigation were done as described in section 2.2. At harvesting, 20 genotypes were selected from each Clone I family based on growth performance, root yield and desirable root shape to advance to Clone II.

Clonal II families were subjected to field evaluations at the following three selected sites: ARI-Tumbi in Tabora Municipal, Nyasha village in Kasulu District and Ndorobo village in Urambo District. The coordinates and physiochemical properties of the study sites are summarised inTable 5.2 whereas the rainfall distribution at the study sites during the study season is presented in Figure 5.2 The 36 Clone II families each represented by 20 genotypes were established at the three sites. The experimental design was a 3 x 12 lattice with two replications at each site. Vine cuttings of 20-30 cm long were planted in a 3 by 1.5 m plot with two ridges at a spacing of 1m inter-row and 0.3m intra-row. Weeding was done twice at each site and fertilizer application was done as presented in section 2.2.

5.2.4 Data collection

Trials were harvested five months after planting and the following agronomic data were recorded: the number of surviving plants per plot, marketable and unmarketable root number per plot which were then expressed as the percentage of the total root number per plot, The total root number per plot, marketable and unmarketable root weight per plot which was then expressed as percentage of the total weight per plot and total root weight per plot (root yield) which was then converted into tons ha^{-1}. Marketable roots were the roots with 5 and above cm in diameter whereas the percentage of marketable yield was calculated from marketable roots.

Figure 5.1. Figures depicting A = Crossing block, B = Mature capsules after crosses, C = harvested sweetpotato seeds, D = drying sweetpotato seeds after scarification, E = sweetpotato seedlings after germnation.

Table 5.2. Geographic coordinates and physiochemical characteristics of the soils at the study sites.

Sites	Soil characteristics											Coordinates	
	pH	Total N (%)	OC (%)	Available P (ppm)	Exchangeable bases (meq/100g)		EC (mS/cm)	Texture (%)			Textural class	Latitude	Longitude
					Mg	Ca		Sand	Silt	Clay			
Nyasha	4.78	0.15	1.88	22.10	0.19	1.05	0.2	40	19	41	SC	4° 49' 59'' S	29° 58' 27'' E
Ndorobo	6.10	0.09	0.14	15.40	0.1	0.54	0.08	75	9	16	SL	5°4'11''S	32° 40'1''E
ARI-Tumbi	6.33	0.05	0.29	18.20	0.23	1.33	0.07	78	7	15	SL	5°5'12''S	32°1'26''E

OC = organic carbon, EC = electrical conductivity, SC = Sandy clay, SL = Sandy loam

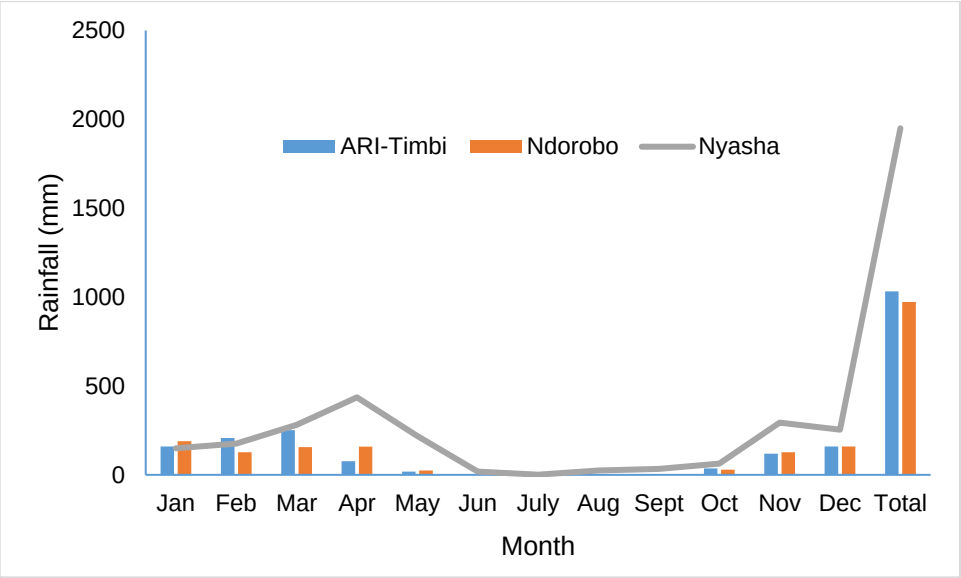

Figure 5.2. Rainfall distribution at the three sites during the study season.

Dry matter content of storage roots of each genotype was determined by taking a sample of 100-200 g fresh storage root mass from five randomly selected healthy roots of each genotype followed by chopping roots into smaller sections. Each sliced root sample was oven dried at 70˚C for 72 hours to constant mass. The dry matter content was determined as the proportion of dry matter relative to fresh mass expressed as a percentage.

Reaction of genotype to weevil infestation was assessed by counting the number of infested roots per plot and its corresponding weight which were then expressed as percentage of total root number and root weight per plot, respectively. Also, sweetpotato damage scoring was done using a scale of 0 to 10 where 0 = no damage, 1 = 1-10% of the root damaged, 2 = 11- 20%, 3 = 21- 30%, 4= 31- 40%, 5 = 41- 50%, 6 = 51- 60%, 7 = 61- 70%, 8 = 71- 80%, 9 = 81- 90% and 10 = 91-100%.

5.2.5 Data analysis

5.2.5.1 Analysis of variance (ANOVA)

The following data: total root number (TRN) per plot, percentage of marketable root number (PMRN) per plot, root yield (RY), percentage of marketable root yield (PMRY) per plot, dry matter content (DMC), percentage of infested root number (PIRN) per plot, percentage of infested root yield (PIRY) per plot and weevil damage score (WDS) were analysed by Statistical Analysis Systems (SAS 9.3)

statistical package (SAS, 2003) using the general linear model (GLM) procedure. Mean separation was computed using the least significant difference (LSD) procedure at the 0.05 probability level.

5.2.5.2 Determination of the GCA and SCA effects

The GCA and SCA effects were estimated following the procedure of NCD II (Hallauer et al., 2010) using the following model:

$Yijkl = \mu + l + rk + gi + gj + sij + gil + gjl + sijl + eijkl$

Where: Yijkl = the observed value of the progeny of the ith male crossed with jth female in the lth location and kth replication, μ = the overall population mean, l =effect of lth location, rk =effect of kth replication nested under lth location, gi = GCA effect of ith male, gj = GCA effect of jth female, sij = SCA effect of ith male crossed with jth female, gil = interaction effect between l and gi, gjl = interaction effect between l and gj, sijl = interaction effect between l and sij and eijkl = random experimental error. The genotypes was considered as a fixed factor whereas environment and replications were considered as random factors.

The GCA and SCA effects were calculated according to (Singh and Chaudhary, 1979) as follows:

$GCA_F = X_F - \mu$, and $GCA_M = X_M - \mu$

Where: X_F and X_M = Mean of male and female parents, respectively
GCA_M and GCA_F = General combining ability of male and female parents, respectively
μ = Overall mean of crosses in the trial

$SCAx = OV - EV$
$= OV - [GCAf + GCAm + \mu]$

Where: OV = Observed mean value of the cross
EV = Expected mean value of the cross based on the 2 GCAs of its parents
SCAx = Specific combining ability of the cross x

The GCA or SCA was significant at 0.05 probability level if it was greater than the the product of ‘t’ value and root mean square error (Dabholkar, 1999).

5.2.5.3 Determination of gene action

The general predicted ratio (GPR) (Baker, 1978) was used to determine the relative importance of GCA and SCA in influencing the expression of the traits. The GPR was computed as follows:

MSQGCA (pooled) / ([MSQGCA (pooled) + MSQ SCA]), where: MSQGCA = mean squares for GCA and MSQSCA = mean squares for SCA. A ratio >0.5 implies that GCA is more important than SCA in the inheritance of the character and a ratio <0.5 implies that SCA is more important than GCA in the inheritance of the character (Baker, 1978).

5.2.5.4 Determination of heritability

From NCD II analysis, narrow sense heritability was determined based on female additive variance (Dabholkar, 1999) as follows:

$h^2_F = 4\ \sigma^2GCAF / (\sigma e^2/r + 4\ \sigma^2SCA + \sigma^2GCAF)$

Where: h^2_F = family narrow sense heritability, σ^2GCAF = genetic variance for general combining ability based on female parents, σ^2SCA = genetic variance component for specific combining ability, σ^2e = error variance and r = number of replication.

Broad sense heritability was calculated as follows: (Dabholkar, 1999)

$H^2 = 4\ \sigma^2GCAF + 4\ \sigma^2SCA / (\sigma e^2/r + 4\ \sigma^2SCA + \sigma^2GCAF)$

The terms are as explained above in the narrow sense heritability.

5.3 Results

5.3.1 Analysis of variance

The combined analysis of variance showed a significant difference (P = 0.01) among the families for all the traits (Table 5.3). There was a significant effect of location on PMRN, PMRY and DMC (Table 5.3). Families also differed significantly (P = 0.001) on all the traits.

Table 5.3. Combined analysis of variance for eight traits of 36 Clone II sweetpotato families evaluated at three locations in Western Tanzania.

Source	DF	TRN	PMRN	RY	PMRY	DMC	PIRN	PIRY	WDS
Loc	2	267.97ns	1616.14***	77.11ns	446.05*	34.02**	48.97ns	287.40ns	64.79ns
Rep(Loc)	3	1084.48***	2346.62***	774.94***	658.95**	61.70***	405.38***	2650.84***	876.10**
Families	35	777.93***	262.16**	200.24***	238.05**	83.65**	487.36***	665.59**	646.60***
Families*Loc	50	62.25ns	38.84ns	18.89ns	21.80ns	4.10ns	20.60ns	39.49ns	53.39ns
Error	105	156.44	105.13	44.87278	112.2309	6.675331	48.26424	135.64756	137.6056

* = significant at 0.05 probability level, ** = significant at 0.01 probability level, *** = significant at 0.001 probability level, ns = non-significant, DF = degrees of freedom, TRN = total root number, PMRN = percentage of marketable root number, RY = root yield, PMRY = percentage of marketable root yield, DMC = dry matter content, PIRN = percentage of infested root number, PIRY = percentage of infested root yield, WDS = weevil damage score.

Loc = location, Rep (Loc) = replication within location, Families*Loc = Families x location interaction,

5.3.2 Family means for eight agronomic traits across locations

The means for eight agronomic traits of families evaluated across three locations are presented inTable 5.4. There was a significant difference (P = 0.01) among the families for all the traits across locations (Table 5.3). TRN per plot ranged from 16.00 to 61.42 with a mean of 32.48 (Table 5.4). The following families: Masinia x 18-CIP, Jewel x 18-CIP, Jewel x 4-CIP and Ukerewe x 2-CIP had significantly higher TRN per plot of 61.00, 52.00, 50.75 and 50.58 in descending order, respectively. PMRN ranged from 30.52% to 56.27% with a mean of 43.29% among families. Masinia x 8-CIP, Jewel x 8-CIP, Ukerewe x 8-CIP and Ukerewe x 6-CIP had significantly larger PMRN of 56.27%, 53.55%, 53.10% and 52.97% in descending order. RY values of families ranged from 11.26 $tonha^{-1}$ to 35.42 $tonha^{-1}$ with a mean of 22.49 $tonha^{-1}$. Families: Simama x 2-CIP, Ukerewe x 2-CIP, Ukerewe x 2-CIP, Ukerewe x 18-CIP and Jewel x 2-CIP had significantly larger root yield of 35.42, 32.90, 32.62 and 31.65 $tonha^{-1}$, in that order. PMRY ranged from 63.36% to 92.49% with a mean of 78.47%. Families: Masinia x 8-CIP, Ukerewe x 17-CIP, Simama x 4-CIP and Ukerewe x 8-CIP had relatively larger PMRY of 92.49%, 87.77%, 87.31% and 86.15% in descending order. DMC ranged from 28.36% to 45.01% with a mean of 38.95%. Kasinia x 8-CIP, Burenda x 2-CIP, Masinia x 17-CIP and Kasinia x 18-CIP were the better families with larger DMC values of 45.01%, 44.51%, 44.23% and 44.03% in descending order.

In the tested families, PIRN ranged from 0.74% to 27.08% with a mean of 10.59%. Kasinia x 5-CIP, Jewel x 4-CIP, kasinia x 4-CIP and Burenda x 18-CIP were unique families that had significantly lower PIRN of 0.74%, 2.09%, 2.47% and 4.07% in that order. PIRY values varied from 3.26% to 48.19% with a mean of 21.11%.

Response to weevil damage varied from 5.00% to 42.92% with a mean of 21.64% (Table 5.4). Relatively, the following families: Kasinia x 5-CIP, Jewel x 18-CIP, Burenda x 18-CIP and Masinia x 2-CIP displayed lower WDS of 5.00%, 7.50%, 8.75% and 8.75% in a desirable direction. Sweetpotato families with WDS between 0 to 10% were categorised as resistant. This group included families such as Kasinia x 5-CIP, Jewel x 18-CIP, Burenda x 18-CIP, Masinia x 2-CIP and Burenda x 4-CIP. Families with WDS between 10.1 to 15% were categorised as moderately resistant (Table 5.4). This group included Masinia x 17-CIP, Kasinia x 4-CIP, Burenda x 8-CIP, Kasinia x 17-CIP, Simama x 4-CIP and Burenda x 2-CIP. Families with WDS between 15.1 to 25% were categorised as moderately susceptible and those with WDS > 25% were categorised as susceptible. The CVs for PIRN, PIRY and WDS were relatively higher due to many factors affecting the level of weevil infestation. Variations in weevil infestation in the field may be attributed to differences in storage root size, soil moisture, plant canopy, storage root morphology and chemical composition. These factors causes differences

in weevil infestation among trials, locations, seasons and sometimes across replications of the same cultivars (Stathers et al., 2003).

Table 5.4. Means for eight traits of 36 sweetpotato families evaluated across three locations in western Tanzania.

Families	TRN	PMRN	RY	PMRY	DMC	PIRN	PIRY	WDS
Kasinia x 2-CIP	21.58	44.55	18.09	84.70	38.20	8.93	9.57	18.75
Kasinia x 4-CIP	29.38	40.55	22.01	76.86	40.05	2.90	11.48	10.83
Kasinia x 5-CIP	16.92	30.52	11.26	63.36	39.21	0.74	3.26	5.00
Kasinia x 8-CIP	41.79	45.47	29.96	79.61	45.01	11.68	21.74	30.00
Kasinia x 17-CIP	29.04	46.13	20.11	84.09	41.92	5.90	19.15	12.92
Kasinia x 18-CIP	47.96	31.54	21.05	74.14	44.03	6.89	20.48	27.50
Simama x 2-CIP	45.54	46.88	35.42	75.91	38.11	27.08	39.89	42.92
Simama x 4-CIP	33.46	49.54	25.08	87.31	38.34	6.40	11.67	13.33
Siamama x 5-CIP	16.88	41.48	17.85	73.04	36.64	9.00	22.97	22.92
Simama x 8-CIP	38.54	33.13	21.47	64.39	38.59	18.28	35.32	33.75
Simama x 17-CIP	30.67	50.90	26.67	83.19	42.72	12.62	29.75	26.67
Simama x 18-CIP	20.79	35.86	15.16	81.60	39.43	20.97	48.19	40.00
Ukerewe x 2-CIP	50.58	42.29	32.90	74.73	34.28	10.76	20.71	24.17
Ukerewe x 4-CIP	31.33	37.62	22.81	72.24	40.34	9.79	15.23	16.25
Ukerewe x 5-CIP	23.08	52.97	18.89	79.50	39.58	15.24	31.39	30.42
Ukerewe x 8-CIP	34.67	53.10	28.82	86.15	36.63	18.15	31.83	31.25
Ukerewe x 17-CIP	37.13	47.65	27.52	87.77	35.08	11.09	25.98	30.42
Ukerewe x 18-CIP	52.63	37.40	32.62	75.32	42.01	17.07	21.93	27.92
Jewel x 2-CIP	39.38	49.34	31.65	79.29	28.36	16.81	31.50	38.75
Jewel x 4-CIP	50.75	47.79	26.13	78.40	36.24	11.79	23.73	20.83
Jewel x 5-CIP	29.00	46.44	26.95	84.02	34.11	26.97	38.82	39.58
Jewe lx 8-CIP	29.79	53.55	20.71	86.05	31.02	10.46	21.37	21.67
Jewel x 17-CIP	42.96	36.37	27.09	76.87	34.43	4.93	21.00	23.33
Jewel x 18-CIP	29.33	43.02	17.37	81.69	37.91	2.47	5.56	7.50
Burenda x 2-CIP	30.00	41.12	21.28	72.52	44.51	6.26	12.96	14.50
Burenda x 4-CIP	36.42	33.07	15.59	72.55	38.25	4.25	8.70	9.17
Burenda x 5-CIP	16.00	47.52	17.91	73.72	40.98	5.45	9.15	10.83
Burenda x 8-CIP	27.38	37.78	16.65	75.51	39.03	7.03	15.15	11.67
Burenda x 17-CIP	22.58	41.13	16.02	81.47	43.41	8.13	25.82	20.42
Burenda x 18-CIP	41.25	44.60	22.87	74.27	43.29	4.07	9.14	8.75
Masinia x 2-CIP	18.42	45.20	18.54	80.77	39.39	4.99	8.01	8.75
Masinia x 4-CIP	16.38	47.28	16.42	73.44	41.58	12.42	24.01	17.50
Masinia x 5-CIP	23.79	46.14	17.92	84.27	38.50	9.18	16.44	15.42
Masinia x 8-CIP	30.04	56.27	21.88	92.49	37.25	15.42	31.72	27.08
Masinia x 17-CIP	33.42	38.39	21.03	78.23	44.23	5.73	14.17	10.42
Masinia x 18-CIP	61.42	35.94	25.97	75.04	39.40	11.53	22.18	28.33
Grand mean	32.78	43.29	22.49	78.47	38.95	10.59	21.11	21.64
CV (%)	38.15	23.68	29.79	13.50	6.63	65.59	55.17	54.00
LSD (0.05)	14.32	3.39	2.21	3.51	0.85	2.30	3.85	3.86
Site means								
Nyasha	34.19	40.24	21.93	76.92	38.22	10.81	22.00	21.91
ARI-Tumbi	30.59	48.75	23.68	81.34	39.59	9.68	18.82	20.59
Ndorobo	33.57	40.88	21.86	77.14	39.02	11.29	22.50	22.43

CV = Coefficient of variation, LSD = Least significant difference, TRN = total root number, PMRN = percentage of marketable root number, RY = root yield, PMRY = percentage of marketable root yield,

DMC = dry matter content, PIRN = percentage of infested root number, PIRY = percentage of infested root yield, WDS = weevil damage score.

5.3.3 Combining ability effects

There was a significant (P=0.01) general combining ability (GCA) effect of females for all assessed traits except PMRN and PMRY (Table 5.5). A significant (P=0.01) GCA effect for males were recorded for all traits except PMRY. The specific combining ability (SCA) effect of families were significant for all assessed traits. The GCA effect was greater for TRN, RY, DMC, PIRN, PIRY and WDS with a >0.5 general predicted ratio (GPR), whereas the SCA effect was greater for PMRN and PMRY displaying a <0.5 GPR (Table 5.5).

5.3.4 General combining ability effects of parents

The general combining ability effects of both females and males for the eight traits are presented in Table 5.6. Both females and males had varied GCA effects in a desirable or undesirable directions. Ukerewe and Jewel were the only female parents with significantly higher and positive GCA of 0.61 and 0.45 for TRN, respectively (Table 5.6). Ukerewe, Jewel and Simama had higher and positive GCA effect of 0.53, 0.28 and 0.12 on RY in descending order. Jewel, Masinia and Ukerewe had the higher and positive GCA effects for PMRY of 0.29, 0.25 and 0.09 in descending order. Burenda, Kasinia and Masinia had significantly positive and higher GCA effects for DMC of 0.29, 0.27and 0.12 in descending order and in a desirable direction. Burenda, Kasinia and Masinia had significant lower and negative GCA effect of 0.53, 0.49 and 0.08 for PIRN in ascending order making them ideal parents for breeding. Burenda, Kasinia and Masinia also had significant lower and negative GCA effect of 0.85, 0.76 and 0.19 for PIRY. Female parents Burenda, Kasinia and Masinia also had significantly lower and negative GCA effect of 1.01, 0.46 and 0.42 on WDS in ascending order and in a desirable direction (Table 5.6).

Male parents such as 18-CIP, 2-CIP and 17-CIP had higher and positive GCA effect of 1.05, 0.16 and 0.10 in descending order for TNR (Table 5.6). Male parents such as 2-CIP, 8-CIP and 17 CIP had positive GCA effect of 0.42, 0.08 and 0.06 in descending order for RY. 17-CIP and 8-CIP had higher and positive GCA effect of 0.39 and 0.25 in descending order for PMRY. 18-CIP, 8-CIP and 4-CIP had higher positive GCA effect of 0.23, 0.15 and 0.02 for DMC.

Table 5.5. Mean squares and significant tests of combining ability effects for eight traits of 36 sweetpotato families evaluated at three locations in Tanzania.

Source	DF	TRN	PMRN	RY	PMRY	DMC	PIRN	PIRY	WDS
Loc	2	267.97ns	1616.14***	77.11ns	446.05*	34.02**	48.97ns	287.40ns	64.79ns
Rep(Loc)	3	1084.48***	2346.62***	774.94***	658.95**	61.70***	405.38***	2650.84***	876.10**
GCA_F	5	519.34**	230.68ns	404.93***	198.23ns	308.85***	583.10**	1652.36***	1601.85***
GCA_M	5	1673.48***	300.62*	238.04**	189.98ns	79.54***	185.53**	413.01*	481.95**
SCA	25	650.54***	260.77**	151.75***	252.65**	39.44***	186.67***	518.75***	469.23***
GCA_F*Loc	10	77.20ns	25.04ns	88.975	12.77ns	4.99ns	92.28ns	188.25ns	182.83ns
GCA_M*Loc	10	23.19ns	26.61ns	29.09ns	31.15ns	8.60ns	15.41ns	30.85ns	45.61ns
SCA*Loc	50	62.25ns	38.84ns	18.89ns	21.80ns	4.10ns	20.60ns	39.49ns	53.39ns
Error	105	156.44	105.13	44.87278	112.23089	6.675331	48.26424	135.64756	137.60562
GPR		0.53	0.40	0.59	0.34	0.77	0.58	0.57	0.60
h^2		0.58	0.40	0.72	0.34	0.93	0.78	0.78	0.77
H^2		0.24	0.18	0.56	0.13	0.84	0.62	0.62	0.62

* = significant at 0.05 probability level, ** = significant at 0.01 probability level, *** = significant at 0.001 probability level, ns = non-significant, DF = degrees of freedom, TRN = total root number, PMRN = percentage of marketable root number, RY = root yield, PMRY = percentage of marketable root yield, DMC = dry matter content, PIRN = percentage of infested root number, PIY = percentage of infested yield, WDS = weevil damage score.

Loc = location, Rep (Loc) = replication within location, GCAF = general combining ability of female, GCAM = general combining ability of male, SCA = specific combining ability, GCAF*Loc = general combining ability of female x location, GCAM*Loc = general combining ability of male x location, SCA*Loc = specific combining ability x location GPR = General predicted ratio, h^2 = narrow sense heritability H^2 = broad sense heritability.

Table 5.6. Estimated general combining ability effects of female and male parents of swetpotato for eight traits.

Parents	TRN	PMRN	RY	PMRY	DMC	PIRN	PIRY	WDS
Females								
Kasinia	-0.19	-0.39	-0.23	-0.15	0.27	-0.49	-0.76*	-0.46
Simama	-0.20	-0.04	0.12	-0.10	0.00	0.57*	1.13	0.92**
Ukerewe	0.61*	0.21	0.53*	0.09	-0.11	0.34	0.38	0.56*
Jewel	0.45	0.31	0.28	0.29	-0.59*	0.18	0.28	0.40
Burenda	-0.43	-0.27	-0.46	-0.38	0.29	-0.53	-0.85**	-1.01**
Masinia	-0.25	0.18	-0.24	0.25	0.12	-0.08	-0.19	-0.42
Males								
2-CIP	0.16	0.18	0.42	-0.05	-0.20	0.21	-0.07	0.33
4-CIP	0.02	-0.07	-0.13	-0.18	0.02	-0.30	-0.59*	-0.78*
5-CIP	-1.32**	0.10	-0.45	-0.24	-0.09	0.06	-0.09	-0.11
8-CIP	0.10	0.36	0.08	0.25	-0.11	0.32	0.56*	0.47
17-CIP	-0.02	0.02	0.06	0.39	0.15	-0.28	0.17	-0.11
18-CIP	1.05**	-0.58	0.00	-0.16	0.23*	-0.01	0.01	0.19

** = Significant at 0.01 probability level, * = Significant at 0.05 probability level, TRN = total root number, PMRN = percentage of marketable root number, RY = root yield, PMRY = percentage of marketable root yield, DMC = dry matter content, PIRN = percentage of infested root number, PIY = percentage of infested yield, WDS = weevil damage score.

Male parents: 4-CIP, 17-CIP and 18-CIP had the lowest negative GCA effect of 0.30, 0.28 and 0.01 for PIRN in a desirable direction, respectively. Similarly male genotypes 4-CIP, 5-CIP and 2-CIP had the lowest negative GCA effect of 0.59, 0.09 and 0.07 in ascending order for PIRY, in that order. Male parents including 4-CIP, 5-CIP and 17-CIP had the lowest negative GCA effect of 0.78, 0.01 and 0.01 in a desirable order for WDS (Table 5.6).

5.3.5 Specific combining ability effects of families

Table 5.7presents the specific combining ability effects of families for eight agronomic traits. Families Masinia x 18-CIP, Jewel x 4-CIP, Simama x 2-CIP and Ukerewe x 2 had significantly higher and positive SCA effect for TRN with values of 2.38, 1.52, 1.46 and 1.21 in a desirable direction, respectively than the other crosses. The following families: Kasinia x 8-CIP, Simama x 2-CIP, Jewel x 5-CIP and Masinia x 18 were the most promising selections displaying higher and positive SCA effects for RY with 0.98, 0.89, 0.67 and 0.63 in a desirable direction, in that order. Likewise, the families: Simama x 4-CIP, Masinia x 8-CIP, Kasinia x 2-CIP and Masinia x 5-CIP had significantly

higher and positive SCA effect for PMRY with 1.27, 1.06, 0.89 and 0.63 in descending order, respectively. Burenda x 2-CIP, Kasinia x 8-CIP, Masinia x 17-CIP and Simama x 17-CIP were favourable candidates for DMC displaying higher and positive SCA values of 0.53, 0.51, 0.31, and 0.27 in that order.

Jewel x 18-CIP, Simama x 4-CIP, Masinia x 2-CIP and Kasinia x 5-CIP were the best families with significantly lower and negative SCA effects of -2.03, -1.59, -1.19, and -1.14 for PIMRY, in that order. Jewel x 18-CIP, Simama x 5-CIP, Masinia x 2-CIP, and Simama x 4-CIP were the families of choice for lower and negative SCA values of 1.07, 0.8, 0.75 and 0.74 for PIRN, in that order.

The best families with weevil resistance were Jewel x 18-CIP, Masinia x 2-CIP Kasinia x 5-CIP and Simama x 4 CIP. These families had significantly lower and negative SCA values of 2.16, 1.35, 1.28 and 1.07 for WDS, in that order (Table 5.7).

Table 5.7. Specific combining ability effects for eight traits of 36 sweetpotato families used in the study.

Families	TRN	PMRN	RY	PMRY	DMC	PIRN	PIRY	WDS
Kasinia x 2-CIP	-1.22*	0.35	-0.68	0.89	-0.15	0.10	-0.45	-0.19
Kasinia x 4-CIP	-0.21	0.16	0.31	0.15	-0.17	-0.07	0.28	0.04
Kasinia x 5-CIP	-0.26	-1.13**	-0.57	-1.29*	-0.16	-0.66	-1.14*	-1.28*
Kasinia x 8-CIP	1.08*	0.27	0.98*	0.03	0.51**	0.29	0.26	0.92
Kasinia x 17-CIP	-0.21	0.69	-0.10	0.39	-0.09	0.25	0.37	-0.40
Kasinia x 18-CIP	0.82*	-0.34	0.07	-0.17	0.06	0.09	0.67	0.92
Simama x 2-CIP	1.46*	0.26	0.89	-0.13	0.10	1.05*	1.03*	1.11*
Simama x 4-CIP	0.26	0.80	0.29	1.27*	-0.09	-0.74*	-1.59**	-1.07*
siamama x 5-CIP	-0.25	-0.26	-0.19	-0.27	-0.17	-0.80*	-0.84	-0.67
Simama x 8-CIP	0.74	-1.46**	-0.32	-1.71**	0.07	-0.04	-0.12	-0.05
Simama x 17-CIP	-0.02	0.87*	0.28	0.24	0.27	-0.06	-0.34	-0.26
Simama x 18-CIP	-2.18**	-0.21	-0.94*	0.61	-0.18	0.59	1.86**	0.93
Ukerewe x 2-CIP	1.21*	-0.50	0.20	-0.45	-0.21	-0.53	-0.35	-0.62
Ukerewe x 4-CIP	-0.79*	-0.77	-0.37	-0.60	0.24	-0.14	-0.44	-0.39
Ukerewe x 5-CIP	-0.37	0.77	-0.48	0.26	0.26	0.12	0.85	0.52
Ukerewe x 8-CIP	-0.50	0.52	0.09	0.51	-0.04	0.17	0.25	0.03
Ukerewe x 17-CIP	-0.11	0.26	-0.04	0.56	-0.47**	-0.01	-0.01	0.52
Ukerewe x 18-CIP	0.55	-0.28	0.59	-0.28	0.22	0.39	-0.30	-0.06
Jewel x 2-CIP	0.12	0.18	0.32	-0.14	-0.39*	0.30	0.95*	1.17
Jewel x 4-CIP	1.52*	0.26	0.25	-0.11	0.26	0.25	0.60	0.28
Jewel x 5-CIP	0.44	-0.06	0.67	0.57	0.13	1.58**	1.77**	1.70**
Jewel x 8-CIP	-0.89*	0.47	-0.56	0.31	-0.18	-0.52	-0.82	-0.87
Jewel x 17-CIP	0.69	-1.09**	0.17	-0.85	-0.07	-0.53	-0.47	-0.11
Jewel x 18-CIP	-1.89**	0.24	-0.85	0.23	0.24	-1.07*	-2.03**	-2.16**
Burenda x 2-CIP	-0.04	-0.15	-0.10	-0.22	0.53**	-0.16	0.02	-0.12
Burenda x 4-CIP	0.81*	-0.79	-0.18	-0.09	-0.39*	0.12	0.06	0.40
burenda x 5-CIP	-0.12	0.64	0.39	0.09	0.02	-0.10	-0.40	-0.08
Burenda x 8-CIP	-0.28	-0.71	-0.28	-0.19	-0.17	-0.19	-0.38	-0.57
Burenda x 17-CIP	-0.69	0.01	-0.33	0.33	0.05	0.53	1.20*	0.98*
Burenda x 18-CIP	0.32	1.00*	0.50	0.08	-0.04	-0.19	-0.50	-0.61
Masinia x 2-CIP	-1.51*	-0.14	-0.62	0.06	0.13	-0.75*	-1.19*	-1.35*
Masinia x 4-CIP	-1.60*	0.34	-0.30	-0.62	0.15	0.58	1.10*	0.73
Masinia x 5-CIP	0.56	0.04	0.18	0.63	-0.09	-0.13	-0.25	-0.17
Masinia x 8-CIP	-0.16	0.90*	0.09	1.06*	-0.20	0.29	0.80	0.55
Masinia x 17-CIP	0.33	-0.73	0.02	-0.66	0.31	-0.18	-0.75	-0.73
Masinia x 18-CIP	2.38**	-0.41	0.63	-0.47	-0.30	0.19	0.29	0.97*

** = Significant at 0.01 probability level, * = Significant at 0.05 probability level, TRN = total root number, PMRN = percentage of marketable root number, RY = root yield, PMRY = percentage of marketable root yield, DMC = dry matter content, PIRN = percentage of infested root number, PIY = percentage of infested yield, WDS = weevil damage score.

5.3.6 Heritability estimates

The narrow sense heritability (h^2) and broad sense heritability (H^2) estimates for the studied traits are presented inTable 5.5. The narrow sense heritability ranged from 0.18 to 0.84. TRN, PMRN and PMRY had lower h^2 values of 0.24, 0.18 and 0.13, in that order. Root yield, DMC, PIRN, PIRY and WDS had higher heritability values of > 0.50. The broad sense heritability values varied from 0.40 to 0.93. All traits assessed in the study had higher H^2 values of > 0.5 except PMRN and PMRY.

5.4 Discussion

5.4.1 Performance of newly developed families across sites

The mean performance of the tested families differed across locations. Location had significant effect on PMRN, PMRY and DMC (Table 5.3). Families had the highest mean values for PMRN, PMRY and DMC at the ARI-Tumbi site than the Nyasha site (Table 5.4). This was probably caused by the difference in soil physiochemical characteristics at different locations. The ARI-Tumbi site had sandy loam soil (Table 5.2) which is desirable for sweetpotato production (Lebot, 2009). Furthermore the ARI Tumbi site had higher level of available phosphorus and exchangeable cations than the other sites, which might have favoured the development and enlargement of storage roots. Conversely, the Nyasha site had sandy clay soils which tend to limit root development and enlargement due to soil compactness (Lebot et al., 2011). Differences in the environmental conditions was reported to affect the dry matter content, root size and number in sweetpotato production (Tsegaye et al., 2007).

The storage root yield of the new families varied from 11.26 to 35.41 tha^{-1}. The yield levels are relatively better than the potential productivity of the crop reported in Tanzania varying from 15 to 23 t ha^{-1} (Sebastiani et al., 2007). Families with root yield above 20 t ha^{-1} and > 50% PMRY can be considered for further breeding for better yield gains. The DMC of all sweetpotato families were above 28%. This implies that all sweetpotato families had DMC within the range preferred by farmers in sub-Saharan African countries (Grüneberg et al., 2009; Cervantes-Flores et al., 2011). The families Kasinia x 8-CIP, Burenda x 2-CIP, Masinia x 17-CIP and Kasinia x 18-CIP which had DMC above 43% can be considered for further breeding.

The newly developed clones had less weevil infestation under field tests. This was related to PIRN that ranged from 0.74% to 27.08%. The observed low level of weevil infestation might have been attributed to the resistance reaction of the newly developed clones or the relatively shorter time at which the clones remained in the fields after maturity. Field weevil infestation on storage roots increase with increased time of the crop under field conditions. After maturity, the roots slowly crack creating entrance for weevils to access roots. It is reported that weevil population increases four times

more in roots than in vines (Smit et al., 2001), thus it is expected that infestation levels will be even higher when the crop overstays in the field after maturity.

The new families expressed significant differences in both PIRN and WDS. This is probably attributed to the difference in the root morphology, time to maturity (Stathers et al., 2003) and varied chemical composition of the storage roots among families (Muyinza et al., 2012; Anyanga et al., 2013). The following families: Kasinia x 5-CIP, Jewel x 18-CIP, Burenda x 18-CIP, Masinia x 2-CIP and Burenda x 4-CIP were categorized as resistant, while Masinia x 17-CIP, Kasinia x 4-CIP, Burenda x 8-CIP, Kasinia x 17-CIP, Simama x 4-CIP and Burenda x 2-CIP were regarded as moderately resistant. The resistant and moderately resistant families can be advanced for weevil resistance breeding or for direct production in western Tanzania.

5.4.2 Combining ability effects

Female parents had significant GCA effects for all traits except for PMRN and PMRY. Also significant GCA effect of males were observed for all the trait except PMRY. Also significant SCA effects were found for all the traits. The genetic effects indicated that both additive and non-additive (dominance) gene action play important role in controlling the expression of these traits in sweetpotato. This implies that both hybridization and clonal selection breeding strategy can be used to improve these traits in a population (Acquaah, 2012). The calculated general predicted ration (GPR) was >0.5 for TRN, RY, DMC, PIRN, PIRY and WDS suggesting the preponderance of additive gene action in controlling the expression of these traits. The GPR values were < 0.5 for PMRN and PMRY indicating that non-additive gene action contributed more on the expression of these traits than additive gene action (Baker, 1978). Similar to this study, additive gene action was reported to control dry mass content in sweetpotato (Komaki et al., 1998; Ngailo, 2015; Rukundo, 2015) and beta-carotene content than non-additive gene action (Chiona, 2010; Balcha, 2015).

5.4.3 General combining ability effects of parents

This study revealed that some female parents were good combiners displaying GCA effects in a desirable direction. Ukerewe and Jewel were the only good combiners for TRN, PMRY and yield displaying significantly higher and positive GCA (Table 5.6). Simama was a good combiner female parent for RY only, while Masinia was chosen as a good combiner female parent for both PMRY and DMC. Three female parents: Burenda, Kasinia and Masinia were selected as good combiners for DMC, PIRN, PIRY and WDS (Table 5.6). These parents can be used for further breeding of

sweetpotato varieties with resistance to weevils and enhanced DMC. Weevils are one of the most limiting factors to sweetpotato production in sub-Saharan Africa (Muyinza et al., 2012; Anyanga et al., 2013), whereas DMC is the most preferred trait by most farmers in SSA (Grüneberg et al., 2009; Cervantes-Flores et al., 2011).

Male parents, 18-CIP, and 17-CIP were selected as good combiners for TNR expressing higher and positive GCA effect in a desirable direction (Table 5.6). Male parents such as 2-CIP, 8-CIP and 17 CIP were good combiners for both yield and PMRY. Among the male parents, 2-CIP was selected as good combiner for both TRN and PIRY. Male parent 8-CIP was a good combiner for high DMC. Likewise, 17-CIP was selected as a good combiner for PIRN and WDS. Male parents: 18-CIP, and 4-CIP were selected as good combiners for both DMC and PIRN. Male parents: 4-CIP, and 5-CIP were selected as good combiners for both PIRY and WDS showing the lowest and negative GCA effect in a desirable direction (Table 5.6).

5.4.4 Specific combining ability effects of sweetpotato families

As expected, the SCA effects of families varied for assessed traits. The following families: Masinia x 18-CIP, Jewel x 4-CIP, Simama x 2-CIP and Ukerewe x 2 were selected for their favourable TRN displaying higher and positive SCA effects. Kasinia x 8-CIP, Simama x 2-CIP, Jewel x 5-CIP and Masinia x 18 were selected with better RY associated with higher and positive SCA effects. Simama x 4-CIP, Masnia x 8-CIP, Kasinia x 2-CIP and Masinia x 5-CIP were best specific combiners for PMRY. Also, families Burenda x 2-CIP, Kasinia x 8-CIP, Masinia x 17-CIP and Simama x 17-CIP were best specific combiners for DMC showing greater SCA effects.

Lower and negative SCA effects are required with regards to PIMRY. Thus the families Jewel x 18-CIP, Simama x 4-CIP, Masinia x 2-CIP and Kasinia x 5-CIP were selected in a desirable direction for this trait. Similarly, Jewel x 18-CIP, Simama x 5-CIP, Masinia x 2-CIP, and Simama x 4-CIP were selected with desired PIRN showing lower and negative SCA effect.

The best families selected for weevil resistance were Jewel x 18-CIP, Masinia x 2-CIP Kasinia x 5-CIP and Simama x 4 CIP. These families had significantly lower and negative SCA effect for WDS (Table 5.7). Similar to this study, significant positive SCA effect for TRN, RY and DMC have been reported (Chiona, 2010; Balcha, 2015; Ngailo, 2015). The best selected families for WDS, TRN, RY, PMRY, DMC, PIRN and PIRY can be used for development of sweetpotato varieties resistant to weevils with enhanced yield and dry matter content.

5.4.5 Heritability estimates

The narrow sense heritability (NSH) and broad sense heritability (BSH) for the TRN was 0.24 and 0.58, respectively. The NSH value for TRN in this study is relatively higher than the report of (Ngailo (2015) who indicated a value of 0.1. Conversely, the same authors reported BSH of 0.98 which is greater than the present value. The current study calculated NSH and BSH values of 0.56 and 0.72 for RY, respectively. Contrary to the current study, a relatively lower NSH and higher BSH values for root yield were earlier estimated at 34.9% and 96.9% by (Chiona, 2010). Ngailo (2015) reported a NSH of 0.22 and BSH of 0.99 for RY. The NSH and BSH values of DMC were 0.84 and 0.93 respectively. Chiona, (2010) reported higher NSH of 76.3% and BSH of 89.6%. Lower heritability values of 19.0% (NSH) and 20.50% (BSH) were earlier reported for DMC (Balcha, 2015). Except the lower values of heritability reported by Balcha (2015) for DMC, the present study found higher heritability values for root yield, TRN and DMC agreeing to previous studies.

Fairly higher NSH value of 0.62 and BSH of 0.77 were revealed in this study for weevil resistance. The current study also reported additive and non additive gene action to control weevil resistance, dry matter content and storage root yield and yield-related traits in sweetpotato. Additive gene action have been reported to control the expression of weevil resistance trait which is chemical based (Anyanga et al., 2017). The additive and non additive gene actions for the traits reported in this study indicated that both hybridization and targeted selection can be made as a strategy to improve this trait in the existing sweetpotato germplasm.

5.5 Conclusions

The present study examined general combining ability (GCA), specific combining ability (SCA), gene action and heritability of weevil (*Cylass* spp.) resistance, dry matter content (DMC) and yield and yield components of newly developed sweetpotato clones. Both additive and non-additive gene action were important in the expression of TRN, RY, DMC, PIRN and WDS displaying significantly higher GCA and SCA effects in desirable direction. The contribution of additive gene action was greater than non-additive gene action of these traits. The following parents had the best GCA for TRN: Ukerewe, Jewel, 2-CIP, 18-CIP and 17-CIP.The parents with best GCA for RY were: Simama, 2-CIP, 8-CIP and 17-CIP. Burenda, Kasinia, Masinia were best parents for DMC, PIRN, PIRY and WDS whereas 8-CIP was best parent for DMC only. Furthermore, 4-CIP and 5-CIP were best parent for WDS while 17-CIP, 18-CIP and 4-CIP were best parents for PIRN.

The following families were selected for enhanced TRN: Jewel x 4-CIP, Simama x 2-CIP, and Ukerewe x 2-CIP. Kasinia x 8-CIP, Simama x 2-CIP, Jewel x 5-CIP and Masinia x 18 were the best families for RY with higher and positive SCA effect in a desirable direction. The families such as Brenda x 2-CIP, Kasinia x 8-CIP, Masinia x 17-CIP and Simama x 17-CIP were selected for higher DMC associated with significantly positive SCA effect. The families displaying best SCA for weevil resistance were Jewel x 18-CIP, Simama x 4-CIP, Masinia x 2-CIP and Kasinia x 5-CIP. These families had significantly negative SCA effects for PIRN and WDS in desirable direction. The study identified the following families: Kasinia x 5-CIP, Jewel x 18-CIP, Burenda x 18-CIP, Masinia x 2-CIP and Burenda x 4-CIP displaying weevil resistance, followed by the families Masinia x 17-CIP, Kasinia x 4-CIP, Burenda x 8-CIP, Kasinia x 17-CIP, Simama x 4-CIP and Burenda x 2-CIP which were categorized as moderate resistant. The above selected families and parents can be used for development of sweetpotato varieties resistant to weevils with enhanced yield and dry matter content.

Reference

Acquaah, G. 2012. Principles of plant genetics and breeding 2nd ed. Wiley-Blackwell, Oxford USA.

Anyanga, M.O., H. Muyinza, H. Talwana, D.R. Hall, D.I. Farman, G.N. Ssemakula, R.O.M. Mwanga and P.C. Stevenson. 2013. Resistance to the Weevils *Cylas puncticollis* and *Cylas brunneus* conferred by sweetpotato root surface compounds. Journal of Agricultural and Food Chemistry 61: 8141-8147.

Anyanga, M.O., B. Yada, G.C. Yencho, G.N. Ssemakula, A. Alajo, D.I. Farman, R.O.M. Mwanga and P.C. Stevenson. 2017. segregation of hydroxycinnamic acid esters mediating sweetpotato weevil resistance in storage roots of sweetpotato. Frontiers in Plant Science 8. doi:10.3389/fpls.2017.01011.

Baker, R.J. 1978. Issues in Diallel Analysis. Crop science 18: 533-536.

Balcha, F.G. 2015. Breeding of sweetpotato for improvement of root dry matter and β-carotene contents in Ethiopia. PhD Thesis, University of KwaZulu-Natal, Pietermaritzburg.

Bernardo, R.N. 1965. Title Breeding for quantitative traits in plants. Stemma Press, , Woodbury, Minnesota.

Cervantes-Flores, J., B. Sosinski, K. Pecota, R. Mwanga, G. Catignani, V.-D. Truong, R. Watkins, M. Ulmer and G.C. Yencho. 2011. Identification of quantitative trait loci for dry-matter, starch, and β-carotene content in sweetpotato. Molecular Breeding 28: 201-216.

Chahal, G.S. and S.S. Gosal. 2002. Principles and procedures of plant breeding : biotechnological and conventional approaches. Alpha Science International Ltd, Pangbourne, UK.

Chiona, M. 2010. Towards enhancement of B-carotene content of high dry mass sweetpotato genotypes in Zambia. PhD Thesis, University of KwaZulu Natal, Pietermaritzburg.

Clark, C.A., J.A. Davis, J.A. Abad, W.J. Cuellar, S. Fuentes, J.F. Kreuze, R.W. Gibson, S.B. Mukasa, A.K. Tugume and F.D. Tairo. 2012. Sweetpotato viruses: 15 years of progress on understanding and managing complex diseases. Plant Disease 96: 168-185.

Dabholkar, A.R. 1999. Elements of Biometrical Genetics. Concept Publishing Company, New Delhi.

Falconer, D.S. and T.F.C. Mackay. 1996. Introduction to quantitative genetics. Clays Ltd. , Great Britain.

FAOSTAT. 2017. Food and Agriculture Organisation of the United Nations : Crop production data. FAOSTAT Division, Rome.

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

Gruneberg, W., R. Mwanga, M. Andrade and J. Espinoza. 2009. Breeding clonally propagated crops *In*: Ceccarelli, S., E.P. Guimarães and E. Weltzien, editors, *Plant breeding and farmer participation.* Food and Agriculture Oganization of the United Nations, Rome. p. 275-323

Hallauer, A.R., M.J. Carena and J.d. Miranda Filho. 2010. Quantitative genetics in maize breeding. Springer, New York.

Kagimbo, F.M., H. Shimelis and J. Sibiya. 2017. Diversity assessment of sweetpotato germplasm collections for yield and yield-related traits in western Tanzania. Acta Agriculturae Scandinavica, Section B — Soil & Plant Science: 1-9. doi:10.1080/09064710.2017.1372516.

Kapinga, R.E., P.T. Ewell, S. Jeremiah and R. Kileo. 1995. Sweetpotato in Tanzanian farming and food systems: implications for research. International Potato Center, Tanzanian Ministry of Agriculture, Nairobi and Dar-Es-Salaam.

Kapinga, R.E., S.C. Jeremiah, E.J. Rwiza, D. Rees and D. Rees. 2003. Sweet potato postharvest assessment: experiences from East Africa. Chatham, United Kingdom.

Komaki, K., K. Katayama and S. Tamiya. 1998. Advancement of sweetpotato breeding for high starch content in Japan. Tropical agriculture-london then trinidad. 75: 220-223.

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.

Lebot, V. 2009. Tropical root and tuber crops : cassava, sweet potato, yams and aroids. CABI, Wallingford.

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

Muyinza, H., H.L. Talwana, R.O.M. Mwanga and P.C. Stevenson. 2012. Sweetpotato weevil (*Cylas* spp.) resistance in African sweetpotato germplasm. International Journal Of Pest Management 58: 73-81.

Ngailo, S., H.A. Shimelis, J. Sibiya and K. Mtunda. 2016. Assessment of sweetpotato farming systems, production constraints and breeding priorities in eastern Tanzania. South African Journal of Plant and Soil 33: 105-112.

Ngailo, S.E. 2015. Breeding Sweetpotato for Improved Yield and Related Traits and Resistance to Sweetpotato Virus Disease in Eastern Tanzania. PhD Thesis, University of KwaZulu-Natal, Pietermaritzburg.

Rukundo, P. 2015. Breeding of sweetpotato (Ipomoea batatas (L.) Lam.) for drought tolerance and high dry matter content in Rwanda. PhD Thesis, University of KwaZulu-Natal, Pietermaritzburg.

SAS. 2003. Statistical Analysis System. SAS Institute inc., Cary, North Carolina.

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. doi.org/10.1186/1471-2164-11-604.

Schlegel, R.H.J. 2010. Dictionary of plant breeding. CRC Press, Boca Raton London.

Sebastiani, S., 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. *8th African Crop Science Society Conference*, El-Minia, Egypt, 27-31 October 2007.

Singh, R.K. and B. Chaudhary. 1979. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi-Ludhiana, India.

Smit, N.E.J.M., M.C.A. Downham, P.O. Laboke, D.R. Hall and B. Odongo. 2001. Mass-trapping male Cylas spp. with sex pheromones: a potential IPM component in sweetpotato production in Uganda. Crop Protection 20: 643-651.

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

Stathers, T.E., D. Rees, S. Kabi, L. Mbilinyi, N. Smit, 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 sweet potato [*Ipomoea batatas* (L.) Lam.] germplasm collection from Tanzania. African Journal of Plant Science 2: 77-85.

Tsegaye, E., E. Sastry and N. Dechassa. 2007. Genetic variability for yield and other agronomic traits in sweet potato. Indian Journal of Horticulture 64: 237-240.

CHAPTER 6 AN OVERVIEW OF THE STUDY

6.1 Introduction

Sweetpotato [*Ipomoea batatas (*L.) Lam] is an important multi-purpose crop providing various livelihood opportunities to millions of smallholder farmers in sub-Sharan Africa (SSA). It is widely grown in SSA including Tanzania serving for food, feed and industrial raw material. However, sweetpotato production and productivity is affected by a range of constraints including biotic, abiotic and socio-economic factors. Weevil infestation caused by sweetpotato weevil (*Cylas* spp.) is one of the main factors contributing to low yields of the crop under the smallholder framing systems in Tanzania. Farmers use field sanitation, early planting and early harvesting and chemical treatment to control sweetpotato weevils. However, these control options are less effective leading substantial quality and yield losses of the crop. Developing sweetpotato varieties with durable resistance to weevils and enhanced yield and yield components is advocated for sustainable production and productivity of the crop in SSA. This chapter summarises the research objectives and highlights the core findings of the study.

The specific objectives of this study were:

v To identify farmers' perceptions on sweetpotato weevil damage, production constraints and criteria used to select and grow the best sweetpotato varieties in western Tanzania.

vi To determine the genetic diversity present among Tanzania grown sweetpotato germplasm to select promising breeding parents with enhanced yield and yield-related traits and dry matter content.

vii To screen sweetpotato germplasm collections for sweetpotato weevil (*Cylas* spp) resistance in western Tanzania and to select best parents to be used in breeding for weevil resistance.

viii To determine general combining ability (GCA), specific combining ability (SCA), gene action and heritability of weevil (*Cylass* spp.) resistance, dry matter content and yield and yield-related traits of newly developed sweetpotato clones.

6.2 Summary of major findings

The first study identified farmers' perceptions on sweetpotato weevil damage, production constraints and criteria used to select and grow the best sweetpotato varieties in western Tanzania. Surveys were conducted in four selected districts of western Tanzania. Data were collected using a structured questionnaire, focus group discussions and transect walk involving 122 sweetpotato farmers. The main outcomes of the study were:

- Weevil damage was reported by 84% of the respondents being the overriding constraint to sweetpotato production. Sweetpotato diseases and drought were the next production constraints, reported by 57% and 54% of respondents, respectively.
- The main farmers' preferred agronomic traits of sweetpotato included high yield (reported by 25% of respondents), drought tolerance (24%), and disease and pest resistance (21%).
- Farmers' preferred sweetpotato culinary traits in the study areas were: high dry matter content (reported by 21% of respondents), followed by reduced cooking time, taste and fiber content (each reported by 19% of respondents).

The second study determined the genetic diversity present among Tanzania grown sweetpotato germplasm and selected promising breeding parents with enhanced yield and yield-related traits and dry matter content. Seventy six sweetpotato accessions collected from Tanzania and 20 sweetpotato accessions received from International Potato Centre (CIP) in Lima/Peru were characterized in two seasons using a 16 x 6 triple lattice design. The main outcomes of the study were:

- The tested sweetpotato collections differed significantly for storage root yield, dry matter content and number of roots per plot.
- Genotypes New Kawogo, Kiti cha Nyerere and Kisu cha Masai had the highest root yields of 10.14, 9.85 and 9.67 t/ha, respectively.
- Genotypes Ngw'anangusa, Rugomoka and Secondary had significantly higher mean DMC of 43.50%, 43.30% and 43.30%, receptively.
- The studied genotypes were classified into two major genetic groups with genetic diversity of 0.54.
- The selected genotypes can be recommended for future breeding programs to bolster yield and dry matter content of sweetpotato under western Tanzania conditions.

The third study assessed sweetpotato germplasm collections for weevil resistance and selected parents for breeding of weevil resistance varieties. A total of 96 sweetpotato

genotypes were screened using a 12 x 8 lattice design with three replications at each site. The main outcomes of the study were:

- The tested genotypes differed significantly for sweetpotato storage root number, root weight, weevil infestation level and root damage score.
- Nine sweetpotato genotypes (Kibandule, Malulumba, Utitiri, 3-CIP, Madebe, Magunhwa, 5-CIP, Kafu and Chuchu ya nesi) expressing resistance and 10 genotypes (Nyamvuva, sengi, 22-CIP, Rugomoka, Tumauma, Ejumla, Carot C, New Kawogo 2, Haraka and 4-CIP) with moderate resistance to weevils were selected.
- Five genotypes (Magunhwa, Chuchu ya Nesi, Rugomoka, Tumauma and New Kawogo) were selected expressing both weevil resistance and desirable yield and yield-related traits.
- Weevil infestation on storage roots significantly correlated with total root number and weevil damage score, whereas marketable root weight and total root weight were significantly correlated with infested root weight.
- The selected genotypes are recommended for weevil resistance breeding programmes of sweetpotato in western Tanzania or similar agro-ecologies.

The fourth study determined the general combining ability (GCA), specific combining ability (SCA), gene action and heritability of yield and yield-related traits, dry matter content and *Cylas* spp. resistance among newly developed sweetpotato clones. Six weevil resistant and six susceptible parents were crossed using a 6 x 6 North Carolina Design II mating design. The 36 families were evaluated at three locations using a 3 x 12 lattice design with two replications for weevil resistance and yield and related traits in western Tanzania. The main outcomes of the study were:

- The GCA effect of females was significant for the studied traits except for percentage marketable root number (PMRN) and percentage marketable root yield (PMRY).
- Significant GCA effect of males were detected for all traits except PMRY.
- The SCA effect of families were significant for all traits.
- Additive gene action showing a >0.5 general predicted ratio (GPR) was more influential for total root number (TRN), root yield (RY), dry matter content (DMC), percentage of infested root number (PIRN), percentage infested root yield (PIRY) and weevil damage score (WDS), whereas non-additive gene action was more influential for PMRN and PMRY with a <0.5 GPR.
- Good combiner parents for RY were Simama, 2-CIP, 8-CIP and 17-CIP, while good combiner parents for DMC were Burenda, Kasinia, Masinia and 8-CIP. The parents

Burenda, Kasinia, Masinia, 4-CIP and 5-CIP were good combers for WDS in a desirable direction.

- The best selected families for RY were Kasinia x 8-CIP, Simama x 2-CIP, Jewel x 5-CIP and Masinia x 18. The following families: Burenda x 2-CIP, Kasinia x 8-CIP, Masinia x 17-CIP and Simama x 17-CIP were superior for high DMC. The families Jewel x 18-CIP, Simama x 4-CIP, Masinia x 2-CIP and Kasinia x 5-CIP were selected for improved WDS.
- The narrow sense heritability for TRN, RY, DMC, PIRN and WDS were 0.24, 0.56, 0.84, 0.62 and 0.62, while the broad sense heritability for these traits were 0.58, 0.72, 0.93, 0.78 and 0.77, in that order.
- The selected parents and families are useful genetic resources for development of sweetpotato varieties resistant to weevils and enhanced root yield, yield components and dry matter content.

6.3 Implications of the research findings

- The study identified farmers' perceptions on sweetpotato weevil damage, production constraints and criteria used to select and grow the best sweetpotato varieties. These traits should be integrated in future sweetpotato breeding programs to develop and release varieties adapted under western Tanzania conditions. This will enhance acceptance and adoption of the newly developed sweetpotato varieties by farmers.
- The two genetically distinct groups of sweetpotato genotypes with the genetic diversity of 0.54 can be exploited in various crosses to develop new varieties with desired traits of economic importance.
- The selected genotypes with resistant and moderate resistant reactions to weevils can be used as best parents for weevil resistance breeding programmes to develop new varieties in western Tanzania or similar agro-ecologies.
- Presence of both additive and non-additive gene action for weevil resistance, root yield and yield-related components and dry matter content suggests that breeding gain can be realized through hybridization and clonal selection in breeding programmes.
- There is need to undertake further multi-environmental evaluations followed by distinct, uniformity and stability trials for varietal registration and release.