Genetic, Agro-Morphological Diversity and Genome-Wide Association studies in sweetpotato (*Ipomoea batatas* [L] Lam.) Accessions from Zimbabwe

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GENERAL ABSTRACT

Sweetpotato *[Ipomoea batatas* (L.) Lam] is a strategic crop, especially for the developing countries within sub-Saharan Africa (SSA). It serves as a food and nutrition security crop. In Zimbabwe, sweetpotato is mostly grown by smallholder farmers as a shield against hunger and income generation. The crop's productivity is limited by both biotic (pests and diseases) and abiotic factors such as drought and floods. However, no breeding, collection, characterisation, and conservation of available sweetpotato accessions has been done in Zimbabwe. The investigations sought to: understand production constraints as well as farmer preferred varieties and selection criteria, conduct genetic diversity studies using agro-morphological and molecular markers, identify high yielding genotypes with stable performance across sites, as well as identifying SNP markers associated with sweetpotato morphological traits through conducting a Genome-wide association study (GWAS).

The first objective was achieved through conducting a socio-economic survey and collection of sweetpotato accessions from key production regions in Zimbabwe. From a sample size of 225 interviewed farmers, 64% were women compared to 36% men. Results indicated that the majority (42.6%) of farmers were between 30-40 years old. Twenty-two of the 30-40-year-old had completed secondary education, six females with primary level education and one male with tertiary education, which can be an important entry point for participatory breeding efforts since they will be able to appreciate some of the concepts. The main varieties were Chibhahlengwe, Tiribhari, Boarding, Kori, Fost, Mozambique White, Germany2, Chingova, Beauregard, Mafuta, Chizai, Chibikiravaenzi, Mukambachaza, Brondal and Pamhai. Theselection criteria were high yielding capacity (22.58%), taste (16.49%), early maturity (15.77%), resistance to disease and insect pests (15.05%), market demand (11.47%), long shelflife (11.11%), cookability (7.53%) and high dry matter. The main constraints were low selling prices (31.55%), insect pests (25%), diseases (20.83%), shortage of clean planting materials (14.29%), heat and drought (7.14%), shortage of labour (0.6%), and frost (0.6%). About 90% of farmers singled out weevils and moles as the most problematic pests. The farmers used adaptable, high yielding varieties, manure and irrigation, piecemeal harvesting and established own nurseries as strategies to cope with the constraints faced.

For agro-morphological characterisation, 92 sweetpotato genotypes were evaluated using 31 sweetpotato

descriptors. One hundred and seventy-four phenotypic classes were observed from the descriptive statistics. The number of phenotypic classes across all attributes were 174 though the classes within an attribute/ character ranged from 3 to 10. Traits including plant type, vine internode length and pigmentation, leaf lobe type and number, shape of central lobe, mature leaf shape, abaxial leafvein pigmentation, petiole pigmentation, petiole length, storage rootstalk length, storage root per plant, storage root formation, predominant flesh colour, secondary flesh colour, storage root skin colour, storage root shape and size, distribution of secondary skin colour, intensity of predominant skin colour and predominant storage root skin colour, showed great variation among the genotypes. The variables which showed few phenotypic classes were: mature leaf size and colour, immature leaf colour, secondary vine colour, secondary skin colour, storage root surface defects, storage root cortex thickness, vine internode diameter, and vine tip pubescence.

Cluster analysis revealed three distinct clusters. Cluster 1 had 27 genotypes (29.3%), Cluster 2comprised 58 genotypes (63%) in two sub-groups 2a and 2b, and Cluster 3 had seven (7) genotypes (7.6%). Sub-group 2a contained 27 genotypes (29.3%), while subgroup 2b had 31 genotypes (33.7%). Clusters 1 and 2 had genotypes that produced more than 6 roots per plant unlike cluster 3 which had genotypes bearing 5 or fewer roots per plant.

One hundred genotypes were evaluated in four environments. The experiments were laid as a 10 x 10 alpha- lattice design with two replications in all the sites. There was evidence of significant ($p<0.001$) genotypic, environmental and genotype x environment interaction effectson storage root yield. Chiredzi had a yield of 15.213 t ha^{-1}, Shamva (11.539 t ha^{-1}), Africa University (6.594 t ha^{-1}) and Harare (4.876 t ha^{-1}). The mean yield ranged from 0.84 t ha^{-1} to 8.25 t ha^{-1}. Forty-seven per cent of the sweetpotato genotypes had yields which were in the range of mean yield (5.19 t ha^{-1}), with G87 (Mukambachaza), G100 (Beauregard), G13 (Germany 2), and G96 (Drumhead) having the top four yields of 8.25, 8.17, 7.74 and 7.69 t ha^{-1}, respectively.Genotypes G11 (Red Jewel) and G 40 (Unknown13Ngaoni) were the low yielders, with below 10 t ha^{-1}. The results of genotype rankings across environments were non-consistent. Genotype 94 (Murewa2Cross) won in Shamva, while genotypes G100 (Beauregard) and G28 (Chidhumbe dhumbe) won in the other locations. The GEI variance component (1.3% of total variance) forroot yield was smaller than the variance of the genotype (2.33%). However, error variance (0.43%) of total variance was smaller than the GEI variance component. Among the test environments, Chiredzi was the most representative and discriminating site while Harare was the most unsuitable site for

sweetpotato fresh root yield evaluations. The genotype designated G53 (Unknown6Chako) was the most stable. The two principal components (PCs) explained 85.39% of the variance, with PC1 and PC2 accounting for 56.92% and 28% of the variation, respectively. Genetic correlation revealed that marketable yield, non-marketable yield, and total yield were significantly correlated (R^2=0.9999). Phenotypic correlations revealed that total root yield was highly correlated to marketable root yield (R^2 =0.8338) and non-marketable root yield (R^2=0.755). However, the number of roots per plant was not correlated to yield (R^2=0.334). The results indicate that there is potential to initiate a strong sweetpotato breeding program in Zimbabwe through exploiting the variation within the collection and ideal production sites for the betterment of farmers.

A total of 98 introduced and local sweetpotato genotypes in Zimbabwe were subjected to genotyping by sequencing since two samples were contaminated. Two groups were inferred using both structure software and silhouette plots in RStudio. The smaller group had four individuals that included Bosbok, UnknownC4, KwasakwasaC, and Kau7. These individuals had large Gower's genetic distancesof 2.54, 2.37, 1.65, and 3.20, respectively, compared to others. Analysis of molecular variance showed a very low PhiPT value (equivalent to FST value) of -0.017 suggesting that these sub-populations could be from the same major population.

The fifth objective was to identify markers, single nucleotide polymorphism (SNPs) for agronomic and quality traits in sweetpotato using a Genome-wide association study (GWAS).There was correlation between single nucleotide polymorphism markers and agronomic and quality traits. Considering a LOD score of 3, flesh colour and root formation traits had markersat unidentified chromosome positions. However, for the intensity of skin colour, roots, secondary flesh colour and size variability markers were observed on chromosomes 2, 10, 10,and 15, respectively. Chromosome 10 had more influence on root traits and breeding efforts can target this chromosome in marker assisted selection.

In conclusion, the study identified production constraints, farmer preferences, selection criteria, stable and high yielding genotypes, genetic diversity among sweetpotato accession from Zimbabwe. The study also revealed duplicates from both agro-morphological and molecular characterisation. Use of results from this study will lead to development of superior sweetpotato varieties that should be adopted easily since farmers' selection criteria were identified. Use of genome-enabled tools that were applied in this study could lead to expeditious development of new varieties, such as through exploitation of SNP markers associated with important sweetpotato phenotypic traits.

DECLARATION

I, **Victor Chingwara**, 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. The thesis does not contain, other person's data, pictures, graphs, or other information,unless specifically acknowledged as being sourced from other persons.
4. This thesis does not contain other person's writing, unless specifically acknowledged as being sourced from other researchers. Where other written sources have been quotedthen:
    - Their words have been rewritten, but their general information attributed to them has been referenced;
    - Where their exact words have been used, their writing has been placed in italics and inside quotation marks, 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 thereference sections.

Signed……

Victor Chingwara

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

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Professor Julia Sibiya (Supervisor)

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Professor Edmore Gasura (Co-Supervisor)

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DEDICATION

I dedicate this thesis to my family: Sarah Chikangaise, Amah, Tino, Praise, and James; mylate mother and father Neily Moyana and James Chingwara, respectively.

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AFLP	Amplified fragment length polymorphism
AGRA	Alliance for a Green Revolution in Africa
AGRITEX	Agricultural Technical and Extension Services
ANOVA	Analysis of Variance
AVRDC	Asian Vegetable Research and Development Centre
CIAT	International Centre for Tropical Agriculture
CIP	International Potato Centre
CTAB	Cetyl Trimethyl Ammonium Bromide
DAP	Days after planting
DNA	Deoxyribonucleic Acid
EDTA	Ethylene diamine-tetra-acetic acid
FAO	Food and Agricultural Organization (United Nations)
G	Genotype
G x E	Genotype by environment interaction
GoZ	Government of Zimbabwe
GWAS	Genome wide association study
HRC	Horticulture Research Centre
IBPGR	International Board for Plant Genetic Resources
IFAD	International Fund for Agricultural Development

IITA	International Institute for Tropical Agriculture
ISSR	Inter-simple Sequence Repeats
LSD	Least Significant Difference
MAB	Marker Assisted Breeding
NGO	Non-Government Organizations
OFSP	Orange Fleshed Sweetpotato
PCR	Polymerase Chain Reaction
RAPD	Random Amplified Polymorphic DNA
RCBD	Random Complete Block Design
RDA	Recommended Daily Allowance
RFLP	Restriction Fragment Length Polymorphism
SADC	Southern African Development Community
SSA	Sub-Saharan Africa
SSR	Simple Sequence Repeats
UPGMA	Unweighted Pair-Group Method with Arithmetic Average
UZ	University of Zimbabwe

CHAPTER 1
GENERAL INTRODUCTION

1.1 Sweetpotato

Sweetpotato [*Ipomoea batatas* (L.) Lam] is a tropical herbaceous dicotyledonous species with creeping, long-term vines and roots that are adventitious (Katayama et al., 2017). It is of the Convolvulaceae family sometimes known as morning glory flowers and are usually considered and are readily distinguished by their botanical characteristics on the basis of morphological traits (Rosero et al., 2019). Sweetpotato is a hexaploid (2n=6x=90) plant.On their own most varieties are not cross compatible, they have high levels of heterozygosity because of the obligate outcrossing nature of the crop (Ellstrand, 1992; Feldman, 2002). Varieties of sweetpotato vary considerablyin morphological and horticultural characteristics such as size, colour, and shape of leaves and branches as well as a wide range of size, flesh, and skin colour of roots, shape, yield potential. The greatest sweetpotato diversity is reported to be in Central America. The evidence was drawn from molecular marker results that indicate Central America as the primary centre of origin for sweetpotato (Simmonds, 1993; Karuri et al., 2010).

1.2 Importance of sweetpotato

Sweetpotato has many uses and benefits. The parts of most economic importance are immature leaves usedas a relish and the starchy storage roots. The roots are mainly for human consumption as well as feeding animals, with very little directed towards industrial use (Mukhopadhyay et al., 2011; Laurie et al., 2013). In countries such as China, farmers use almost all parts of sweetpotato as livestock feed (Mukhopadhyay et al., 2011). This illustrates the potential of sweetpotato, which is unexploitedin many African countries, Zimbabwe included. Sweetpotato as a root crop is regarded as the most important in the tropics because of its flexibility in a number of production aspects (Mukhopadhyay et al., 2011).

Sweetpotato is adaptable to different soils including acidic soils (Mukhopadhyay et al., 2011) can give economic yields under those harsh conditions (Parwada et al., 2011). It is possible to grow sweetpotato all year round provided the areas are frost-free and have adequate water for its growth (Chivenge et al., 2015b). Sweetpotato has a short growing season of 3-5 months, which allows

multiple cropping and the vines are used as planting material (Six, 2011). Sweetpotato is also comparable to other economic crops in terms ofimportance and is ranked fifth after rice, wheat, maize, and cassava. It comes sixth in dry matter production, seventh in digestible energy production and ninth in protein production in developingcountries (Esan and Omilani, 2018).

The government of Zimbabwe declared sweetpotato as one of the staple crops due to its importance. Motsa et al. (2015a) and Chandrasekara and Josheph Kumar (2016) indicated that in some African countries, sweetpotato among starchy crops, is the staple food while other countries use it as food security or supplementary food. This later part is in agreement with earlier reports by Gibson et al. (2011) that storage roots of sweetpotato were often kept in the ground and only harvested when needed. The sweetpotato crop is mainly harvested in piecemeal and stored on a flexible time schedule, which qualifies it as a food security crop (Motsa et al., 2015a). This suggests a continuous food supply that can be provided during the off-season with no requirement for storage infrastructure (Low et al., 2001). This is very important for a month or two when grain stock from the previous season has been exhausted and just before major grain harvests (Roncoli et al., 2001; Motsa et al., 2015a). The crop is also good as a food reserve when the main staple has been adversely affected by drought and other biotic factors such as pests and diseases (Reynolds et al., 2015).

1.3 Sweetpotato utilization.

Sweetpotato is a nutritious food crop. Both the storage roots and tender leaves areedible to humans (Allemann et al., 2004; Van Der Hoeven et al., 2016). Sweetpotato can be consumed as vegetables, boiled, baked or roasted, fried, or dried, and ground into flour to make biscuits, bread,and baby weaning foods, while other people prefer eating them raw (Oniang et al., 2003; Bao and Fweja, 2020). asserted that sweetpotato leaves may possibly have some medicinal properties due to the polyphenol-rich green extracts reported to play a role in reducing prostate cancer. China, the world's leading potato producer uses 40% of its products for animal feed, while Brazil and Madagascar use 35% and 30%, respectively (Laurie et al., 2009) . In China, farmers are contracted by companies to produce sweetpotato for both domestic consumption and export.

1.4 Justification of the study

Sweetpotato is grown throughout the tropical, sub-tropical and frost-free temperate zones (Kristjanson et al., 2012). The crop is one of the world's most important, versatile,yet underutilized food crops grown for its roots and leaves at subsistence level (Chivenge et al., 2015a; Motsa et al., 2015b). Despitethe increase in sweetpotato demand as a result of rapid population growth and price increase of staple food, sweetpotato yields in Zimbabwe are still low (6-10 t ha^{-1}). The impact of the advent of climate change on food availability and plant genetic loss in Zimbabwe is not yet known. Agriculture in the sub-Saharan region is identified as particularly vulnerable to ongoing climate change (Cooper et al., 2008). However, sweetpotato is a rustic crop that produces well in poor nutrient soil conditions, and it is known to have low incidence of pests and limiting diseases, high drought tolerance and low production costs (Low, 2017)). The genetic diversity of sweetpotato in Zimbabwe is not known, yet it is important for conservation and breeding. In addition, systematic collection, conservation, and characterization of sweetpotatoin Zimbabwe have not yet been done. In general, systematic plant breeding and efficient utilizationof agricultural inputs have increased crop productivity in the past century (Chivenge et al., 2015a). However, the effect of the increased intensification on the crop genetic diversity inclusive of sweetpotato in Zimbabwe has not yet been established.

Most farmers in Zimbabwe have not been trained in sweetpotato production and much of what is known comes from traditional knowledge. Improvement work in sweetpotato can be limited by a lack of knowledge of available genetic diversity (Tairo et al., 2008). Traditional naming systems of the landraces are often based on traits that are perceived subjectively, and therefore in doing so, it is uncommon to find confusion between varieties or use of different names for the same cultivar (Cleveland et al., 2000). This calls for proper identification of the existing sweetpotato genotypes through characterization so as to avoid such confusion that is associated with the traditional naming of varieties (Jenkins, 2015; Ochieng, 2019). Furthermore, the variation within the collection of sweetpotato germplasm available in Zimbabwe is largely unknown since no previous studies on sweetpotato characterization have been done. The phenomenon of occurrence of the same cultivar withdifferent names or vice versa is quite common (OECD, 2016). Characterization of sweetpotato accessions will provide information on conserved germplasm, placing it in the most effective form of use, and it is important to emphasize that the value of germplasm increases as it becomes known

and documented (Li et al., 2004; Massucato et al., 2020). Accessions identified could be promoted as superior varieties to farmers or used as parents in the comprehensive breeding programs for improved nutrition in sweetpotato varieties without a negative impact on crop yields (Gasura et al., 2008).

The highly variable environments in Zimbabwe have led to highly complicated genotype by environment (G x E) interactions. Genotype by environment analysis is key in selection and cultivar recommendation, and in identifying suitable production and test environments (Asfaw et al., 2009). It would be important to determine the level of G x E interaction for sweetpotato root yield in Zimbabwe and this would allow for region-specific recommendations. A significant G x E interaction would mean that a selection from one environment may perform poorly in another environment (Via and Lande, 1985). This would entail breeding for specific adaptation. Genotypes thatshow little interaction with environments would be desired as they are stable (Kawecki and Ebert, 2004).

Subsequently, to enhance the potential for adoption of varieties by growers, farmers' constraints and their preferences for sweetpotato cultivars need to be identified through participatory breeding.

1.5 Overall Objective

The study aimed at increasing the understanding of sweetpotato diversity in Zimbabwe as a way of laying a foundation for sweetpotato breeding, productivity and conservation measures.

1.5. 1 Specific objectives

The following specific objectives were pursued:

1. To identify challenges faced by sweetpotato farmers in Zimbabwe and attributes considered to be central in retaining sweetpotato cultivars;
2. To assess agro-morphological variability of the sampled sweetpotato germplasm;
3. To evaluate the population structure and diversity at the molecular level of local and introduced sweetpotato accessions in Zimbabwe using the genotyping by sequencing approach;

4. To identify high yielding sweetpotato genotypes with stable performance across sites.
5. To identify single nucleotide polymorphism (SNP) markers for agronomic and quality attributes of sweetpotato using a Genome-wide association study.

1.5.2 Research hypothesis

The following hypotheses were tested:

1. Farmers are rational in their choice of sweetpotato cultivars for production and utilization.
2. Diversity in morphological traits exists among the sampled sweetpotato genotypes.
3. Diversity at the DNA level exists among the collected sweetpotato genotypes.
4. Variability in adaptation to different agro-ecological areas exists among sweetpotato genotypes collected in Zimbabwe.
5. There are associations between single nucleotide polymorphism (SNP) markers and agronomic and quality traits

1.5.3 Outline of thesis

Eight chapters constitute this thesis and only five chapters are independently crafted and can be read as research papers. However, all five chapters have a common overall objective of investigating sweetpotato variability in Zimbabwe. The respective objectives constituted were fulfilled in the different chapters. The chapters are as follows:

Chapter 1: Introduction and Overview

This chapter covers the background information, problem statement, the origin, importance, nutritional benefits, and botanical attributes of sweetpotato. It also covers the aim, objectives, and explains why the study area is important for breeding efforts for Zimbabwe.

Chapter 2: Literature Review

Relevant previous works are highlighted on sweetpotato variability, the threats posed by the advent of climate change food systems and nutrition security, conventional and current methods of measuring sweetpotato variability are highlighted under this chapter.

Chapter 3: Identification of farmers' key sweetpotato production constraints and desired attributes in sweetpotato cultivars.

This chapter covers the methodology used to collect information from key stakeholders, sweetpotato constraints faced by sweetpotato farmers in Zimbabwe, and characteristics considered important in different sweetpotato genotypes.

Chapter 4: Morphological variability

This chapter reveals the results of a systematic analysis of sweetpotato variability using morphological descriptors. It also covers the importance of conventional approaches to the investigation of variability within plant genotypes which is critical in plant breeding.

Chapter 5: Genetic variability analysis using genotyping–by–sequencing (GBS).

This chapter covers the most recent approach to investigating plant genetic variability. It complements the findings of the morphological approach. This complements the results obtained through morphological analysis. It covers the benefits of using the most recent approaches to investigating sweetpotato genetic diversity.

Chapter 6: Genotype x environment interaction and root yield stability of sweetpotato germplasm across different stress environments.

This chapter covers the importance of sweetpotato, various factors which distinguish test areas where sweetpotato is grown in Zimbabwe, the challenges posed by the existence of significant genotype x environment interaction to plant breeding. It confirms the existence of a strong genotype x environment interaction among the different sweetpotato genotypes across different test areas.

Chapter 7: Genome-wide Association study

This chapter covers the application of a Genome-wide association study to identify Single Nucleotide Polymorphism markers for agronomic and quality traits in sweetpotato in order to investigate genetic diversity among sweetpotato genotypes.

Chapter 8: General Discussion, Conclusion and Recommendation

This chapter contains a summary of the major findings of the study and their meaning for the sweetpotato sector. Deductions are also made about the achievements and limitations of the study and it feeds into recommendations for future research in sweetpotato characterization.

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CHAPTER 2
LITERATURE REVIEW

2.1 Introduction

This chapter reviews the sweetpotato taxonomy, dispersal, anatomy, sweetpotato production in Southern Africa, nutritional contribution of sweetpotato, sweetpotato as a food security crop, genetic diversity of sweetpotato germplasm, morphological and molecular characterization, Diversity AraysTechnology (DArT), genotype x environment interaction, statistical procedures to account Gx E and value chain actors 'perspective on Sweetpotato.

2.2 Taxonomy

Sweetpotato (*Ipomoea batatas* [L.] Lam.) is a tropical crop that belongs to the Convolvulaceae family (Reddy, 2015). Sweetpotato is believed to be a hexaploid (2n=6x=90) plant (Reddy, 2015). In Zimbabwe, there are different sweetpotato cultivars that exhibit huge morphological and growth habit variations. Nevertheless, polyploidization is believed to have aided the attainment of its hexaploidy status, though cytogenetic evidence suggested an autohexaploid structure with a B genome (Bourke et al., 2018) from 2X *Ipomoea leucantha*, 4X *Ipomoea littoral*is.

2.3 Sweetpotato dispersal

Glato et al. (2017) indicated that sweetpotato came from tropical America and was dispersed around the world as a result of migration. Rossel et al. (1999) hypothesised that the rapid spread of the sweetpotato in the sixteenth century was a result of the Portuguese voyagers. Glato et al. (2017) also suggested that sweetpotato was introduced in Africa by the Portuguese in the 16th century. However, Brecht (2002) indicated that Europeans introduced the crop into Africa in the early 1500s. Gichuki et al. (2003) believed that secondary introductions were made from India between the seventeenth and nineteenth centuries.

2.4 Anatomy of sweetpotato

In terms of growth habits, Nwankwo et al. (2015) reported sweetpotato as erect, semi- erect,

spreading, and very spreading. In Zimbabwe, people consume both sweetpotato tender leaves and storage roots. However, the storage root is the most economic part of the sweetpotato plant. Gajanayake et al. (2013) defined the swollen root as the storage root. In his studies, (Villordon et al. 2009) indicated that accumulation of starch marked the initiation of root formation. It is believed that root formation starts within seven to nine days post-transplant and this varies with variety in question. Reddy et al. (2018) and Somda and Kays (2019) reported that sweetpotato yield was a function of environmental factors and is highly variable. In addition, Shumbusha et al. (2017) pointed that sweetpotato yield depends on the number of roots formed per plant, and the number of roots varied from 4 to 6. Laurie et al. (2013) observed that the sweetpotato storage roots shape varied from round to irregular mainly because of environmental factors. In most cases, storage root skincolour varies from white to dark purple yet flesh colour ranges from white to orange.

Sweetpotato stems are cylindrical and their lengths and internodes are functions of the genotype and moisture availability. Maquia et al. (2013) observed variation in stem diameters ranging from thin to very thick. In Zimbabwe, stem colour ranges from green to purple. FAO et al (2019) reported that some stems totally hairy yet other stems are only hairy at the tip. Sweetpotato plants exhibit three types of branching which are primary, secondary and tertiary during their periods of growth. Sweetpotato genotypes differ in the number of branches and these range from three to 20 branches. Fanzo et al. (2013) observed that the branching habit is influenced by planting spacing, photoperiod, soil moisture and nutrient supply.

Sweetpotato leaves are simple and spirally arranged around the sweetpotato plant. The sweetpotato leaves could be serrated, toothed, entire, or lobed. The leaf outline might be round, reniform(kidney-shaped), cordate (heart-shaped), triangular, hastate, lobed and almost divided. The Lobe number of sweetpotato leaves varies from 3 to 7. Maquia et al. (2013) observed that petiole length varied widely with genotype and may range from approximately 10 cm to 40 cm.

2.5 Sweetpotato production in Southern Africa

Sweetpotato is a very important root crop for Southern Africa including Zimbabwe. Zawedde et al. (2015) reported 3 million hectares are under sweetpotato production with an estimated annual production of ca. 13 million tonnes worldwide. In a separate study, (Kays, 2005) reported sweetpotato production of 131 million tonnes per year on approximately 9 million hectares with a

mean yield of 13.7 tonnes per hectare. In addition, Saranraj et al. (2019) also reported sweetpotato as the most widely grown root crop, resulting in 9.9 million tonnes of storage roots produced on an estimated 2.1 million hectares in Sub-Saharan Africa (SSA). In Zimbabwe, sweetpotato is mainly grown under low input dryland farming. Motsa et al. (2015) reported that sweetpotato is an attractive crop partly because of its low input requirements and tolerance to harsh conditions. Bashaashaetal.(1995) cited that sweetpotato was widely adapted to the tropics, subtropical, and warm temperate originswhere it is grown by smallholder farmers on marginal land with minimal inputs. In Zimbabwe, sweetpotato is a food nutrition security crop. Bashaasha et al. (1995) and Mukhopadhyay et al. (2011) raised the point that sweetpotato is regarded as a food security crop, mainly because of its reliable yields; its ease of propagation and low requirements for production inputs. Mukhopadhyay et al. (2011) indicated that among the major starchy staple crops such as maize, bananas, potatoes, cassava, sweetpotato has one of the highest rates of dry matter production per unit area and unit time, thus making it attractive to farmers who have small land areas. Low (2017) pointed out that rural women grow sweetpotato near their homes to feed their families and as a source of income if they produce more than the family needs. Truong et al. (2018) indicated that these attributes render the crop appealing to low-income farmers, resulting in increasing importance of the crop over other crops in recent years in sub-Saharan Africa (SSA).

The government of Zimbabwe declared sweetpotato a staple crop and this resulted in the area under sweetpotato increasing. Ngailo et al. (2016) reported a sweetpotato yield potential of 20-50 tonnes per hectare of storage roots in the tropics. However, this yield potential is yet to be realized as farmers in SSA produce on average less than 10 t ha^{-1} of sweetpotato partly because of several socio-economic, biotic, and abiotic constraints. Chandrasekara and Josheph Kumar (2016) cited socio-economic constraints in the production of sweetpotato which include, poor post-harvest handling and storage facilities, lack of processing skills, lack of clean seed, and poor seed distribution system, and poor varieties. Laurie et al. (2005) implicated pests (sweetpotato weevil, weeds, and nematodes) and diseases (viruses, Alternaria, blight, and root rots among others) as the most common constraints limiting high productivity. Murugan et al. (2012) reported yield losses of 20- 78% due to viruses (and 45% due to sweetpotatoweevil (*Cylas formicarius*). A different study by Gurmu et al. (2014) pointed that SADC countries(South Africa, Namibia, Botswana, Zimbabwe, Swaziland, and Lesotho) realize low yields mainlybecause of planting old local landraces and virus infections due to recurrent use of material for years.

2.6 Nutritional contribution of sweetpotato

The nutritional benefits of sweetpotato have been mentioned by different investigators (Kivuva et al., 2014). Chandrasekara and Josheph Kumar (2016) in separate studies on sweetpotato storage root reported that sweetpotato is rich in macro-and micro-nutrients. He also indicated that sweetpotato had substantial amounts of vitamin C, vitamin B complex (Vitamin B1,B2, B5, and B6) and folic acid. In a related study, Kivuva et al. (2014) found that deep orange-fleshedsweetpotato roots were rich in Fe (50 ppm DM) and Zn (40 ppm DM). In separate studies, Ukpabi (2012) recommended the consumption of orange-fleshed sweetpotato varieties as rich sources of pro-vitamin A. Baba et al. (2017) found that dried sweetpotato vines were comparable to alfalfa as an animal feed. Ewell (2002) revealed that sweetpotato leaves were excellent sources of lutein, while Hochmuth et al. (2021), reported that sweetpotato leaf protein content was twice as much as that from storage roots.

2.7 Sweetpotato as a food security crop

A number of studies on the food security role of sweetpotato have been cited by several authors (Motsa et al., 2015b; Makini et al., 2018). According to Veasey et al. (2007), food security has three pillars which include food availability, food access, and food use (utilization andstability). In Zimbabwe, smallholder farming contributes immensely to food security. The government of Zimbabwe elevated sweetpotato to a strategic staple crop due to its contribution to food security which is anchored on its ability to survive under harsh conditions. Sweetpotato hasthe capacity to give a decent yield under a low input production system. Sweetpotato can survivewhere other crops such as maize fail. It contributes to food security by improving rural livelihoods Makini et al. (2018), especially those involved in small-scale agriculture. Mgcibelo,(2014) indicated that sweetpotato had higher energy than maize products. In addition, Chandrasekara and Josheph Kumar (2016) pointed that sweetpotato derives its food security status through its ability to grow and survive in different edaphic environments. Maquia et al. (2013) associated the food security ability of sweetpotato to its short growing period (3-5 months) which allows for multiple cropping. Namanda (2011) reported that sweetpotato is a food security crop because its precocity makes it possible for farmers to escape from hunger. Related to this assertion, Dellasala and Goldstein (2017) reported that sweetpotato derives its food security from its abilityto be propagated through vines.

Reduction (2019) indicated that when cassava was attacked and destroyed by an unknown virusin the 1990s, sweetpotato saved the Ugandan rural communities from devastating hunger. Thornton et al. (2011) reported that among the starchy crops such as bananas, maize, cassava, andIrish potatoes, sweetpotato produces the greatest dry matter per unit area. Finally, van Niekerk and Nemakonde (2017) reported that sweetpotato was a source of income whenever surplus was realized.

2.8 Genetic diversity studies of sweetpotato germplasm

The aim of plant characterization is to identify the individuality of each genotype in a collection (Nadeem et al., 2018). This reveals similarities within and among plant populations, and also show how the genotypes are structured and aid in their utilization (Govindaraj et al., 2015). Future crop improvements are dependent on the exploitation of the diversity within plant populations. The development of core collections of various crops was made possible by focusing on areas of greatest genetic diversity (Zawedde et al., 2015). Information on genetic diversity is central in the design of plant improvement programs (Ochieng, 2019).

2.8.1 Morphological characterization

The most common method for characterization is dependent on morphological attributes partly because it is easy and cheap to implement (Huaman, 1999). This method has standard descriptors developed for sweetpotato (Vigouroux et al., 2002; Placide et al., 2015). Takagi (1994) pointed that these standard descriptors create a common language internationally. Morphological characterization entails the evaluation of leaf, flower, and storage root characteristics (Laurie et al., 2013b). In sweetpotato, Morphological characterization has been widely used in sweetpotato and has given reliable results (Ochieng, 2019). Nearly 8000 accessions of sweetpotato have been collected and maintained at various genebanks worldwide (Khoury et al., 2015).

Morphological characterization is capable of isolating duplicates and defining the structure of sampled genotypes (Prasad et al., 2020). In Tanzania, morphological characterization was successfully used on sweetpotato (Maquia et al., 2013). Nadeem et al. (2018) pointed that morphologicalcharacterization is the first step in the evaluation of sweetpotato diversity. However, morphological attributes are subject to environmental factors such as soil fertility, light intensity, temperature, and available moisture and developmental stages (Prakash et al., 1996; Rossel et al., 1999b; Zhang et al., 2000; Motsa et al., 2015).

2.8.2 Molecular characterization

Molecular characterization offers a complementary tool to the morphological approach (Zawedde et al., 2015; Ochieng, 2018) . Molecular characterization offers more accurate informationthan morphological assessments and it is capable of establishing genetic distances in a case of significant interaction between genotype and environment (Mohammed et al., 2015; Ngailo et al., 2016).

Molecular markers are a result of changes in DNA sequences such as deletions, substitutions, or insertions, or abnormal replications (repeats) (Govindaraj et al., 2015). In addition, molecular markers are environmentally stable and are unlimited in their numbers (Nadeem et al., 2018). Microsatellites are highly polymorphic due to the presence of huge numbers of repeats (Nadeem et al., 2018). Polymorphism is shown by the banding pattern in the Polymerase chain reaction (Gonçalves-Vidigal and Rubiano, 2011; Kumar et al., 2016). Simple Sequence repeats markers are favourable to investigators due to high reproducibility and the fact that they are co-dominant and their abundance in the genomes (Sajid et al., 2019). The use of SSR markers in evaluating the diversity of sweetpotato genotypes started recently (Talseth-Palmer and Scott, 2011) and it has been successful in revealing sweetpotato genetic diversity (Vieira et al., 2016). The use of SSRs markers in evaluating the diversity of sweetpotato genotypes started recently (Talseth-Palmer and Scott, 2011). However, SSR markers have been successfully used to reveal sweetpotato genetic diversity (Nair et al., 2017).

Single Nucleotide Polymorphism markers, on the other hand, do not always demand the use of electrophoresis. According to Koopaee and Koshkoiyeh (2014), SNPs are the most abundant form of variation within Deoxyribonucleic acid. These are differences between genomes due to differences in a single nucleotide by individuals within a common species. For this technique to be effective there is a need for whole-genome data which serves as a reference for picking polymorphism among genotypes (Sajid et al., 2019). The reference data allows identification of any changes happening within the genome as a result of different factors (Scheben et al., 2017). According to Andrade et al. (2009)), SNPs are available within the entire genome. Single nucleotide polymorphisms are very important in revealing phenotypic variations within both plants and animals (Placide et al., 2015) and have not been fully utilized in sweetpotato in sub-Saharan Africa particularly Zimbabwe.

2.8.3 Diversity arrays technology (DArT) and SNP identification

A Diversity Arrays Technology marker is part of genomic DNA and occurs in a biallelic manner. The gene is either present or absent and functions as co-dominant (Fuentes-Pardo and Ruzzante, 2017. It is the most current method for analysing plant genetic diversity. Genotyping by sequencing (GBS) is one of the latest methods for detecting single-nucleotide polymorphisms. This technique is reliable, cheap with minimum chances of errors, and does not require high-quality DNA in order to identify SNPs (Jiang et al., 2016; Sajid et al., 2019). There isa need to verify SNPs for their functionality (Harvey et al., 2016). However, GBS is weak when important parts of the genome are not captured in genomic libraries and is also liable to errors during sequencing (Li et al., 2019).

Chromatin immunoprecipitation is another fifth-generation technique for identifying SNPs. Unlike the GBS, the CHIP technique does not require a reference genome to be able to identify SNP (Grüneberg et al., 2015). This technique calls for a P1 barcoded adapter to be attached to DNA strands which are products of DNA digestion by restriction enzymes. P2 adapter primers get attached to the Deoxyribonucleic acid in order to amplify the DNA segmentsso that sequencing libraries are created (Park, 2009). Andrew et al. (2010) reported that this method requires high-quality DNA and loss of restriction sites may occur due to sequence polymorphism. The Diversity Arrays Technology (DArT) is a powerful tool for marker identification and is worth trying in sweetpotato.

2.9 Genotype x environment interaction

The outward appearance of an organism is a product of genetic and environmental effects (Jung and Sang, 2007). Yan and Hunt (2001) defined the summation of the conditions which envelop an organism as the environment. These conditions can be humidity, temperature, soil fertility, light intensity, amount of rainfall, and other biotic factors such as pests and diseases around an organism (Yadav et al., 2018). Tadesse et al. (2010) indicated that the environment may vary within years, seasons, andsites. Tumwegamire et al. (2016) defined Genotype x Environment (G x E) as the way individualsrespond to genetic and environmental effects.

As reported by Singh et al. (1999). G x E interaction can be crossover or non- crossover. Of the

two types of interactions, the most important type is the crossover interaction since it results in changes in rank and size of the genotypes across test environments. Mohammed et al. (2015) defined G x E as a measurement of the relative responses of genotypes in terms of the expression of specific phenotypes in response to variable environmental influences. Gurmu et al. (2017) indicated that significant interaction compels investigators to interrogate agronomic stability of genotypes across test sites. Gurmu et al. (2014) also reported that G X E affects the entire decision-making process of plant breeding including identification of the most ideal testing sites and allocation of resources within a breeding program, and selection of genotypes and breeding strategies. In separate studies, (Zakir, 2011) pointed that Genotype-by-environment interaction analysis is key to selection and cultivar recommendation, and to identifying suitable production and test environments. In his studies on sweetpotato, Esuma et al. (2016) found that storage root yield and quality are affected by environmental changes- partly because of genotype-by-environment interaction. Yet, Kumar et al. (2016) revealed that G x E results in different responses by genotypes across test environments and couldconfound the selection process. Singh et al. (2020) concluded that G x E analysis is an essential component of varietal selection.

2.10 Statistical procedures to account for G x E

A number of scientists published ways of accounting GEI (Xavier et al., 2018). Malosetti et al. (2013) reported that Multi-Environmental Trials can also help in the identification of production environments that best suit certain genotypes. Yet, Sandhu et al. (2014) recommended breeding for specific adaptation, which entails selecting genotypes best adapted to specific environments in order to optimize productivity. Another way of dealing with GEI as reported by Ngailo et al. (2019) is to select homogenous subgroups of environments (that is, environments with similar soil types, temperature, rainfall, day lengths, biotic and abiotic stresses)and make recommendations for the different subgroups.

Balalić et al. (2011) reported non-parametric methods which measure stability. One of the methods for measuring interaction and main effects is the combined analysis of variance. Laurie et al. (2015) reported thatthe Linear Regression model was the commonly used method. Mohammed (2020) reported that most researchers are currently using additive main effects and multiplicative interaction (AMMI). The AMMI is mainly used in conjunction with genotype and genotype by environment (GGE) biplot analysis (Yan and Hunt, 2001; Yan et al., 2007). Zobel et al. (1988)

indicated that when using the AMMI model main effectsare treated as additive effects yet the GEI is treated as the multiplicative effect.

Hongyu et al. (2014) described the AMMI model as a composite model which combines the analysis of variance (ANOVA) as an additive part and the principal component analysis (PCA) as the multiplicative component and it is responsible for analysing the genotype x environment interaction. Sandhu et al. (2014) indicated that the AMMI is the best model for investigating G x E interaction for multi-locational trials since it does not just approximate the interaction but also reveal the contribution of the environment in the interaction. Sa'diyah and Hadi (2016) pointed that the objective of using AMMI analysis is to obtain an improved estimate of the performance of a genotype in a particular environment. Dyulgerova and Dyulgerov (2019) also indicated that biplots have been used with AMMI analysis for visually interpreting the performance of genotypes in different environments.

Yan and Hunt (2001) reported that the AMMI model was successfully used for GEI and stability analysis among sweetpotato clones across different environments in Turkey. In addition, Gedif and Yigzaw (2014) used GGE biplots and identified suitable sweetpotato genotypes and representative environments in South Africa.

Sharma et al. (2020) reported that GGE biplot analysis has the capacity to analyse within-environmentgenotype-by-environment data (GED). Kaguongo et al. 2008 and Tena et al. (2019) also indicated that the GGE model is used in breeding programs for site regression of genotype plus genotype x environment interaction. Wie et al. (2017) reported that the most recentmethod GGE bi-plot model provides researchers with the pictorial representations of the data by creating a bi-plot that simultaneously represents both mean performance and stability. Yan et al. (2007) pointed that this multiplicative model combines the two main effects, i.e., genotypes (G) plus the G x E interaction (GE). This model is capable of picking cultivars that managed to win atvarious trial sites and this is important in selecting high yielding, stable genotypes and discriminating and identifying representative test environments. Kennedy et al. (2004) claimed that nowadays, it is a common practice by sugarcane breeders to use GGEmodels in explaining G x E interaction and analysing the performance of genotypes and test environments. For this study, both AMMI and GGE biplots were used.

2.11 Value chain actors' perspectives on sweetpotato

A value chain can be viewed in the context of an agri-food system. Sugri et al. (2017) defined an agri-food system as a set of activities and relationships between value chain players. Ezin et al. (2018) applauded the perspective of a food system since allows traceability and understating how global forces are impacting world food systems. In Tanzania, Wie et al. (2017) identified farmers, brokers, transporters, wholesalers, vendors/ retailers, processors, and consumers as active participants in the sweetpotato value chain. However, Sugri et al. (2017 and Kolech et al. (2017) noted that neighbouring countries could have exporters as additionalactors within the value chain. There are many actors in the Zimbabwean sweetpotato value chain.

Low (2017) indicated that agro-input dealers play the role of availing inputsto producers of sweetpotato thus ensuring the smooth functioning of the value chain. Sugri et al. (2017) indicated that a value chain is either producer-driven or buyer-oriented in its mode of governance. Sugri et al. (2017) reported that activities within the value chain are interdependentand challenges within it affect all actors within the value chain. Sugri et al. (2017) acknowledgedthe poor coordination which is common in most sweetpotato value chains. Poor coordination makes farmers more vulnerable since farmers would be ignorant of market expectations and market forces at play.

Gichuru and Dijk (2015) pointed out that sweetpotato is a subsistent crop and it is internationally traded but in very small quantities. Hotel (2010) claimed that the main challenge faced by farmers was the shortage of quality planting material. This point was also raised by Hall and Nahdy (1999). Rees (2000) reported a shortage of improved planting materials while working on sweetpotatoin Ethiopia. In addition, Sugri et al. (2017) pointed that access to quality sweetpotato plantlets during the onset of planting was a key problem in Kenya.

Sweetpotato has a limited market mainly because it competes with well-established roots and tubers such as yam, Irish potato, and cassava that consumers have developed a better taste. Zhang et al. (2018) and Zhang et al. (2019) revealed that poor shelf life and absence of proper storage facilities are other challenges experienced by all value chain actors. However, Sugri et al. (2017) reported that traders in Uganda are able to sell the sweetpotatoes within 3-4 days before the onset of rot. Low (2017) reported that producers have resorted to piecemeal harvesting and storing roots underground in order to avoid loss of the produce.However, Singh et al. (2008) stated that variety improvement is the only lasting solution to prolonged shelf life. Poor shelf life creates

a time of gluts resulting in depressed prices and periods of scarcity when prices are very high. Thiele et al. (2009) reported that sweetpotato is less favouredby some consumers due to the presence of flatulence. However, Mukhopadhyay et al. (2011) indicated that there is a need to investigate how the degree of cooking influences the occurrence of flatulence.

In SSA, sweetpotato value chain players are motivated by profit. This in turn affects sweetpotato accession diversity as farmers only retain high yielding varieties. Aliguma et al. (2007) asserted that sweetpotato was only important in cities like Kampala in Uganda. Mussoline and Wilkie (2017) reported that theadoption of sweetpotato was partly influenced by the lower quality of its flour as compared to wheat flour and the need for washing and peeling. Markos (2016) discovered that chipping withwhite-fleshed sweetpotato was not a profitable venture. However, Sugri et al. (2017) from sweetpotato studies in Kenya found that sweetpotato products that appeal to consumers.

An efficient marketing system for agricultural produce is one of the top priority areas in most developing economies. Low (2017) reported that underlying causes of persistent poverty in developing countries stem from a lack of incentives for smallholder producersto invest in more efficient and organized markets. Sugri et al. (2017) implicated the absence of functional marketing systems and pro-farmer policies in Uganda to the uptake of technologies. Baafi et al. (2017) raised that due to the bulky nature of sweetpotato it is very expensive to transport it to distant markets. Farmers in remote areas usually sell their produce within their localities and they end up being price takers.

Adoption of different sweetpotato varieties of different maturity times can solve the challenge of gluts and make sweetpotato production more profitable. Hall and Nahdy (1999) reported that growing of diverse sweetpotato cultivars with different maturity times ensures the availability of sweetpotato throughout the season. On the other hand, when soilsare of poor drainage it is advisable to plant sweetpotato on ridges to facilitate good drainage. Pillay et al. (2018) cited the use of pre-rooting techniques as a way of removing the dead and minimize crop failure. Sugri et al. (2017) recommended intercropping sweetpotato and maize as a way ofdiscouraging leaf blight and rust in the maize crop.

Low adoption of technologies is caused by releasing what is not preferred by end users. We need to understand what end users want before formulating solutions. The inclusion of farmers in research work is key to the adoption of new technologies. Sibiya et al. (2013) raised the importance

of factoring in farmer preferences and perception of the characteristics of new technologies. (Sibiya et al. 2013) reported that younger farmers are more likely to adopt new varieties than older farmers. Mafouasson and Bassi (2015) reported that younger families with children are more permeable to new technologies than older people. Sabel and Toledano (2017) cited those previous studies that have shown the positive role of extension services for the adoption of new varieties.

Sugri et al. (2017) reported that farmers were a heterogeneous group as a result their preferences were bound to be different. Sugri et al. (2013) pointed that farmers' selection depends on the final product attributes, socioeconomic variables, opinions and attitudes, risk perception, the socio-cultural environment, and the amount of information they have access to. Accordingly, the best strategy to increase the improved seeds is to develop appropriate technologies that take into consideration the heterogeneity of farmers, their production constraints, and what really influences their final decisions in farming activities (Sugri et al., 2017).

Farmers also have different perspectives regarding important constraints to crop production. Most farmers do not consider leaf miner as a major pest in sweetpotato production. This is supported by Ochieng (2018) who reported that ninety-seven percent of farmers did not control insect pests mainly because they were not aware of any control measures. Grzywacz et al. (2014) attributed the failure to control insect pests to a lack of technical know-how. However, Sugri et al. (2017) learned that in Kenya 63.8% of the farmers saw *Cylas* species as the most aggressive pest followed by sweetpotato butterfly (27.6%), leaf miner (8.6%), and vine borers (8.6%).

In another study on sweetpotato, Kaguongo et al. (2008) and Garbero et al. (2018) cited several benefits of observing sweetpotato-based cropping systems such as; i) it is precocious ii) it can produce economic yields under harsh conditions, iii) it is a low input crop unlike other staple crops, iv) and it is a good substitute for expensive cereals and other vegetables and it is nutritious. Mwololo and Ajambo (2019) reported that even though sweetpotato has a yield potential of 50 -60 tonnesper hectare under Ethiopian conditions farmers are still realizing about 6 to 8 tonnes per hectare. Mwololo and Ajambo (2019) attributed the low yields to challenges in accessing improved vines, pests and diseases, and poor post-harvest treatment. Consequently, Mwololo and Ajambo (2019) recommended the application of fertilizers as a viable option for increasing sweetpotato productivity.

2.12 Conclusion

Literature review revealed that sweetpotato is a very strategic staple crop for rural and urban people of Zimbabwe. However, its production and productivity are limited mainly by lack of improved varieties. Sweetpotato breeding efforts in Zimbabwe are still in its formative stage to the extent that systematic collection, multiplication and conservation of sweetpotato genotypes have not yet been conducted. Morphological and molecular characterization of sweetpotato have been used to strengthen breeding initiatives in other countries with the exception of Zimbabwe.

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CHAPTER 3

IDENTIFICATION OF FARMERS' KEY SWEETPOTATO PRODUCTIONCONSTRAINTS AND TRAITS DESIRED IN SWEETPOTATOGENOTYPES

Abstract

In Zimbabwe, sweetpotato (*Ipomoea batatas* L.) production is hampered by numerous biotic, abiotic, economic, and social factors. A baseline survey was conducted in sweetpotato growing areas of Zimbabwe namely Manicaland, Mashonaland East, Mashonaland Central, and Masvingoduring the 2017-2018 season to collect sweetpotato germplasm from farmers; to determine farmers' selection criteria of sweetpotato varieties, production and marketing value chain constraints and farmers' coping strategies. A structured questionnaire was administered to 100 farmers,and 130 farms were visited in 15 collection expeditions, in addition to seven focus group discussions. One hundred (100) genotypes were collected. Results indicated that 64% of the farmers were women and the majority (42.6%) were between 30-40 years old. Twenty-two of the 30-40years old had completed secondary education, 6 females with primary level education and one male with tertiary education which can be an important entry point for participatory breeding efforts since they will be able to appreciate some of the concepts. About 91.5% of the respondentshad more than 3 years' experience in sweetpotato production. The sweetpotato yield ranged from3.5-8 t ha^{-1}. The preferred sweetpotato varieties were Chibhahlengwe, Tiribhari, Boarding, Kori, Fost, Mozambique White, Germany 2, Chingova, Beauregard, Mafuta, Chizai, Chibikiravaenzi, Mukambachaza, Brondal, and Pamhai. Farmers' selection criteria were high yielding capacity (22.58%), taste (16.49%), early maturity (15.77%), resistance to disease and insect pests (15.05%),market demand (11.47%), long shelf life (11.11%), cookability (7.53%) and high dry matter. The important constraints were low prices (31.55%), insect pests (25%), diseases (20.83%), shortage of clean planting materials (14.29%), and heat anddrought (7.14%). Major pests and diseases were weevils, moles and sweetpotato virus disease (SPVD) as indicated by 90% of the farmers. Farmers use adaptable, high-yielding varieties, manure and irrigation application, piecemeal harvesting, and establishing their own nurseries as some coping strategies for production constraints. The results of this study can serve as a baseline reference for strategic breeding and other interventions to develop sweetpotato varieties according to the needs of the farmers of Zimbabwe.

Keywords: *Ipomoea batatas* L., farmers' preferences, sweetpotato selection criteria, sweetpotato production constraints, sweetpotato germplasm.

3.1 Introduction

Sweetpotato is an important crop for developing countries including those in Sub-Saharan Africa (SSA). The majority of smallholder farmers grow landraces and white-fleshed sweetpotato genotypes are more dominant than other colours. East Africa is rich in different sweetpotato genotypes and is believed to be a secondary centre of diversity (Ngailo et al., 2013; Rodriguez-Bonilla et al., 2014). Osiru et al. (2009) reported that sweetpotato was adapted to warm cold-free regions where it is mainly grown by resource-poor smallholder farmers. Andrade et al. (2009) and Ngailo et al. (2013) pointed that unimproved sweetpotato cultivars were beneficial because they are adapted to local conditions and have developed resistance towards pests and diseases found within their areas of adaptation. Sweetpotato was considered to be a food security crop partly because of its reliable yields, ease of propagation and low input requirements. Andrade et al. (2009) indicated that most rural farmers grow sweetpotato near their homes for security and ease of watering. Sweetpotatohas a short maturity time which allows it to fit in numerous cropping systems. Chipungu et al. (2017) reported that these attributes of sweetpotato make the crop favourable to resource-poor farmers hence increasing its importance over other staple crops in SSA (McEwan et al., 2015).

Mutandwa (2008) reported that sweetpotato has gained prominence in Zimbabwe partly because of the ever-increasing prices of other staples such as maize and Irish potato. In addition, Mutandwa (2008) estimated that between 1-7 kg of sweetpotato are consumed in towns whilst rural households consume between 3-5 kg of sweetpotato per capita. In Zimbabwe, sweetpotatois grown in all provinces. However, the main producing provinces are Manicaland, MashonalandCentral, Masvingo, Midlands and Matabeleland North.

The average sweetpotato yield in Zimbabwe is 3.5 to 8 tonnes per hectare. According to Mutandwa (2008) the depressed yields are a result of failure to practice crop rotation, poor qualityplanting material coupled with increased pests and diseases. However, Mutandwa (2008) indicated that these yields are comparable with Africa's average of 6 tonnes per hectare but is farbelow the world average yield of 14 tonnes per hectare. Low et al. (2020) quoted an average crop yield of 6 tonnes per hectare in rainfed management, while irrigated sweetpotato registered 25 tonnes per hectare.

In addition, however, plant breeders have focused more on raising yields of different crops under optimal agronomically well-managed conditions and farmers either perceive little advantage in

growing them because they are not designed for their needs (Sibiya et al., 2013). Sibiya et al. (2013) reported that most of the time breeders fail to factor in the aspirations of end-users of technologies by not recognizing their importance. Therefore, in order to enhance the adoption and relevance of technologies, farmers' perceived constraints and their preferences have to be thoroughly interrogated Hall and Nahdy (1999) defined participatory research as a collaboration of farmers and scientists in agricultural research and development. Kolech et al. (2017) advocated for participatory methods as they recognize the valuable input of all key stakeholders.

Weltzien et al. (2000) reported that farmers are a reliable source of useful crop ideotypes based on preferable characteristics favoured by farmers. For example, in SouthernAfrica, Worku (2010) and Strobl et al. (2020) reported that apart from yield-related traits, farmers frequently mentionearly maturing varieties, hard endosperm (flint) types, and good husk cover for the maize varietiesthey would prefer. An example was drawn by (Abebe, 2005) working on maize in South Africa, where farmers also revealed that generally, they have their own way of selecting cultivars for their localities. However, in some instances, farmers' preferences coincide with breeders' selections. Including farmers in evaluations of cultivars increases adoption rates of the varieties in the target communities. The aims of the study were focused on: i) establishing the preferred sweetpotato characteristics by smallholder farmers from sweetpotato main growing areas of Zimbabwe that can be used for selection in breeding programs, and ii) identifying and analysing the constraints andcoping strategies to sweetpotato production and marketing from sweetpotato main growing areasof Zimbabwe.

3.2 Research Methods

3.2.1 Study sites

This study was conducted in seven districts during the 2017-2018 growing season. The areas chosen are all rural and without all-season roads. However, they are all accessible through dusty roads. Choice of study areas was prompted by being the main sweetpotato producing areas and expect the greatest sweetpotato diversity from them. Areas covered included Chinyaduma (Chipinge district), Tamandai (Chipinge district), Ngaoni (Chimanimani district), Kopa (Chimanimani district), Murewa (Murewa district), Chigondo (Hwedza district), Domboshawa (Goromonzidistrict), Africa University (Mutare district), and Chiredzi Research Institute (Chiredzi

district). The season starts from mid-October and ends in late March. The main limiting factors are mid- season droughts, cold winters, and acidic soils which threaten sweetpotato vine survival.

3.2.2 Ethical considerations

The principal researcher obtained informed consent from sweetpotato farmers and there was an agreement in maintenance of confidentiality and privacy of participants.

3.2.3 Data collection

One hundred sweetpotato genotypes were collected from main growing areas of Zimbabwe and the collections are presented in Appendix 1.

3.2.4 Structured survey

A participatory approach was used in this study. The information was obtained through the use of questionnaires to the sweetpotato farmers. The questionnaire was initially tested on five extensionstaff and 10 farmers from the Marondera district and amendments were made accordingly. Information on age and gender of respondents, education levels, experience in sweetpotato production, cropping systems used, sources of planting material, sweetpotato cultivars grown, genotypes that have disappeared, and reasons for disappearance, characteristics preferred by farmers, and production constraints faced by the farmers was gathered (Appendix 2).

3.2.5 Focus group discussions

The approach used included focus group discussions with 125 sweetpotato farmers. The surveyed areas were Hwedza, Marondera, Chipinge, Chimanimani, Mutare, Domboshawa and Murewa. The proportion of farmers who participated in focused group discussions in the seven selected districts are indicated in Figure 3.1. The research team was made up of the agronomist, a biometrician, and a facilitator who happened to be the local extension staff. The extension staff of the respective areas with the help of a biometrician facilitated the discussions. Each group consisted of an average of 20 farmers mostly with a ratio of female to male of 2: 1. The local extension staff informed the selection of the members within a group. One hundred and thirty farmers' fields were visited during the sweetpotato germplasm collection.

During collection expedition, the principal investigator encouraged discussions on how the farmers utilize thesweetpotato and challenges they face in sweetpotato production, the cropping

systems, the state of roads, water sources, and the condition of fields. The genotypes were collected during field visits after asking for permission from the farmers. In some cases, the extension staff informed the sweetpotato farmers to bring samples of different sweetpotato vines from their fields or gardens. The farmers involved in these surveys were a mixed group of males and females of all ages who grow a diversity of crop varieties.

The first goal of the focus group discussions was to identify sweetpotato genotypes and traits that were considered by the farmers as important for each type. The farmers brought samples of the sweetpotato germplasm they grow in their farm holdings. Then the farmers were requested to name the sweetpotato genotypes where possible, and indicate why they preferred those genotypesto others. The second goal was to identify the main problems or constraints to sweetpotato growing. The third objective of this chapter was to investigate sweetpotato diversity from the Zimbabwean collection.

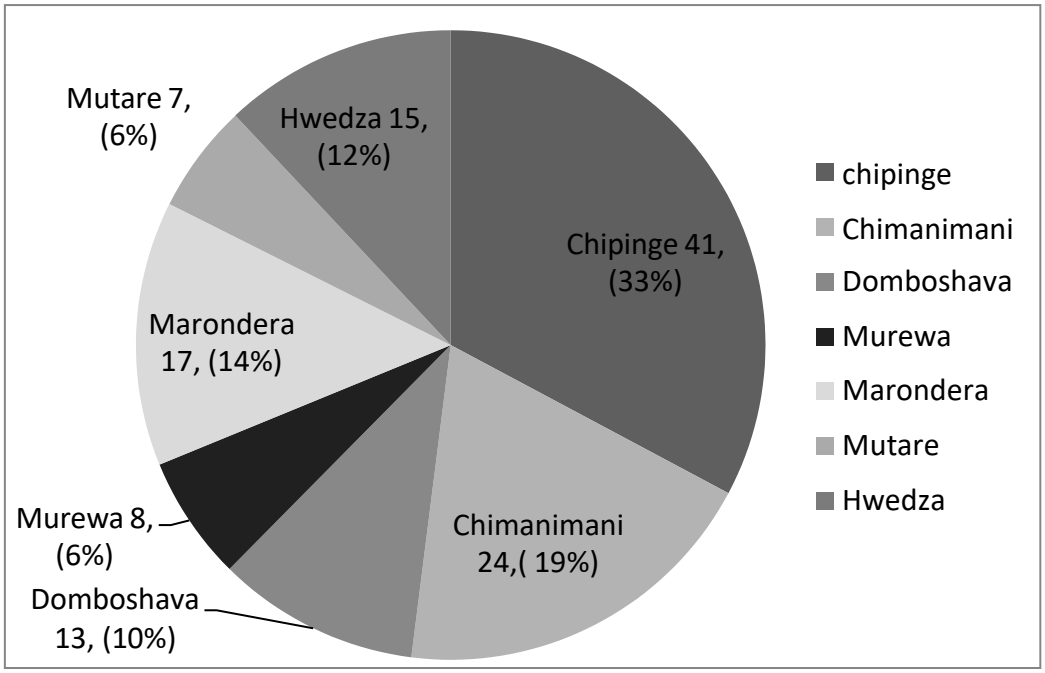


Figure 3.1 Proportion of farmers who participated in focused group discussions in seven selected districts

3.2.6 Data Analysis

The collected data were checked for outliers, verified then analysed using Statistical Package for Social Scientists (SPSS version.20). Frequency graphs mean, and percentages of the identified variables were generated.

3.3 Results

This study investigated sweetpotato diversity, farmers' selection criteria, farmer's preferred sweetpotato attributes, and production constraints. In total 225 farmers participated in the study as indicated in Table 3.1. Sixty-three percent of the respondents who participated in the structured survey were females and 37% males from all districts/ villages. Overall, 64% of the respondents in the focus group plus questionnaires, were females, and 36% were males. The motivation for growing sweetpotato was to get food during lean periods and also secure some income whenever there is a surplus.

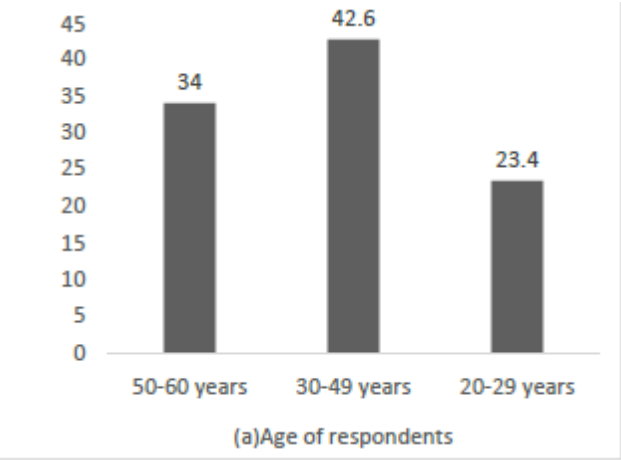
Table 3.1. Disaggregated data of farmers interviewed during the structured survey and thosewho participated in focus group discussions

Gender	Focus Group Discussion	Respondents for Questionnaires	Total
Females	81 (64.8%)	63 (63 %)	144 (64%)
Males	44 (35.2%)	37 (37 %)	81 (36%)
Total	125	100	225

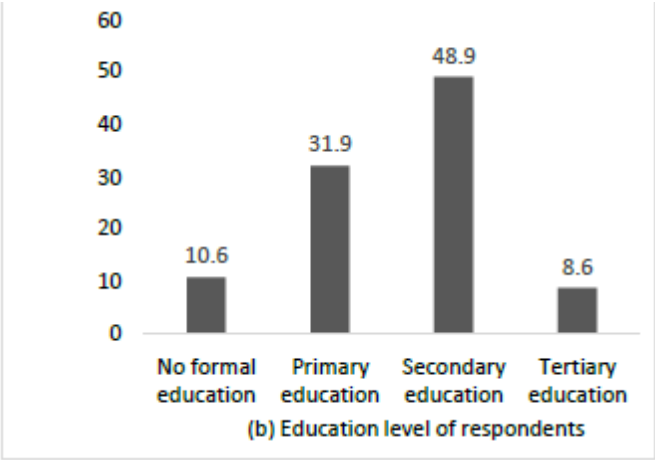
3.3.1 Demographic information

Most of the farmers (42.6%) were between 30-40 years old, seconded by a 50-60-year age-group (34%) and lastly, 23.4% consisting of respondents in the 20-29 years age group (Figure 3.2a). Twenty-two of the 30-40 years old had secondary school education, six, all females had primary school education and one male had tertiary education. Forty-eight percent of the respondents had secondary school education, 31.9% ended at primary school level, 8.6% with tertiary education, and 10.6% had no formal education (Figure 3.2b). However, 63% ofthe house heads were males and 37% were female-headed (Figure 3.2c). The majority (70.2%) had formal training in sweetpotato production with 29.8% without formal training in sweet production(Figure 3.2d).

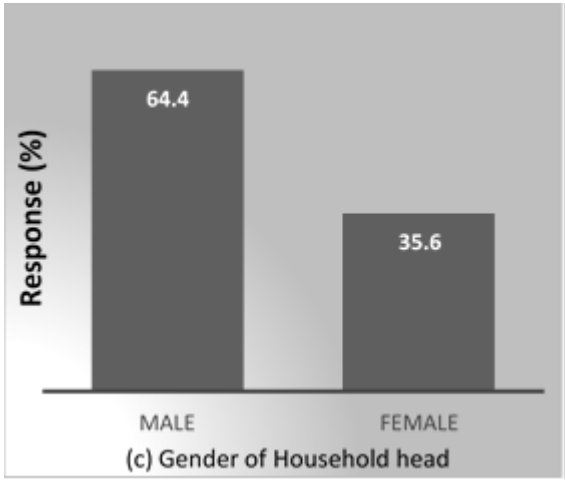
However, 91.5% of the interviewees had grown sweetpotato for a time exceeding 3 years, seconded by 4.3% who had 3 years of experience and 2.1% had 1 year and 2 years of experience each (Figure 3.2e). Extension workers were the main source of sweetpotato productioninformation and training (56.10%), seconded by research (29.3%) and the donor community camethird with 14.60% (Figure 3.2f). The majority of farmers (51.1%) had no formal training in rapid multiplication of sweetpotato against 48.9% who had formal training in sweetpotato vine multiplication (Figure 3.2g).



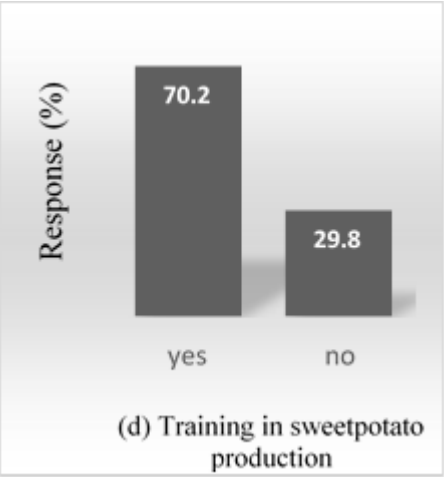
(a)Age of respondents



(b) Education level of respondents



(c) Gender of Household head



(d) Training in sweetpotato production

(e) Experience in sweetpotato production

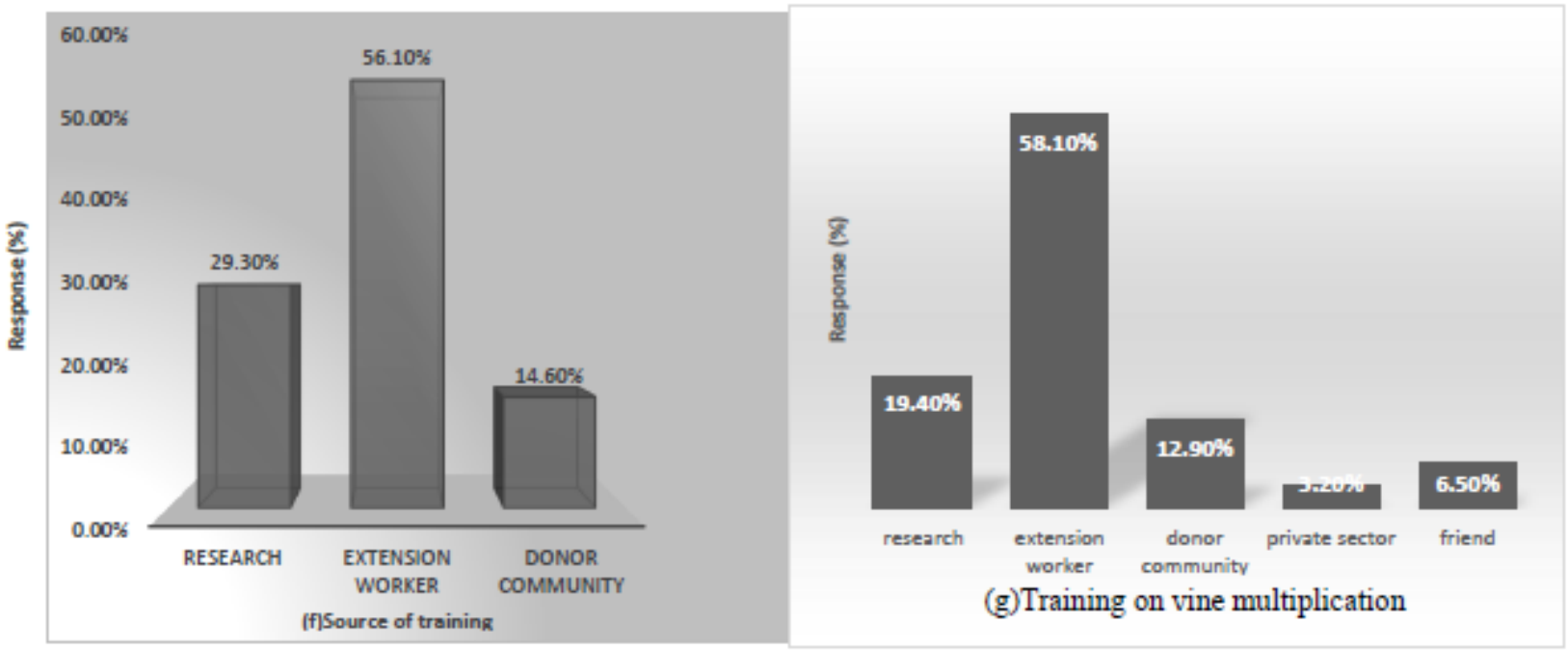


Figure 3.2. (a) age of respondent, (b) education of house hold head, (c) gender of house hold head, (d) training in production, (e) experience in sweetpotato production, (f) source of sweetpotato production training, (g)Training in vine production

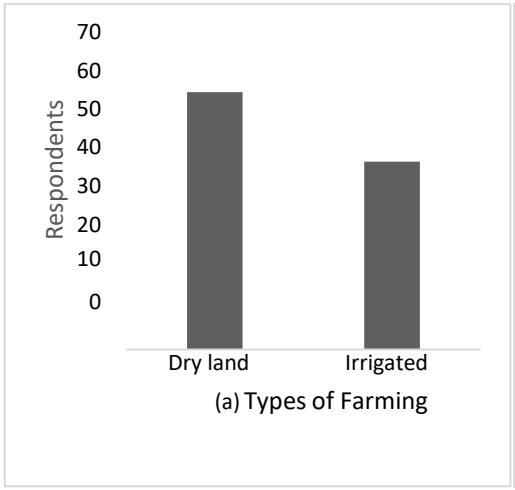
3.3.2 Cultural practices

Most farmers bury sweetpotato stems during harvesting as a way of preserving plantlets for the oncoming year (Figure 3.3). The majority of farmers in the Chipinge district planted sweetpotato vines in such away that the crop receives maximum exposure to the sun (Figure 3.4). Farmers used a piece-meal harvesting method.

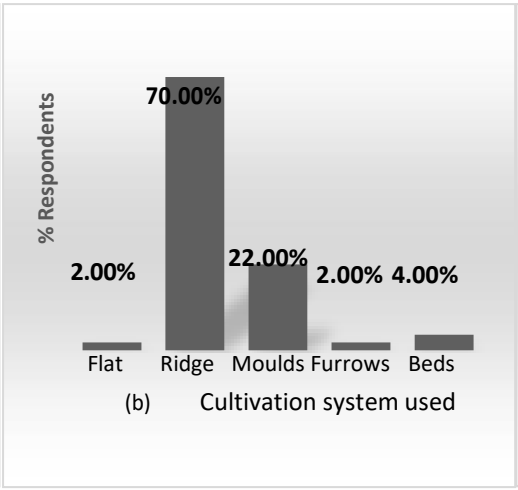
Most farmers (57.8%) practiced dryland farming while 42.2% produced sweetpotato under irrigation (Figure 3.5a). Most respondents (70%) plant sweetpotato on ridges, while 22% plant on mounds (stools) and only 4% of respondents plant sweetpotato on beds, and those who plant on flat and furrows constituted 2% each (Figure 3. 5b). Seventy- six percent of respondents used their own planting material, 2% of respondents got planting material from relatives, 17% from neighbours and only 5.7% of respondents got planting material from registered nurseries (Figure3.5c). The majority of respondents (50.9%) used hand hoes, 43.6% used ox-drawn ploughs, and only 5.5% used tractor-drawn implements for land preparation (Figure 3.5d). The majority of respondents (72.2%) cited that access to planting material was not an issue yet 27.8% had difficulties in accessing planting material (Figure 3. 5e). The bulk of the respondents (46%) used inorganic fertilizer in the form of Compound S (7:21: 7) and Ammonium nitrate (34.5% N) while 37% of the respondents use both inorganic and organic fertilizers and 17% using organic fertilizers mainly manure and grass mulch (Figure 3.5f). The dominant weed control method was hand hoeing practiced by 52.9% of the respondents seconded by hand pulling cited by 43.2% of the respondents and only 3.9% of the respondents indicated that they use herbicides (Figure 3.5g). Fifty-three percent (53%) of respondents rotated sweetpotato with maize, 36.4% with ground nuts,and finger millet and sorghum constituting 7.6% and 3%, respectively (Figure 3.5h). Most farmers(56%) preserved their sweetpotato planting material through mulching with grass and 46% of thefarmers leave their nurseries unearthed (overwintering) (Figure 3.5i). About 35.7% of the famers intercropped sweetpotato with maize, 21.4% with finger millet, 28.6 with ground nuts and 14.3% with sorghum (3.5j). About, 89.1% of the respondents did not intercrop, unlike 10.9% who indicated that they intercropped with crops such as leafy vegetables and maize (Figure 3.5k).

Figure 3.3. Replanting at harvesting to ensure availability of planting material for the following season.

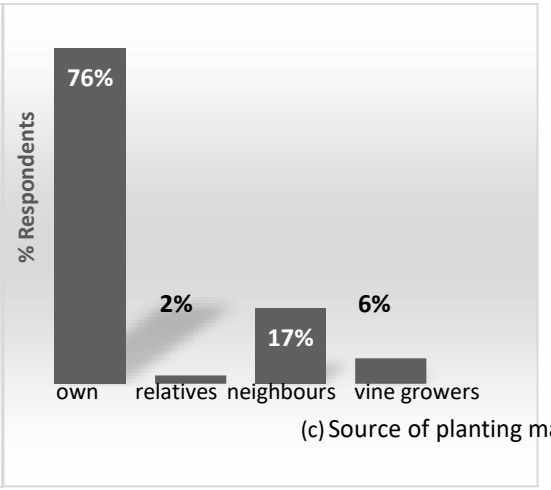
Figure 3. 4. Sweetpotato on ridges at Merino-Chipinge planted facing east.



(a) Types of Farming

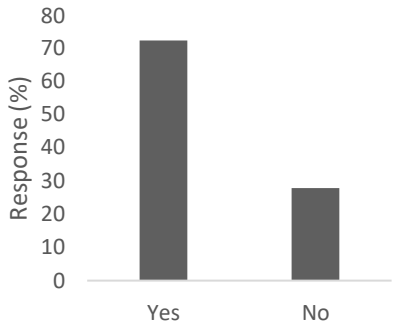


(b) Cultivation system used

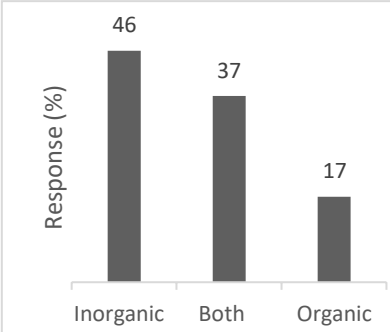


(c) Source of planting materials

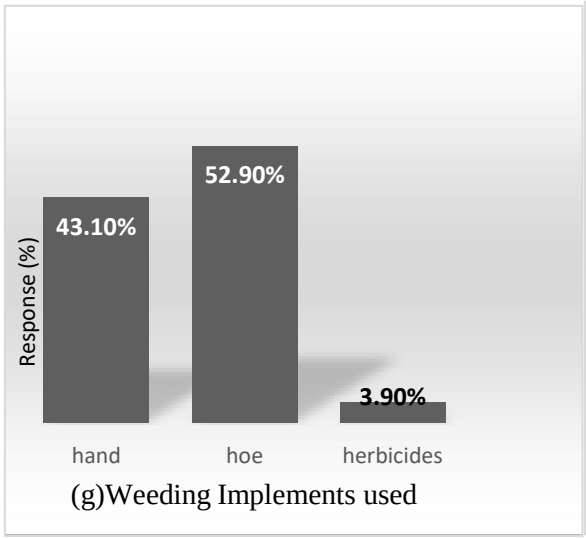
(d)Type of farm implements used for land preparation



(e) Ease of Access to Planting

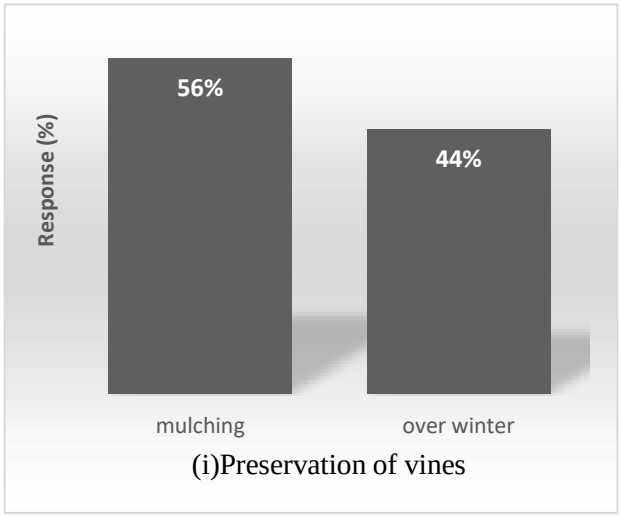


(f)Type of fertiliser used

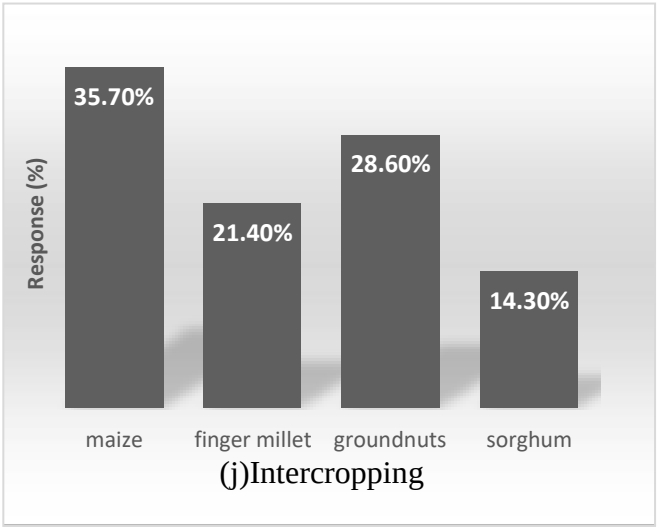


(g)Weeding Implements used

(h)Rotation



(i)Preservation of vines



(j)Intercropping

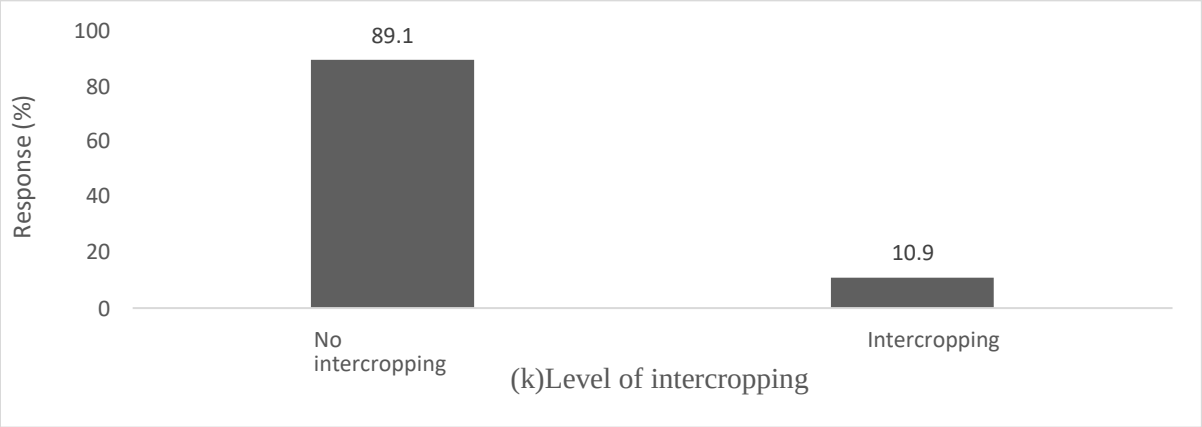
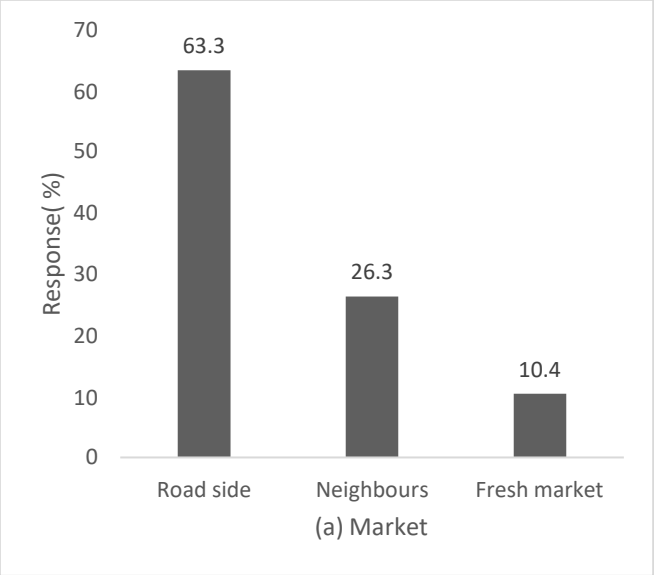


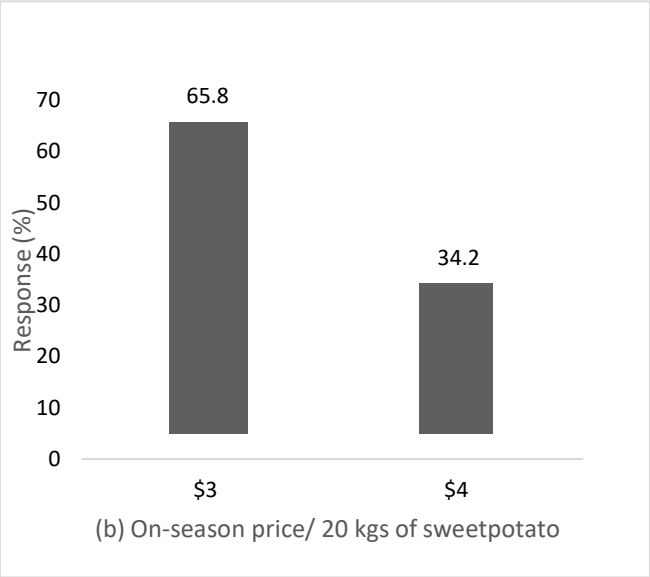
Figure 3. 5. (a) Type of farming, (b) Cultivation system used (c) Source of planting material, (d) Types of farm implements (e) Ease of access of planting materials (f) Type of fertilizers used (g) Weeding implements used (h) Rotation (i) Preservation of planting materials (j) intercropping, (k) Level of intercropping

3.2.2 Sweetpotato marketing

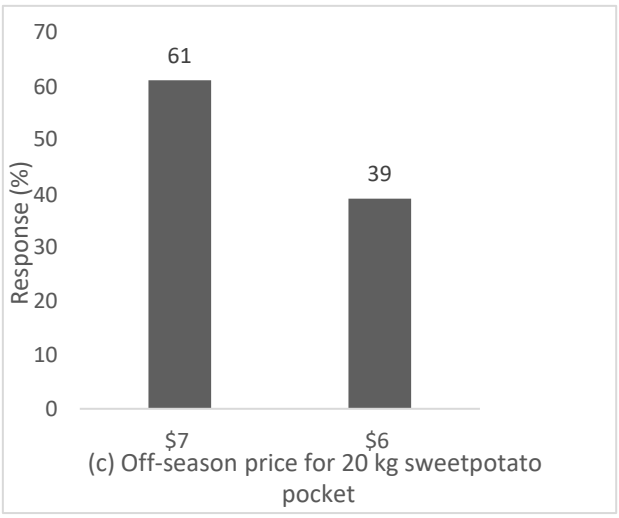
The majority of respondents (63.3%) indicated that they sell their produce by the roadside, 26.3% sell to their neighbours and 10.4% sell their sweetpotato to fresh markets (Figure 3.6a). Most sweetpotato growers in surveyed areas (65.8%) cited $3-00 per 20 kg of sweetpotatoes during the on-season period while 34.2% cited $ 4-00 per 20 kg for the same period (Figure 3.6b). However, 61% pegged the 20 kg of sweetpotato at $7-00 and 39% put it at $6-00 during the off-season period (Figure 3.6c). The majority (79.6%) indicated that they boiled and consumed sweetpotato with tea, yet 5.6% used it as a side dish and 14.8% consumed it in the form of chips (Figure 3.6d). Most respondents (52.2%) indicated that they ate sweetpotato about 3 to 5 days a week when they are in season yet (47.8%) stated that they consumed sweetpotato twice per week for the same period (Figure 3.6e).

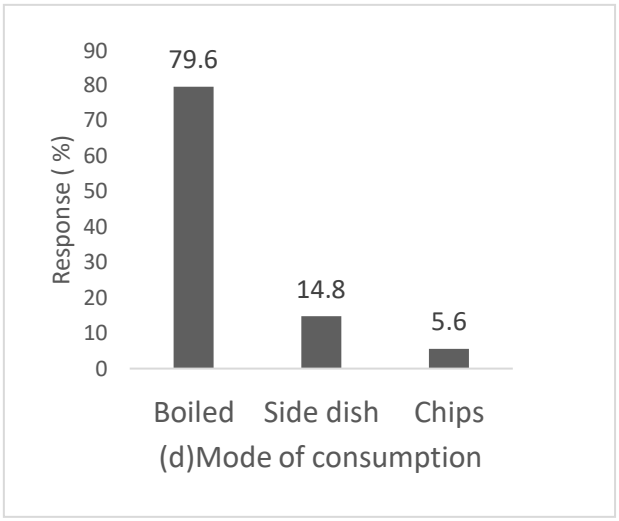


(a) Market



(b) On-season price/ 20 kgs of sweetpotato





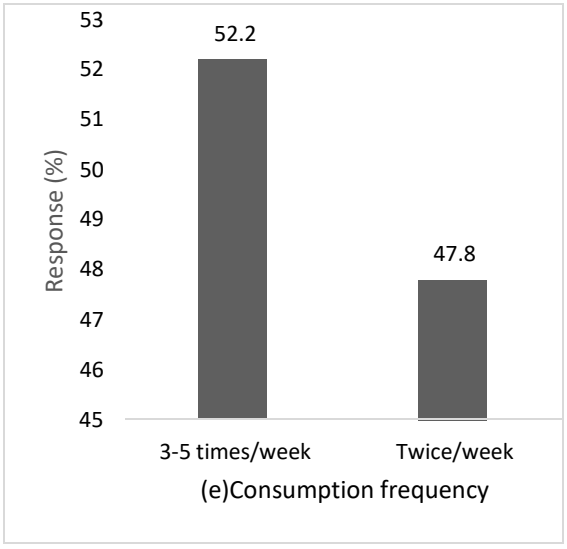


Figure 3. 6.(a) Type of market, (b) on-season price, (c) off-season price, (d) mode of consumption, (e) consumption frequency

3.2.3 Sweetpotato production constraints from respondents

Major constraints identified during focus group discussions are drought which hardened the soil rendering land preparation and harvesting difficult, shortage of clean planting material and higher yielding varieties resulting in poor yields, high input costs compounded by lack of funds, lack of machinery to reduce drudgery, weed pressure and high labour costs rendering sweetpotato production unviable and deep-rooted varieties which make harvesting difficult. The main pests

farmers complained about were sweetpotato weevil, moles, ants, whiteflies, aphids and red spider mites, while the major diseases identified were Alternaria blight and fungal black rot (Table 3.2).

Table 3. 2. A list of sweetpotato production constraints derived from focus group discussions

Land Preparation	**Harvesting**	**Pests**	**Diseases**
Drought resulting in hard soil	Drought causing hard pan	Sweetpotato weevil	Alternaria blight (*A.bataticola*)
Lack of high yielding varieties	shortage of clean planting material	Moles	Fungal Black Rot (*C. fibriata*)
High input costs	Lack of funds	Ants	Sweetpotato virus disease (SPVD)
Lack of machinery	Weevil infestation	Whitefly (*Bemisaia tabaci*)	
Weed pressure	Ants	Aphids (*Aphis gossypii*)	
High labour costs	Damaged roots at harvesting	Red spider mite	
	Mole attack		
	High labour cost		
	Lack of funds		
	Low root yields		
	Deep rooted varieties		

The majority of respondents (31.55%) in the structured survey identified low prices as a major constraint, as well as insect pests (25%), diseases (20.83%), and shortage of clean planting material (14.29%) came fourth, with heat and drought viewed by 7.14% of the respondents as a limitation to increased productivity. Very few respondents (0.6%) regarded shortage of labour and frost constraints in sweetpotato production in surveyed areas (Table 3.3).

Table 3.3. Different Production constraints identified by respondents in structured survey

Production Constraints	**Number of Farmers**	**Rank**	**Percentage of Farmers (%)**
Low prices	53	1	31.55
Insect-pests	42	2	25.0
Diseases	35	3	20.83
Shortage of clean planting material	24	4	14.29
Heat and drought	12	5	7.14
Shortage of labour	1	6	0.6
Frost	1	6	0.6
Total	168		100

The evaluated farmers indicated that their sweetpotato varietal selection criteria are based on: root yield (22.58%), taste (16.49%), time to maturity (early maturity 15.77%), resistance to diseases and insects (15.05%), market demand (11.47%), storage quality (11.11%) and cookability (7.53%) (Figure 3.7).

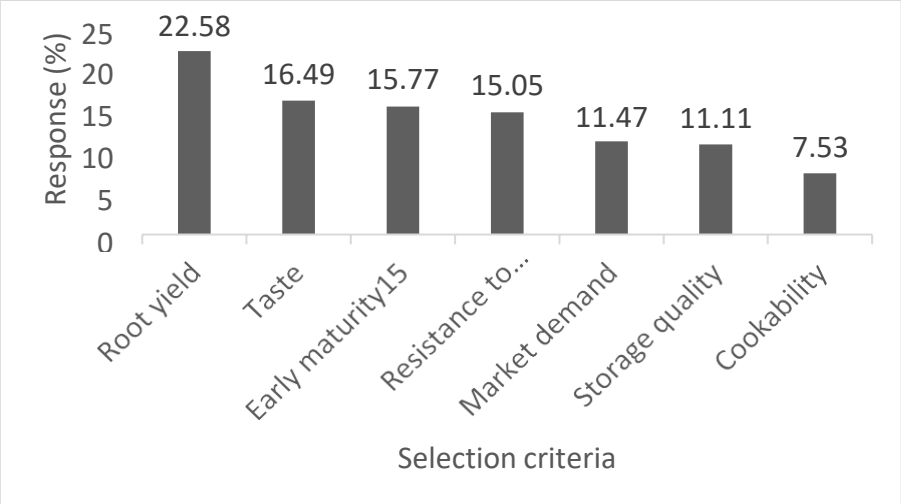


Figure 3.7. Farmers' sweetpotato selection criteria

3.2.4 Preferred sweetpotato varietal attributes

Farmers grew different sweetpotato varieties in each district with some similarities between Chipinge and Chimanimani districts. The agronomic attributes, earliness, high production/ productivity, good taste, cooking quality, pest and diseases resistance and storage quality featuredin all surveyed areas (Table 3.4).

Table 3.4. Farmers' preferred varieties according to districts and provinces

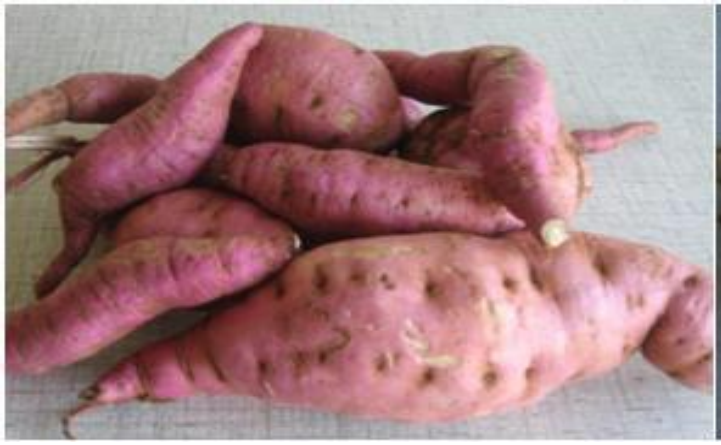
Cultivar	Chipinge	Chimanimani	Goromonzi	Wedza	Total percentage	Why preferred
Chibhahlengwe	8	3	1	0	12	EM, HY, PR, CD, CQ, SQ, GT, NO
Kori	10	2	1	0	13	EM, HY, CD, CQ, SQ, GT
Tiribhari	3	1	4	0	8	HY, CD, CQ, SQ
Chizai	2	0	2	4	8	EM, PR, CD, SQ, GT
Chidhumbedhumbe	2	1	0	0	3	EM, HY, CD, SQ, GT, NO
Chibikira vaeni	1	0	0	0	1	EM, NO
Chimarata	3	2	1	0	6	EM, DR, CQ, SQ, GT, NO
Mutengangehuku	1	0	0	0	1	SQ, GT
Gwasharandima	1	2	0	0	3	EM, CD, SQ, GT
Zadzangoro	0	0	2	0	2	EM, DR, HY, GT
Mutari	3	2	0	0	5	HY,GT
Brondal	1	0	0	0	1	CQ
Muzvareshonga	0	0	0	10	10	EM, HY, CD, SQ, GT, NO
Chingova	0	0	0	7	7	EM, HY, CQ, GT, NO
Chigogo	0	0	0	7	7	HY, PR, SQ, GT
Germany 2	0	0	1	0	1	SQ, HY, NO
Kwasa kwasa	0	0	0	4	4	HY, CD, GT
Makope	0	0	1	0	1	CD, GT
Shirikadzi	0	0	0	1	1	EM, HY
Jubheki	0	0	0	1	1	EM, HY
Dambaradzi	0	0	1	2	3	HY, PR, GT
Germany 1	0	0	1	1	2	HY,PR,GT,NO
Total (%)	35	13	15	37	100	

NO= do not overcook, EM= Early maturity, GT= Good taste, CQ= Good cooking quality, PR= Pest resistant, DR= Disease **resistant**, SQ= Storage quality, HY= Highyielding

Roadside marketing has gained currency especially in Chipinge and Chimanimani (Figure 3.8).

Boarding (White)

Chibhahlengwe



Germany II

Chingova

Figure 3.8. A sample of sweetpotato accessions

3.3 Discussion

3.3.1 Demographic information

Most farmers who participated in the study went through schooling. Ninety-eight percent of farmers had at least primary education. Educated farmers may be more innovative and can easily adopt new farming practices. About forty-three percent of farmers were of the 30-40 years age group and 34% were within the 50-60 years of age group. Twenty-two of the 30-40 years old had completed secondary school education, six females had primary school level education and one male had tertiary education which can be an important entry point for participatory breeding efforts since they will be able to appreciate some of the concepts. The adoption of new farming methods also varies with age of the person and level of education. The study revealed that the majority of sweetpotato farmers are women which supports the fact that sweetpotato is dominated by females. This can help in sustainable conservation of different sweetpotato genotypes since women are good at tendering delicate but precious things. However, most household heads were men. Kosmowski et al. (2016) reported that sweetpotato production is mostly women-dominated. Unlike in other farming activities, the youths had a taste for growing sweetpotato which might guarantee sustainable production of this crop. The participation by youths in sweetpotato production might be due to the absence of other jobs. The area dedicated to sweetpotato was smaller than that of other staple crops such as maize and this could be due to their different contribution to food security. Mmasa et al. (2012) recommended more land for sweetpotato in an attempt to increase production and productivity. In Chimanimani, much land was under cereal and fruit crops partly because fruit trees bring more household income. However, the removal of marketing hurdles might be the solution to an increased area under sweetpotato since most farmers are discouraged by low selling prices offered by the market.

3.3.2 Cultural practices

Sweetpotato varieties grown by farmers differed from region to region. Chipinge and Chimanimani districts showed some similarities in conserved sweetpotato accessions (Table3.4). Chibhahlengwe, Kori, Tiriburi, Chimarata were mainly grown in Chipinge and Chimanimani districts. The selection criteria of sweetpotato varieties were similar to considerations for preferred attributes which a variety should possess. The largest number of respondents considered high yield/ yield stability (22.58%), taste (16.49%), earliness (15.77%), insect and disease resistance

(15.05%), market demand/ preference(11.47%), storage quality (11.11%) and cookability (prefer varieties with high dry matter) (7.53%)as the most important selection criteria in the surveyed districts. Additional consideration identified during focus group discussions is the ability of a variety to produce profuse vines which guarantees the availability of planting material at the onset of the season. Taste and earliness are very important considerations for trade and subsistence purposes in Zimbabwe. About 16 percent of respondents preferred early maturing varieties which might be a good attribute to escape hunger. Donatelli et al. (2017) reported that earliness serves several purposes, including allowing for an increase in cropping intensity as well as reducing the crop's exposure to pests and diseases. The common weed control method was the hand hoe practiced by 52.9 % of the respondents seconded by hand weeding cited by 43.2 % of the respondents and only 3.9 % of the respondents indicated that theyuse herbicides. This could be due to limited disposable income to buy herbicides. Mukhopadhyay et al. (2011) reported that weeding was beneficial during early growth stages.

Most farmers in Zimbabwe grow sweetpotato accessions that are preferred by the market. This market consideration is good for the farmers who are motivated by more income but it results in the neglect of less productive sweetpotato accessions that might be good for future breeding efforts. Consumer preference of sweetpotato is determined by texture when cooked, cooking time, sweetness, and skin and flesh colour. In Zimbabwe, Chibhahlengwe,a cultivar from Mozambique is the most preferred cultivar by both farmers and buyers mainly because of its; early maturity, medium-sized roots, disease, pest and drought tolerance, high dry matter, and long shelf life. Talsma et al. (2017) reported that consumers determine the adoption and acceptance of sweetpotato which is the same in Zimbabwe. Gurmu et al. (2014) and Neela and Fanta (2019) reported that consumers preferred sweetpotato with high dry matter content (greater than 27%) and with high starch content. However, different uses of sweetpotato varieties are also an important factor for retaining sweetpotato varieties. In Chipinge and Chimanimani some varieties such as Chibikiravaenzi, Mutengangehuku, and Boarding are used for sweetening sweet beer and porridge yet other varieties such as Dambaradzi and Gwasharandima have tender leaves which are consumed as a relish. The choice of sweetpotato varieties by farmers in districts such as Domboshawa, Murewa, Marondera, and Hwedza is mainly influenced by proximity to the Horticulture Research Centre in Marondera which multiplies improved sweetpotato varieties such as Chingova, Germany 2, and Mozambican White. The majority (94%) of sweetpotato in

Zimbabwe are white or cream-fleshed and fewer (6%) being orange-fleshed which is a result of continuous selection by farmers. However, most farmers had more than one sweetpotato cultivars at their homesteads partly because they save different purposes.

The study revealed that sweetpotato cultivars grown by farmers are not constant due to a lot of introductions from other countries and loss due to natural attrition. This is partly explained by interactions with developmental agents such as donors, extension and research officers, markets, and introductions from nearby countries along the borders. There was more sweetpotato genotype diversity in Chipinge than the rest of the other districts. This could be due to genetic drift from Mozambique as most farmers from Mozambique sell their produce in Zimbabwe. Some sweetpotato genotypes such as Chimararata and Chibhutata are disappearing in Chipinge area and the disappearance could be a result of neglect by farmers due to low productivity. Beauregard an orange-fleshed improved variety dominated areas around Harare where it is commercially grown mainly for export.

Most farmers in surveyed districts acknowledged that sweetpotato is a food security crop. Farmers eat sweetpotato at least once per day when in-season partly because that will be the only affordable food around. This explains why early maturing and high-yielding varieties are preferred by most farmers so that they can escape the hunger period which occurs just before harvesting period of the main staple crop like maize. Ebregt et al. (2004) and Ezin et al. (2018) reported that sweetpotato is important for food security, and increasingly, as a cash crop.

However, on-farm sweetpotato yield in Zimbabwe is generally low ranging from 3.5 - 8 tonnes per hectare. Kapinga et al. (2007) reported that the unavailability of quality material was a big constraint in Namibia. Ngailo et al. (2019) also reported the scarcity of land, improved genotypes, funding and training on best practices, poor communication systems and expensive inputs as other contributing factors to poor productivity which is the same situation with Zimbabwe.

The majority of farmers in Zimbabwe use retained or recycled planting material. This is supported by a small proportion of farmers who possess registered nurseries. However, most farmers were aware of the value of clean planting material. The majority of farmers also cited the prevalence of pests and diseases which might be partly explained by the use of recycled planting material. Ezin et al. (2018) reported a lack of clean and adequate planting material as a major constraintin most African countries. In a study by Agbede and Adekiya (2009) increased sweetpotato yields were

realized when sweetpotato was planted on flatbeds or on mounds and ridges. In this study, most farmers plant sweetpotato on ridges. However, farmers from Chimanimani plant sweetpotato on mounds. The adoption of mounds in Chimanimani might be due to the sloppy and rocky nature of the terrain and land shortage which is not the case in other districts. However, the size of ridges differed with regions. Farmers from Chipinge district plant sweetpotato on bigger ridges than those constructed using ox-drawn ploughs in other districts such as Murewa and Marondera. Mukhopadhyay et al. (2011) and Makini et al. (2018) reported that cultivation on mounds or ridges results in better yield partly because it promotes good drainage. Another notable difference between farmers in Chipinge and the rest of the districts is that farmers from Chipinge plant sweetpotato vines with respect to the sun so that they benefit from maximum light. In this study, the majority of farmerspreferred the use of inorganic fertilizers for sweetpotato destined to the market yet subsistent farmers favour the use of organic manure and grass in order to maximize taste. Those farmers who prefer organic fertilizers to inorganic fertilizers indicated that inorganic fertilizers and chemicals such as pesticides were expensive and they render the storage roots tasteless. This study revealed limited intercropping with vegetables mainly planted on the same ridge with sweetpotato. This could be explained in part by the need to allow the sweetpotato crop to benefit from maximum sunlight for improved yields. Mukhopadhyay et al. (2011) and Nedunchezhiyan et al. (2012) reported the beneficial effects of intercropping cereals or vegetables with sweetpotato. Unlike other districts understudy, Chirinda farmers in Chipinge district grow sweetpotato throughout the year-the reason being that it receives rain showers most part of the year. Chirinda farmers also observe sweetpotato-based cropping systems, unlike Chimanimani farmers whose cropping systems are horticulturally based.

3.3.3 Sweetpotato production and marketing constraints experienced in Zimbabwe

The marketing system in Zimbabwe is largely informal and is still in the formative stage of development. Major markets are fresh produce markets located in Harare, Bulawayo, Beitbridge, Gwanda, and Mutare. Sweetpotato farmers in Zimbabwe have no grower association hence the marketing value chain is dominated by middlemen who travel to producing areas and dictate the farm gate price. Mukhopadhyay et al. (2011) reported that post-harvest losses, marketing systems, low prices, lack of organized markets, high labour costs, and unavailability of transport were cited as common bottlenecks in the sweetpotato value chain system. Farmers are forced to be price takers by middlemen. However, due to the bulkiness of the roots, the majority of the marketable

roots are sold by the roadside. Producers prefer roadside marketing partly because consumers or buyers do not have an opportunity to influence the price downwards. Women also dominate the roadside marketing of sweetpotato partly because they have the patience to wait for buyers. Vendors use plates, buckets or just heap the roots on a plastic sheet as the measurement for sale. Some vendors are not honest they arrange the roots in a manner that leaves hollow spaces at the centre of the bucket and create a noticeable heap at the top thus deceiving the buyer. This could be a way of trying to make the business profitable. However, this practice has got a negative effect in that consumers will shun buying from such vendors. In Chipinge district, sweetpotato prices are pushed down due to a glut since Mozambique farmers cross the border and flood the market with sweetpotato. The glut lowers the price of a 20 kg-bucket of sweetpotato to the US $2-00–US$ $3-00 during in-season periods. This has a demotivating effect on sweetpotato farmers resulting in loss of less productive varieties hence loss of genetic diversity. Middlemen dispose of a 20 kg-bucket of sweetpotato at US$ 5-00 – US$ 10-00 at fresh markets. This study concurs with the works of Thiele et al. (2009), Mitchell (2011) and Mitra et al. (2018) in Uganda who reported that middlemen made a profit of 5% of the farm gate price.

There is a severe shortage of infrastructure for the production of clean planting material such as tissue culture laboratories leading to low sweetpotato production and productivity by farmers. The absence of a reliable market that offers viable producer prices, and drought conditions are some of the major constraints faced by sweetpotato farmers in Zimbabwe. Most growers regarded sweetpotato production as an unviable activity mainly because of the low prices offered by buyers. Through interaction with farmers, it was evident that lack of technical support, high input costs, pests, and diseases were part of the constraints limiting sweetpotato production and productivity.In addition, most of these farmers rely on their farm-retained vines, which mainly have pests and diseases leading to poor yields, hence the reason why they cited low yield as the number one factor inhibiting sweetpotato production in Zimbabwe. There is a need for deliberate farmer training on good agriculture practices since most of them did not observe crop rotation. These results are in agreementwith the findings of Mmasa et al. (2012) who implicated a lack of quality planting material, fundingopportunities, pests and diseases, and drought in Tanzania.

The use of hand hoes for land preparation and harvesting is a backbreaking task due to the drought-induced hard surface. Therefore, researchers need to generate innovative ways of breaking the hard surface with ease. Mechanization and irrigation facilities can go a long way in easing backbreaking

tasks. The United States of America farmers mechanized weed control Weiner et al. (1988), Mrema (2008), and Adeleke and Idrisu (2018). Farmers in Murewa employ ox-drawn ploughs for ridge construction and harvesting. However, very few farmers have livestock that can be harnessed for these activities. There is a need to intensify efforts on developing control measures of moles and sweetpotato weevils. As a coping strategy, some farmers use phostoxin tablets for the control of moles.Ants were more prevalent in the Rusitu area of Chimanimani district partly because this area is warmer than the rest of the surveyed districts.

Moles and weevils were cited by 90% of the farmers as the most problematic pests of sweetpotato. The sweetpotato virus was the most devastating disease of sweetpotato in Zimbabwe since its symptoms (chlorotic leaves and stunted growth) were prevalent in most growing areas. This validatesthe findings of Ngailo et al. (2013), who indicated that sweetpotato virus disease depressed sweetpotato yields by 50-80% in Tanzania. Namanda (2012) and Rono et al. (2017) reported the common challenges in Uganda as unavailability of quality of planting material, the incidence of drought, and sweetpotato virus attack. The cheapest control method that can be helpful to resource-poor farmers is breeding for resistance to major pests and diseases. In this study, most farmers control weevils through the construction of big ridges which are not prone to cracking, covering cracks atthe earliest occurrence of cracks, and avoiding delayed harvesting. However, information gatheredduring focused group discussions showed that most farmers were unable to identify diseases and pests in their fields. As a result, there is a need to strengthen the technical capacity of farmers.

Most farmers from all surveyed districts called for improved, high-yielding, early maturing cultivars with tolerance to drought, pests, and diseases since they are tired of low production and productivity. However, some farmers especially in Chipinge indicated that varieties which become soft upon cooking are good for the young and the old. These findings concur with observations by Zawedde et al. (2014) who reported the importance of a cultivar to be high yielding, have good taste, early maturity, and pest and disease tolerance. This is a challenge to sweetpotato breeders to prioritize targeted breeding as well as the promotion of clean planting material. Most farmers from surveyed areas indicated a willingness to adopt improved varieties adapted to their respective geographical locations and preferred by the market. This implies that farmers are not stuck to white, cream, or yellow-fleshed cultivars with the high dry matter but are open to new introductions as long as they are nutritious and have a reliable market.

3.4 Conclusion

One hundred diverse sweetpotato genotypes were collected from sweetpotato producers and public institutions from Zimbabwe and preferred characteristics identified were: early maturity, high yielding, pest and disease tolerance, market preference, taste, cooking quality (prefer varieties with high dry matter), and varieties that are able to produce adequate planting material by the start of the season. The identified production and marketing constraints were low selling prices, insect pests, diseases, shortage of clean planting materials and labour, heat, drought, and frost attack, and low production and productivity.

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CHAPTER 4

MORPHOLOGICAL CHARACTERIZATION OF SWEETPOTATO [*IPOMOEA BATATAS* (L) LAM.] ACCESSIONS FROM ZIMBABWE

Abstract

Morphological and genetic diversity investigations lay the foundation for any plant breeding initiative. In addition, understanding the genetic diversity available in a germplasm collection helps breeders to identify and isolate duplicate genotypes resulting in efficient genetic resources utilization. Ninety-two sweetpotato accessions collected from the main growing areas of Zimbabwe and institutions were evaluated using sweetpotato descriptors. Eight accessions failed to establish resulting in ninety-two accessions for evaluation. The number of phenotypic classes across all attributes were 174 though the classes within an attribute/ character ranged from 3 to 10. Plant type, vine internode length and pigmentation, leaf lobe type and number, the shape of central lobe, mature leaf shape, abaxial leaf vein pigmentation, petiole pigmentation, petiole length, storage rootstalk length, storage root per plant, storage root formation, predominant flesh colour, secondary flesh colour, storage root skin colour, storage root shape and size, distribution of secondary skin colour, the intensity of predominant skin colour and predominant storage root skin colour, showed great variation among genotypes. The variables which showed few phenotypic classes were: mature leaf size and colour, immature leaf colour, secondary vine colour, secondary skin colour, storage root surface defects, storage root cortex thickness, vine internode diameter, and vine tip pubescence. Cluster analysis revealed three distinct clusters. There were 27, 58, 7 accessions in clusters 1, 2, and 3, respectively. Cluster 2 had two subgroups; 2a and 2b containing 27 accessions (29.3%) and 31 accessions (33.7%), respectively. Of interest is that the accessions were randomly clustered-thus accessions were grouped irrespective of where they were collected. The study revealed important information useful for initiating a robust sweetpotato breeding program based on the collection since it revealed diversity among accessions in addition to isolating duplicates such as Bosbook and Unknown CA; Hwedza 1 and Hwedza 5H; Birchenough and Muzvareshonga.

Keywords: Sweetpotato morphological traits, genetic diversity, germplasm collection, sweetpotato characterization, *Ipomoea batatas* L, sweetpotato descriptors

4.1 Introduction

Sweetpotato is one of the staple crops of Zimbabwe. It saves as a food and nutrition security crop grown mainly by smallholder farmers. It can be grown and harvested any time of the year provided the area is frost-free. Zimbabwe is endowed with diverse sweetpotato genotypes. The main sweetpotato producing areas in Zimbabwe are found in natural regions; I, II and III with adequate rainfall and better soils (Mudombi, 2007). Mutandwa (2008) reported that national sweetpotato production levels generally had not exceeded 10,000 tons/year, with an average yield per hectare ranging from 5 to 8 t ha^{-1}. Most of the sweetpotato isgrown on raised ridges, mounds, and beds.

Morphological characterization is the initial step in differentiating plant genotypes Revilla and Tracy (1995) and Osawaru, et al. (2014). In addition, Talukder and Saha (2017) indicatedthat the differentiation of plants through their morphology is important in revealing desirable attributes. Some et al. (2014) also reported that numerous studies based on morphological characteristics such as vine, leaf, flower, and storage root revealed significant morphological differences in sweetpotato. Mbithe et al. (2016) defined morphological characterization as a method based on evaluating leaf, flower, and storage root characteristics and has been traditionallyused for the identification of the crop's cultivars. In support, Moulin et al. (2012), Mbithe et al. (2016) and Felistus et al. (2017) documented that morphological characterization is essential in isolating duplicates and identification of unique characteristics.

Jackson et al. (2012) recommended the adoption of sweetpotato for food security due to its ability to give good yields in rugged conditions, marginal soils, resistance to pestsand diseases, and drought tolerance. Sweetpotato owes its adaptability to the great phenotypic andgenotypic variability which is an indispensable asset for breeding in the current climate change situation. The advent of climate change buttresses the need for plant germplasm collection and conservation. In Zimbabwe, there is no systematic collection and conservation initiatives of sweetpotato germplasm in place, yet it is a strategic crop in the lives of both rural and urban populations. In addition, there is little documented information about sweetpotato diversity that is available. The objective of this study was to assess sweetpotato from main growing areas of Zimbabwe andinstitutions for genetic diversity through morphological characterization and to identify and eliminate duplicates from the collection in order to enhance conservation strategies.

4.2 Materials and Methods

4.2.1 Plant collection

One hundred sweetpotato accessions (Appendix 1) were collected from identified main growing areas of Zimbabwe: Manicaland, Mashonaland East, Masvingo, Matabeleland North, Harare, and Mashonaland Central (Figure 4.1). The guiding principle was to collect as many sweetpotato accessions as possible from the target main growing areas. The study was conducted in seven districts during the 2017-2018 growing season. The areas chosen are all rural but accessible through feeder roads. The districts were selected solely as they belong to the main sweetpotato producing areas and are rich in sweetpotato diversity. The areas included, Chinyaduma (Chipinge district), Tamandai (Chipinge district), Ngaone (Chimanimani district), Rusitu (Kopa) (Chimanimani district) Murewa (Murewa district), Chigondo (Hwedza district), Domboshawa (Goromonzi district), Africa University (Mutare district), sweetpotato gene bank at Chiredzi Research Institute (Chiredzi district, Masvingo) and a collection from the University of Zimbabwe (germplasm mainly from Matabeleland and Mashonaland West). The rainy season for these areas normally lasts from mid-October to March. The main limiting factors are mid-season droughts, cold winters, and acidic soils which threaten sweetpotato vine survival.

The approach included random visits to households from the main sweetpotato growing areas and purposive visits to institutions known to have active sweetpotato gene banks. In some cases, the extension staff requested sweetpotato farmers to bring samples of different sweetpotato vines from their fields or gardens to a central meeting place. Farmers volunteered to bring two to five vines of all genotypes at their respective homesteads. The farmers involved in these surveys werea mixed group of males and females who grew a diversity of crop varieties. Landholdings varied from small (0.5 ha) to large (50 ha).

The information collected included, the name of the enumerator, location, genotype number, date of collection, province, district, village, and ward. Unfortunately, vines brought by farmers had no such information, however, this does not compromise the objective of the study since the aim was not to associate certain attributes to areas of the collection. Nevertheless, the sweetpotato germplasm brought by farmers during focused group discussions had no passport data and some genotypes were not known by farmers.

4.2.2 Characterization site

The germplasm consisted of 94 white-fleshed and six orange-fleshed varieties and was evaluated in a field experiment from December 2018 to August 2019 at the Harare Research Centre farm located at Harare (17º 48` S, 31º 03`E, altitude 1506 metres above sea level). The texture of the soil was medium grain, sandy clay and the average rainfall was 100.54 mm with the lowest June temperature of 4.4˚C and October highest temperature of 34˚C. the accessions were further multiplied within a nursery so as to raise adequate planting material for field evaluation.

4.3 Experimental procedure

Soil sampling was conducted at 20 cm depth. Chemical and physical analysis results were: soil pH ($CaCl_2$) = 6, 2, organic matter content 0.84 dag/ dm^3, Ca^{+2+} =7.57 mg/100g, Mg^{+2+}= 3.61 mg/100g and K_2O_5 = 3.61 mg/100 g. There was no need for lime application since the soil pH was ideal for sweetpotato production. One hundred kilograms per hectare of potassium nitrate was applied as supplementary fertilizer. Ridge construction was done using hoes. The trial was established as a 10 x 10 alpha lattice and replicated twice. One hundred sweetpotato genotypes were randomly assigned to the plots. Each plot had a single three-metre ridge with 0.3 m width and height. Ten vines of 3 to 4 nodes each were planted at 0.3 m depth covering two-thirds of the vine. All vines were spaced at 0.3 m within a ridge. The ridges were spaced at 0.9 m. Compound S (7:21:8 ratio of NPK) was the basal fertilizer applied at 300 kg per hectare. Top dressing was done with ammonium nitrate fertilizer (34.5 % N) three weeks after transplanting at a rate of 150 kg per hectare. Before field establishment, rapid multiplication was done on sandy beds in the greenhouse.

4.3.1 Data collection

Sweetpotato descriptors as recommended by Low (2017) were used for morphological characterization. The characterisation covered 30 attributes composed of 16 aerial and 14 from the root system (Table 4.1). Characters were scored on five plants per plot randomly selected from each accession. The aerial parts were characterized at 90 days post-transplant as recommended by Some et al. (2014). The aerial attributes included plant type, vine internode length, vine internode diameter, predominant vine colour, secondary vine colour, vine tip pubescence, mature leaf shape, leaf lobe types, leaf lobe number, the shape of central lobe, mature leaf size, abaxial leaf vein pigmentation, mature leaf colour, immature leaf colour, petiole pigmentation and petiole length.

Morphological characterization for the root system was done at 145 days after planting in thefield. The characterization was conducted following recommendations by Some et al. (2014). The 14 descriptors included: storage root shape, storage root surface defects, storage root cortex thickness, storage root skin colour, intensity of predominant skin colour, secondary skin colour, predominant flesh colour, secondary flesh colour, distribution of secondary skin colour, storage root formation, storage rootstalk, number of storage roots per plant, variability of storage root shape, variability of storage root size and storage root cracking. Five roots of medium to large size were considered for the evaluation.

4.3.2 Data analysis

Descriptive analysis was done for all agro-morphological traits. All data were checked, verified, and analysed with a statistical package for social scientists (SPSS version 21). The descriptive statistics were: frequencies, means, and percentages of the identified variables. Morphological factorial analysis and cluster analysis were done using Darwin version 6. The trees were drawn using the unweighted pair group method with arithmetic mean (UPGMA) and neighbour-joining algorithms with bootstrap values of more than 80%.

Table 4.1. Morphological descriptors used to evaluate vegetative parts and roots of sweetpotatoaccessions from main producing areas of Zimbabwe.

Descriptor	**Phenotypes**
Plant Type	Erect= (< 75 cm); Semi-erect = (75-150 cm); Spreading = (151-250 cm); Extremely spreading = (> 250)
Vine Internode Length	Very short = (< 3 cm); Short= (<3-5 cm); Intermediate= (6-9 cm); Long= (10-12 cm); Very long = (> 12 cm)
Vine Internode Diameter	Very thin (<4 mm); Thin = (4-6 mm); Intermediate= (7-9 mm); Thick (10-12); Very thick = (>12 mm)
Predominant Vine Colour	1= Green; 3= Green with few purple spots; 4= Green Many purple spots;5= Green with many dark purple spots; 6= Mostly purple; 7=e Mostly dark purple; 8= Totally purple; 9=Totally dark purple
Secondary Vine Colour	0= Absent; 1= Green base; 2=Green tip; 3=Green nodes; 4= Purple base; 5= Purple tip; 6= Purple nodes; 7= other
Vine Tip Pubescence	0= Absent; 3= Sparse; 5= Moderate; 7= Heavy
Leaf	
General Outline	1=Round; 2=Reniform; 3= Cordate; 4=Triangular; 5= Hastate; 6=Lobed;7= Almost divided
Lobe Type	0= No lateral; 1= Very slight 9teeth); 3= Slight; 5= Moderate; 7= Deep; 9= Very deep
Leaf Lobe Number	1=One; 3= Three; 5= Five; 7 Seven
Shape of Central Lobe	0= Absent; 1= Toothed; 2= Triangular; 3= Semi- Circular; 4= Semi-elliptic; 5= Elliptic; 6=Lanceolate; 7= Oblanceolate; 9= Linear (Narrow)
Mature Leaf Size	3=Small (<8 cm); 5=Medium (8-15 cm); 7= Large (16-25 cm); 9=Very large (> 25cm)
Abaxial Leaf vein pigmentation	1= Yellow; 2= Green; 3=Purple spot in the base of main rib; 4=Purple spots in several veins; 5= Main rib partially purple; 6= Main rib mostlyor totally purple; 7= All veins partially purple; 8= All veins mostly or totally purple; 9= Lower surface and veins totally purple
Mature Leaf Colour	1=Yellow- Green; 2= Green; 3= Green with purple edge; 4=Greyish-Green; 5= Green with purple veins on upper surface; 6= Slightly purple;7= Mostly purple; 8= Green upper, purple lower; 9= purple both

Descriptor	Phenotypes
	Surfaces
Immature Leaf Colour	1= Yellow – Green; 2=Green; 3= Green with purple edge; 4= Greyish-green; 5= Green with purple veins o upper surface; 6= Slightly purple; 7= Mostly purple; 8= Green Upper, Purple lower; 9= Purple both Surfaces
Petiole Length	1=Very short (<10 cm); 3= Short (10-20 cm); 5= Intermediate (21-30 cm); 7= Long (31-40 cm); 9= Very Long (> 40 cm)
Petiole Pigmentation	1= Green; 2= Green with purple near stem; 4=Green with purple at bothends; 5= Green with purple spots throughout petiole; 6= Green with purple stripes; 7=Purple with green near leaf; 8= Some petioles purple, others green; 9= Totally/ mostly purple
Storage root	
Shape	1=Round; 2=Round elliptic; 3= Elliptic; 4=Ovate; 5=Obovate; 6=Oblong; 7= Long oblong; 8= Long elliptic; 9= Long irregular orcurved
Variability of storage root shape	3=Uniform; 5= Slightly variable; 7=Moderately variable
Surface defects	0=Absent; 1Alligator-like skin; 2= veins; 3= Shallow horizontal constrictions; 4=Deep horizontal constrictions; 5= Shallow longitudinal grooves; 6= Deep longitudinal grooves; 7== Deep constrictions and Deep grooves; 8= Others
Root cortex thickness	14= very thin 9 (< 1mm); 3= Thin (1-2mm); 5= Intermediate (2-3 mm); 7=Thick (3-4 mm); 9=Very thick (> 4mm)
Skin colour	1= White; 2= Cream; 3= Yellow; 4= Orange; 5= Brownish orange; 6= Pink; 7=Red; 8= Purple- red; 9=Dark purple
Skin colour intensity	1= pale; 2= intermediate; 3= dark
Secondary skin colour	0= Absent; 1=White; 2= Cream; 3= Yellow; 4= Orange; 5=Brownishorange; 6= Pink; 7= Red; 8=Purple-red; 9=Dark purple
Flesh colour	1= White; 2= Cream; 3= Dark cream; 4=Pale-yellow; 5=Dark yellow; 6= Pale orange; 7= Orange; 8= Pigmented; 9= Strongly pigmented
Secondary Flesh colour	0= Absent; 1= White; 2=Cream; 3=Yellow; 4= Orange; 5=Pink; 6= Red; 7 = Purple-red

Descriptor	Phenotypes
Distribution of secondary flesh colour	0= Absent; Narrow ring in cortex; 2= Broad ring in cortex; 3=Scatteredspots in flesh; 4=Narrow ring in flesh; 5=Broad ring in flesh; 6=Ring and other areas in flesh; 7=In longitudinal sections; 8= Covering all flesh
Storage formation	1= Closed; 3=Open cluster; 5= Dispersed; 7= Very dispersed
Storage root stalk	0= Sessile/ absent; 1= Very short (< 2cm); 3= Short (2-5 cm); 5= intermediate (6-8 cm); 7= Long (> 12 cm)
Variability of storage root size	3=Uniform; 5=Slightly variable; 7= Moderately variable
Storage root cracking	0=absent; 3= few cracks; 5= medium number of cracks; 7= many cracks
Secondary skin colour	0=absent; 1=white; 2= cream; 3= yellow; 4=orange; 5= brownish orange; 6= pink; 7= red; 8 =purple-red; 9=dark purple
Flesh colour	1= white; 2= cream; 3= dark cream; 4= pale yellow; 5= dark yellow; 6= pale orange; 7= intermediate orange; 8= dark orange; 9= strongly pigmented with anthocyanins
Secondary flesh colour	0= absent; 1= white; 2= cream; 3= yellow; 4= orange; 5= pink; 6= red; 7= purple-red; 8= purple; 9= dark purple
Distribution of secondary flesh colour	0= absent; 1= narrow ring in cortex; 2= broad ring in cortex; 3= scattered spots in flesh; 4= narrow ring in flesh; 5= broad ring in flesh; 6= ring and other areas in flesh; 7= in longitudinal sections; 9=covering all flesh
Storage formation	1= closed cluster; 3= open cluster; 5= dispersed; 7= very dispersed
Storage root stalk	0= sessile or absent; 1= very short (< 2 cm); 3= short (2-5 cm); 5= intermediate (6-8 cm); 7= long (9-12 cm); 9= very long (> 12 cm)
Variability of storage size	3= uniform; 5= slightly variable; 7= moderately variable
Storage root cracking	0= absent; 3= few cracks; 5 = medium number of cracks; 7= many cracks

4.4 Results

4.4.1 Morphological characterisation

Part of the collection team discussing different sweet potato accessions from Chimanimani district (Figure 4.1)

Figure 4.1. Survey team collecting sweetpotato germplasm at Kopa Rusitu–Chimanimani district, Manicaland Province

The total number of phenotypic classes across all attributes was 174. However, classes within an attribute ranged from 3 to 10. There was evidence of a wide range of phenotypic classes (Figure 4. 2.1- 30).

Plant type, vine internode length and pigmentation, leaf lobe type and number, the shape of central lobe, mature leaf shape, abaxial leaf vein pigmentation, petiole pigmentation, petiole length, storage rootstalk length, storage root per plant, storage root formation, predominant flesh colour, secondary flesh colour, storage root skin colour, storage root shape and size, distribution of secondary skin colour, the intensity of predominant skin colour and predominant storage root skin colour, showed great variation among genotypes. The variables which showed few phenotypic classes were: mature leaf size and colour, immature leaf colour, secondary vine colour, secondary

skin colour, storage root surface defects, storage root cortex thickness, vine internode diameter, and vine tip pubescence.

For growth habit/ plant type, 13% of the genotypes had erect vines, 50% semi-erect vines, 37% had spread and no extremely spreading (Figure 4.2.1). For internode length, 4% of the accessions had very short (≤ 3cm) internode, 50% (3-5 cm), 44% were intermediate (6-9 cm), only 2% were long (10-12cm) and none were very long (>12 cm) (Figure 4.2 .2). In terms of vine internode diameter, 78% of the accessions had thin (4-6 mm) vines, 16% had intermediate (7-9 mm) and 6% had very thin (<4 mm) vines (Figure 4.2.3). Most genotypes (53%) had green vines, 18% had green vines with few purple spots, 6% green with numerous purple spots, 1% green vines with many dark purple spots, 17% had mostly purple vines, 2% had mostly dark purple vines, 1% had complete purple vines and 2% had totally dark vines (Figure 4.2.4). For the secondary vine colour, 77% of the genotypes had green tips, 3% had purple bases, 5% had purple tips, 7% had purple nodes, 2% had green nodes and 2% of the genotypes had other colours (Figure 4.2.5). The majority of accessions (69%) had sparse vine tip pubescence, 23% had no tip pubescence, 6% had moderate tippubescence and 2% of the accessions had heavy vine tip pubescence (Figure 4.2.6).

In relation to mature leaf shape, 7% of the genotypes had cordate leaves, 21% with triangular leaves, 1% had hastate leaves, 47% of the genotypes had lobed leaves, 24% had almost divided leaves (Figure 4.2.7). For leaf lobe type, 2% of the accessions had no lateral lobes, 18% of the accessions were very slightly lobed, 14% of the accessions were slightly lobed, 22% of the accessions showed moderate lobes, 28% of the accessions showed deep lobes and 16% had very deep lobes (Figure 4.2.8). With respect to the number of leaf lobes, 22% of the genotypes had only one lobe, 11% had three lobes, 55% of the genotypes had five lobes, 8% had seven lobes and 4% of the genotypes had nine lobes (Figure 4 .2.9). With regards to shape of central leaf lobe,18% of the genotypes had toothed central leaf lobe, 7% triangular, 1% semi-circular, 20% semi-elliptic, 27% with elliptic central leaf lobe, 16% lanceolate, 3% oblanceolate, and 8% linear/ narrow (Figure 4. 2.10). The accessions exhibited different mature leaf sizes, with 3% of the genotypes having small (≤ 8cm), 75% had medium (8-15 cm) leaves, 21% with large (16-25 cm) leaves and1% with very large (25 cm) (Figure 4.2.11).

Great variability was observed in abaxial leaf vein pigmentation, with 8 classes: 59% were green, 13% had purple spots at the base of the main rib, 1% with purple spots in several veins, 7% had partially purple main rib, 7% of the accessions had mostly or totally purple main rib, 3% of the

accessions had all veins partially purple, 9% had all veins mostly or totally purple, and 1% of the accessions had lower surface and veins totally purple (Figure 4.2.12).

Sixty-nine percent of the mature leaves were green, 6% green with purple edges, 7% green with purple veins on upper surfaces, 1% were slightly purple, 5% were mostly purple, 10% green on the upper surface, and purple on lower surfaces, and 2% purple on both surfaces (Figure 4.2.13). Most of the immature leaves were green (76%), 7% green with purple edges, 7% green with purple venison upper surface, 1% with mostly purple immature leaves, 7% being green on the upper surface and on the lower surface of leaves and 2% purple on both surfaces (Figure 4.2.14).

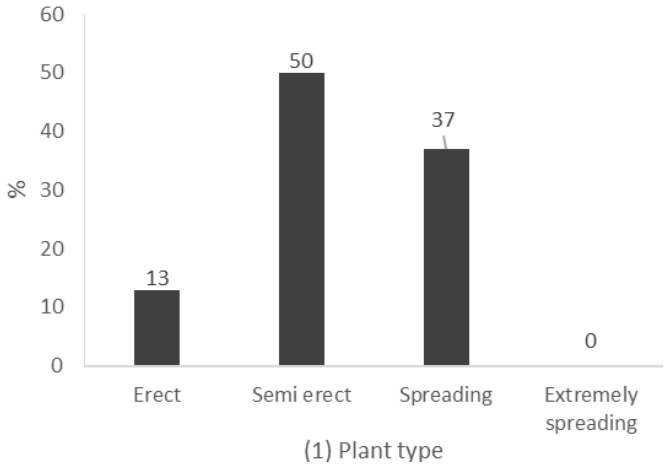
Fifty nine percent of the genotypes had intermediate (21-30 cm) petiole length, 2% with very short (≤ 10cm), 31% with short petioles (10-20 cm) and 8% long (31-40 cm). None of the accessions had very long (> 40 cm) petioles thus exhibiting pronounced variability on this attribute (Figure 4.2.15). High variability was observed for petiole pigmentation with 7 classes: 58% of the accessions had green colour, 11% had green with purple colour on both ends, 8% had green with purple colour near the stem end, while 8% had green colour and purple near the leaf, 2% with green and purple stripes, 4% had purple petioles with green colour near the leaf end and 9% of the accessions had totally or mostly purple (Figure 4.2.16).

Five classes were observed on root shape. One per cent was round, 10% round elliptic, 18% elliptic, 41% long elliptic and 30% had long irregular/curved shape (Figure 4.2.31). The intensity of skin colour was characterised as 44% pale, 35% intermediate and 21% dark (Figure 4.2.21). There wasno secondary skin colour for 74% of the genotypes, 12% white, 1% cream, 1%yellow, 1% orange,7% pink and 4% red (Figure 4.2.22). High variability was detected for distribution of secondary skin colour: absent in 45% of the accessions, 2% of the accessions had a narrow ring in the cortex,2% had the broad ring in the cortex, 16% had spots scattered in the flesh, 3% had the narrow ringin the flesh, 1% had the broad ring in the flesh, 7% had the ring in the cortex and in other parts ofthe flesh, 1% in longitudinal sections, 19% covering most of the flesh, and 4% covering all other parts of the flesh (Figure 4.2.25).

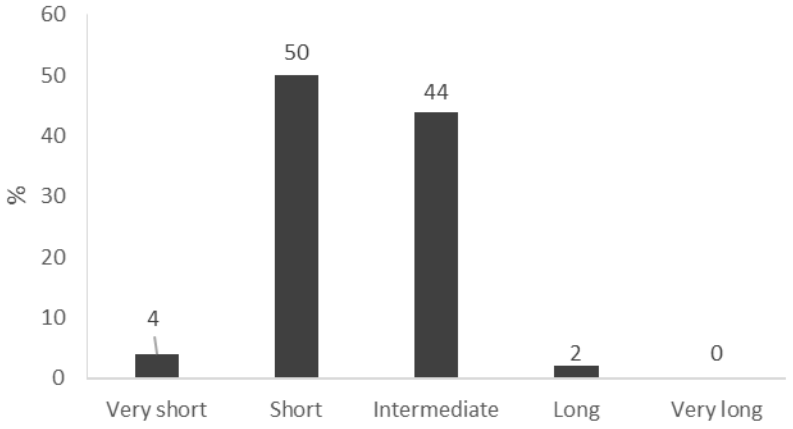
There was a great variation in storage root flesh colour. Fifty-four per cent of the genotypes had white pulp, 35% had cream pulp, 4% pale yellow; 7% pale orange pulp (Figure 4.2.23). Forty-six per cent of the genotypes had no secondary flesh colour. However, 26% had cream colour, 8% white, 7% orange, 6% yellow, 3% purple, 1% pink and 1% red (Figure 4.2 .24). Eleven per cent

of the genotypes had no surface defects. However, 6% of the genotypes had vein-type defects, 69% shallow horizontal constrictions, and 14% shallow longitudinal grooves (Figure 4.2.18). With regards to storage root cortex thickness, 31% of the accessions exhibited very thin (< 1mm) cortex, 5% had thin (1-2 mm), 61% with intermediate (2-3 mm) and 3% had thick (3-4 mm) cortex (Figure 4.2.19).

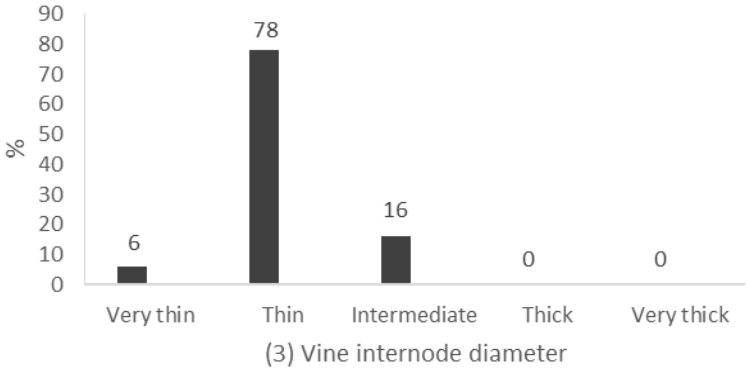
The predominant storage root skin colour of the accessions characterized was classified as purple (34%), white (28%), cream (27%), pink (4 %), red (3%); dark purple (2%), orange (1%) and brownish-orange (1% (Figure 4.2.20). The predominant storage root formation was the open cluster with 52%, seconded by very dispersed roots (28%), dispersed (8%), and (2%) with closed cluster (Figure 4.2.26). The majority (52%) of the accessions had short (2-5 cm) root stalks, 31% intermediate, 9 % long, 6 % very short, and 2% very long (Figure 4.2.27). There were significant differences in the number of roots per plant. Forty-seven percent of the accessions having 4 roots per plant, 23% with 3, 11% with 6, 9% with 5, 9% with 7, 6% with 8, 6% with 2, 6% with 1root, 2% with 9 roots and 1% with 10 roots per plant (Figure 4.2-28). In terms of variability of storage root shape, 50% were slightly variable, 27% uniform, and 23% moderately variable (Figure 4.2.31 In relation to the variability of storage root size, 43% were moderately variable, 40% slightly variable, and 17% uniform (Figure 4.2.29). Low variability for storage root cracking was observed, 80% of the accessions had no cracks (absent), 15% with few cracks, and 5% with medium cracks (Figure 4.2.30).



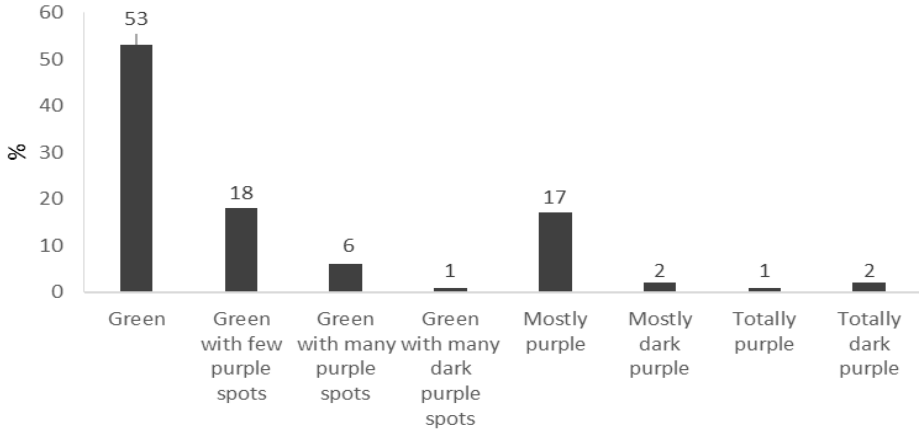
(1) Plant type



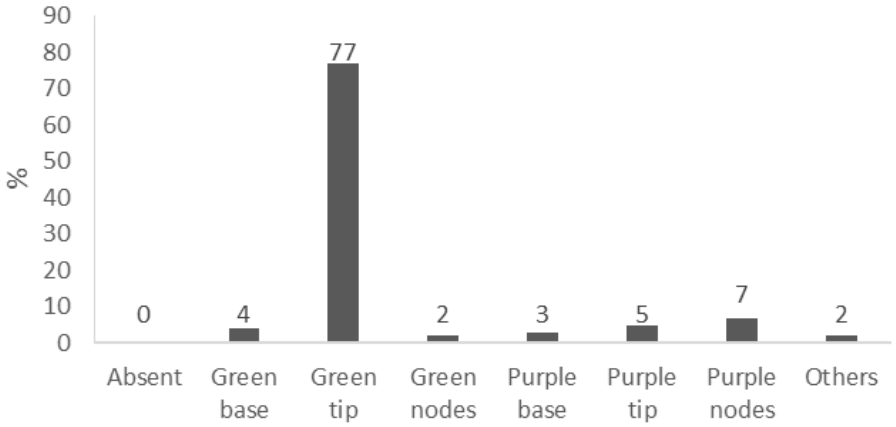
(2) Vine internode length



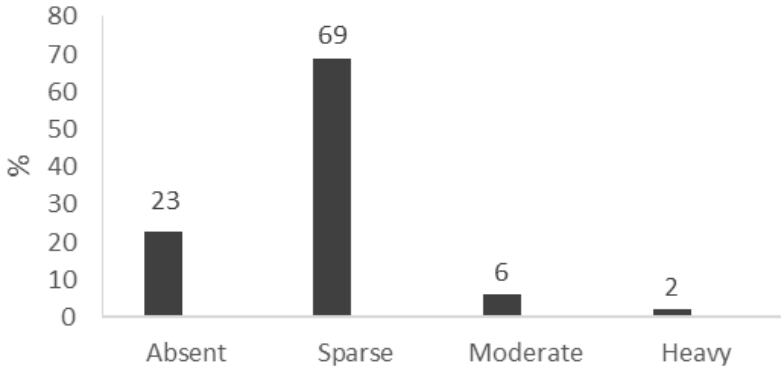
(3) Vine internode diameter



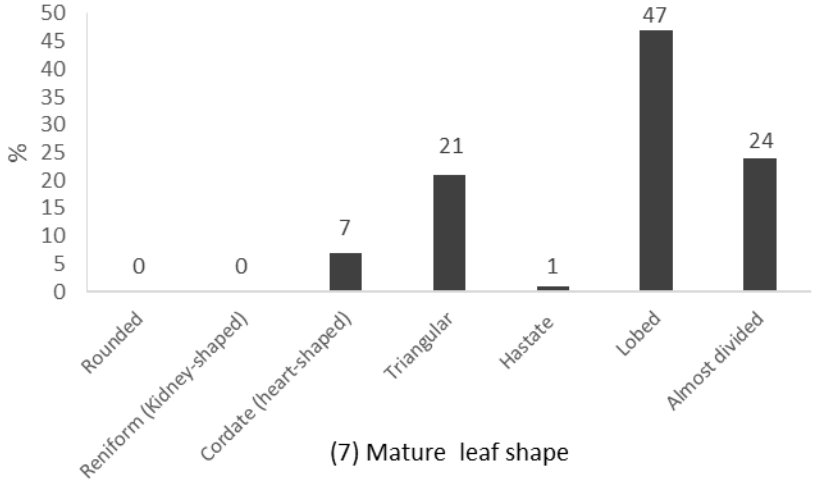
(4)Vine pigmentation



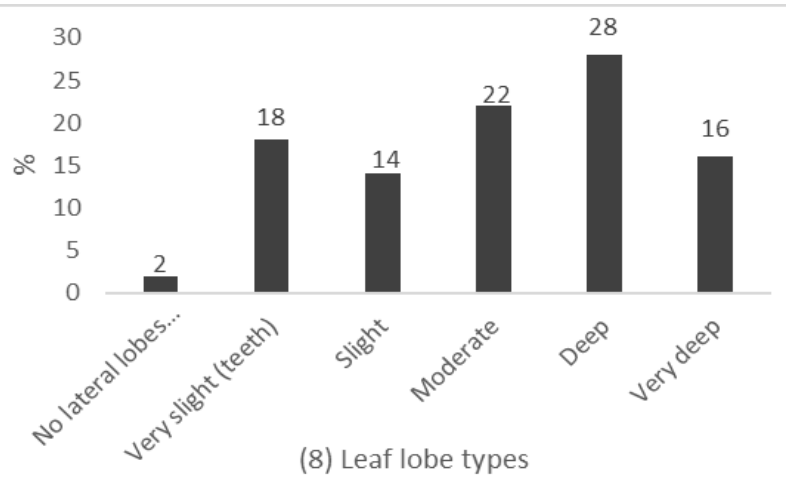
(5) Secondary vine colour



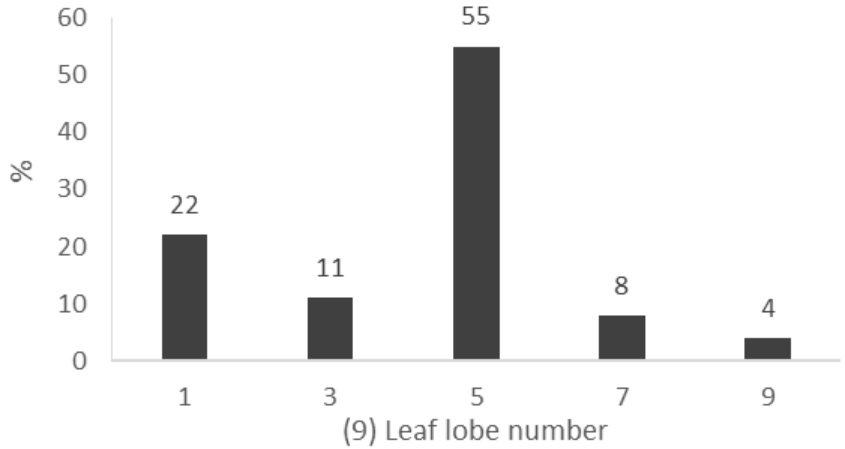
(6) Vine tip pubescence



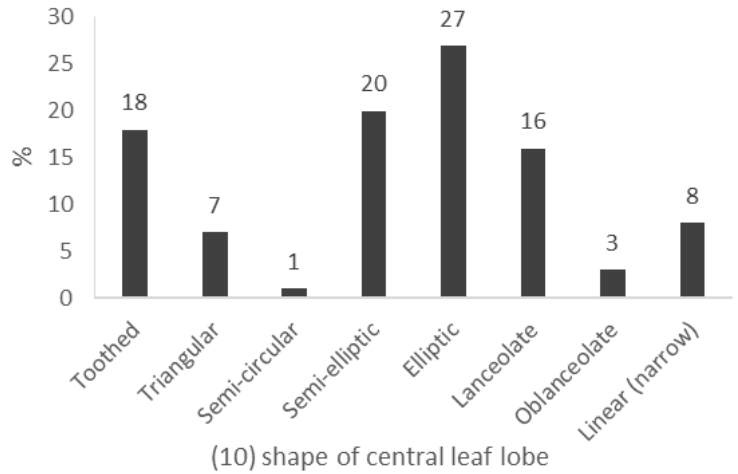
(7) Mature leaf shape



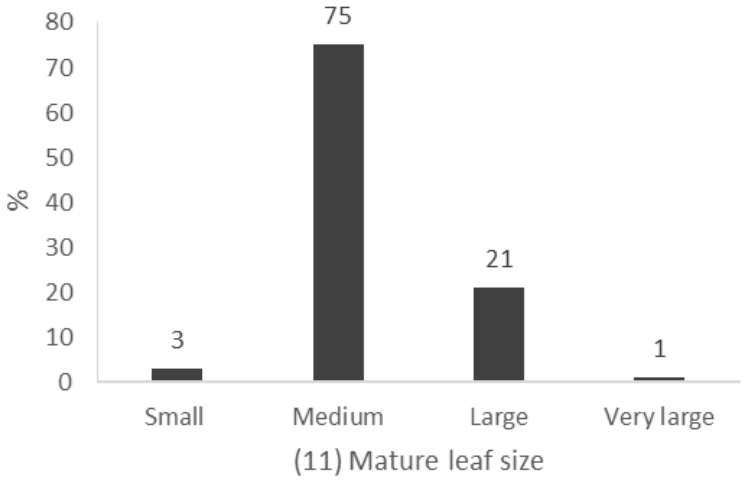
(8) Leaf lobe types



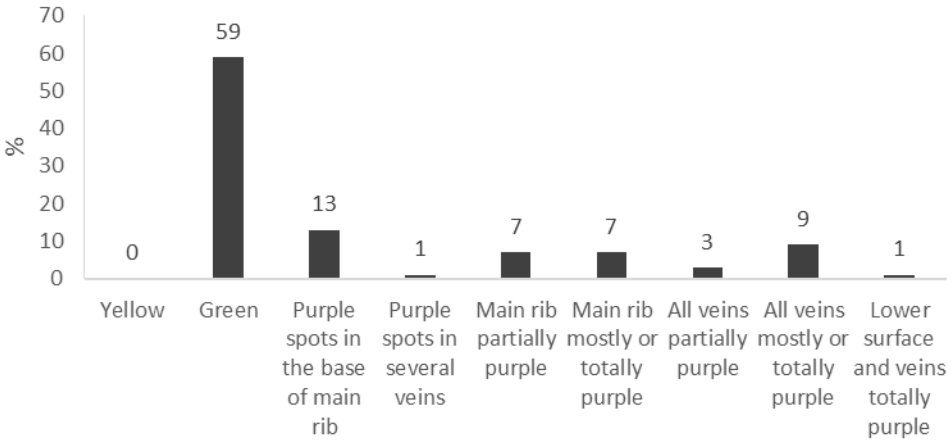
(9) Leaf lobe number



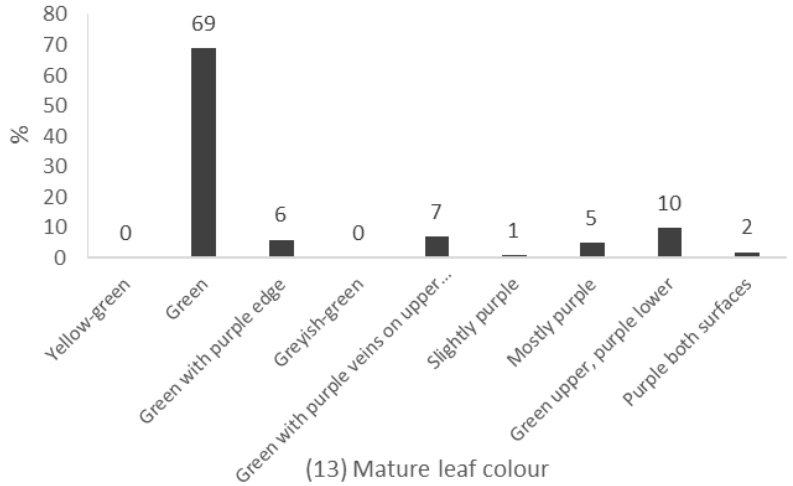
(10) shape of central leaf lobe



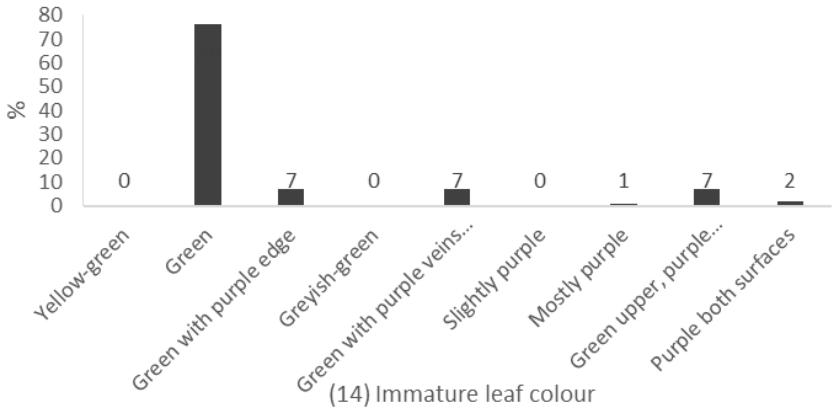
(11) Mature leaf size



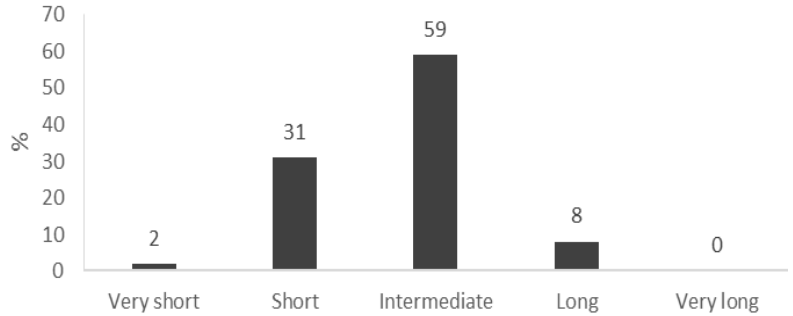
(12) Abaxial leaf vein pigmentation



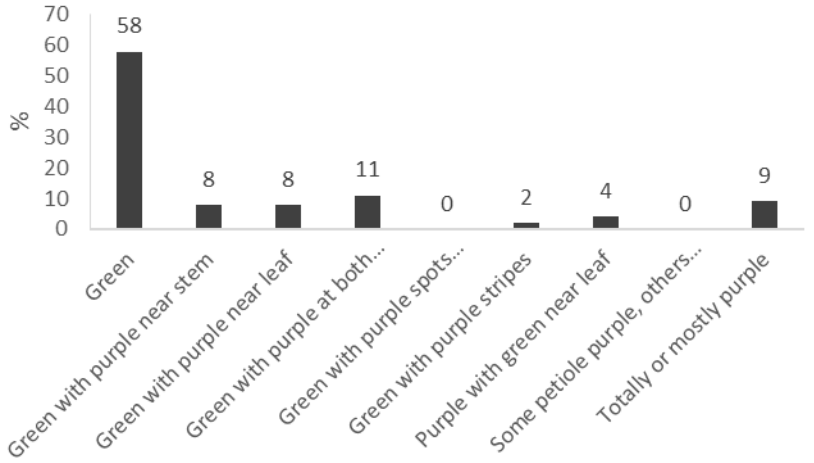
(13) Mature leaf colour



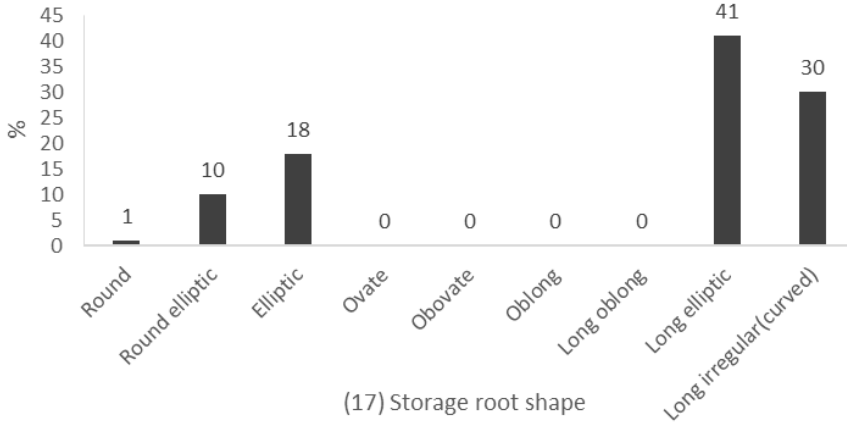
(14) Immature leaf colour



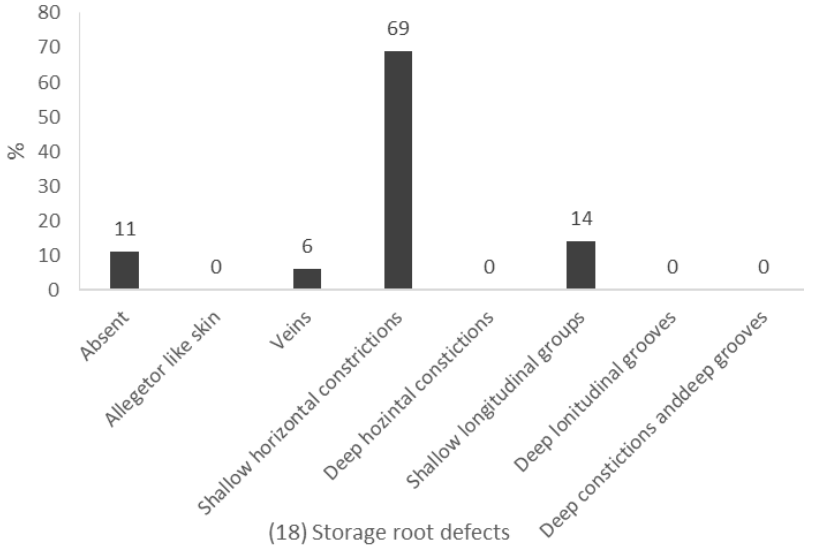
(15) Petiole length



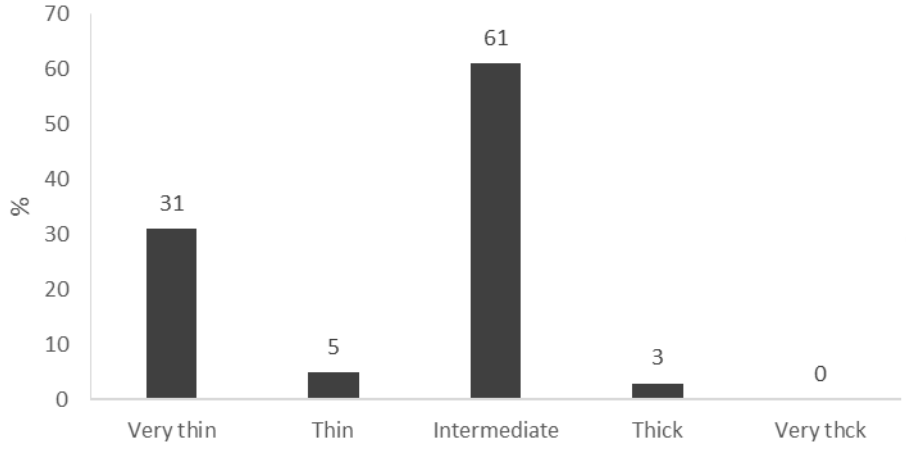
(16) Petiole pigmentation



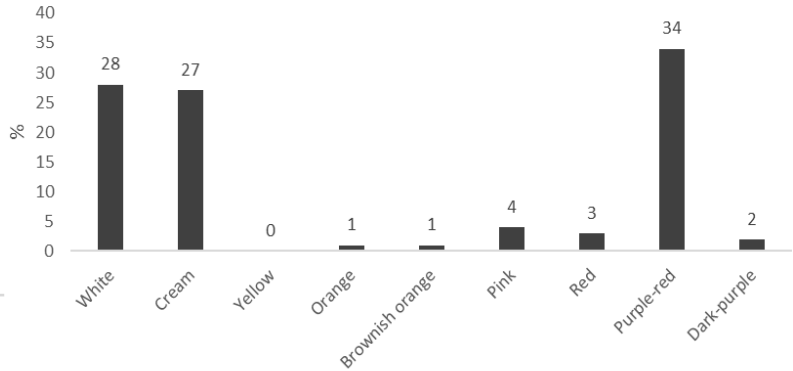
(17) Storage root shape



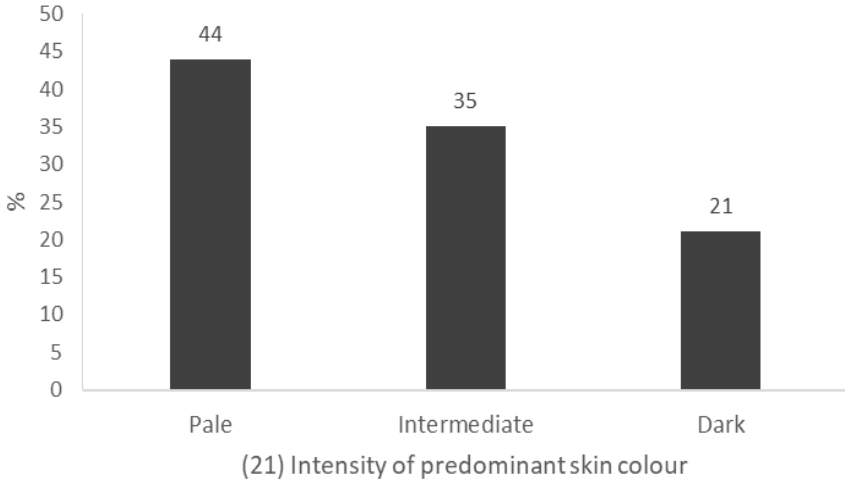
(18) Storage root defects



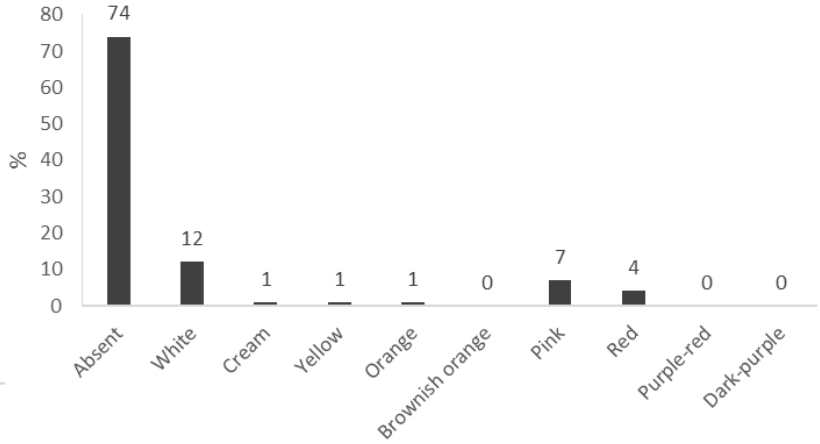
(19) Storage root cortex thickness



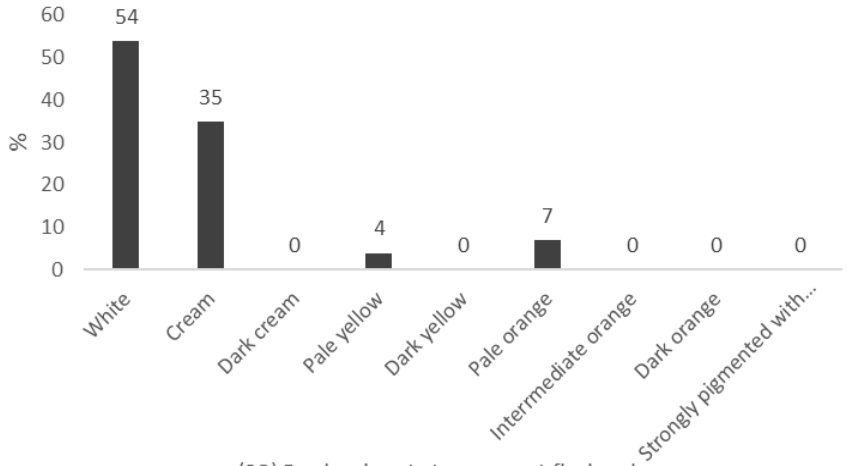
(20) Storage root skin colour



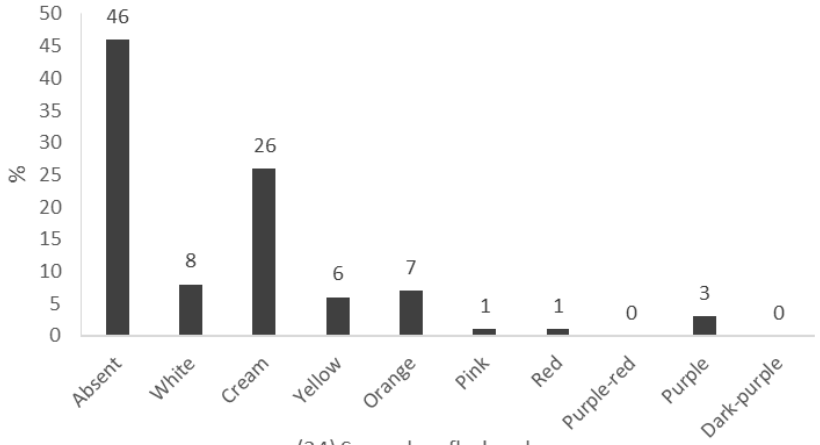
(21) Intensity of predominant skin colour



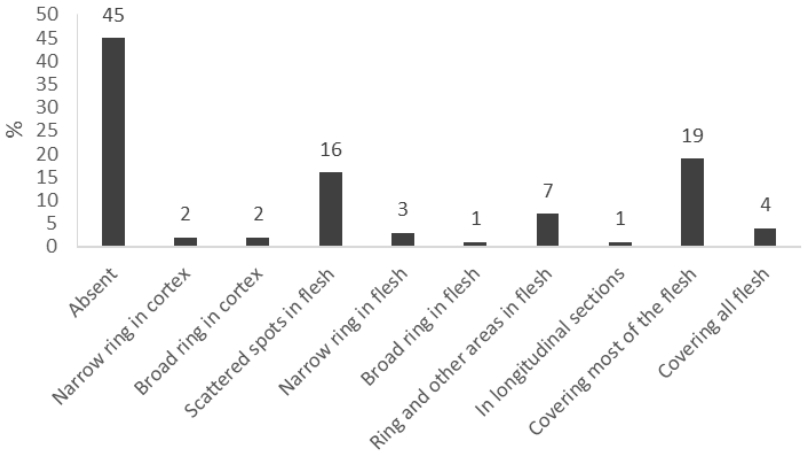
(22) Secondary skin colour



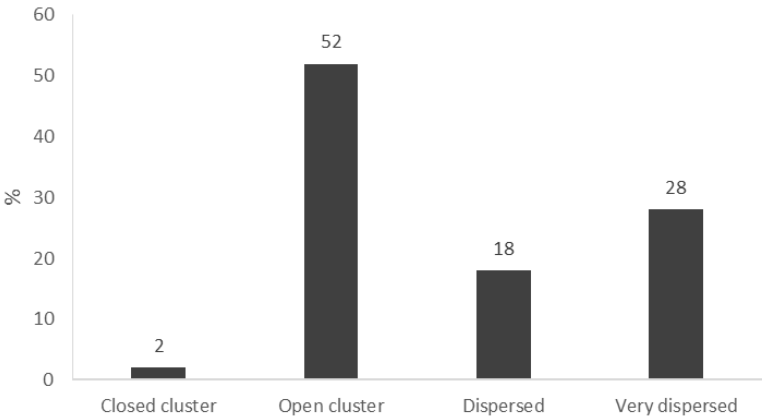
(23) Predominant storage root flesh colour



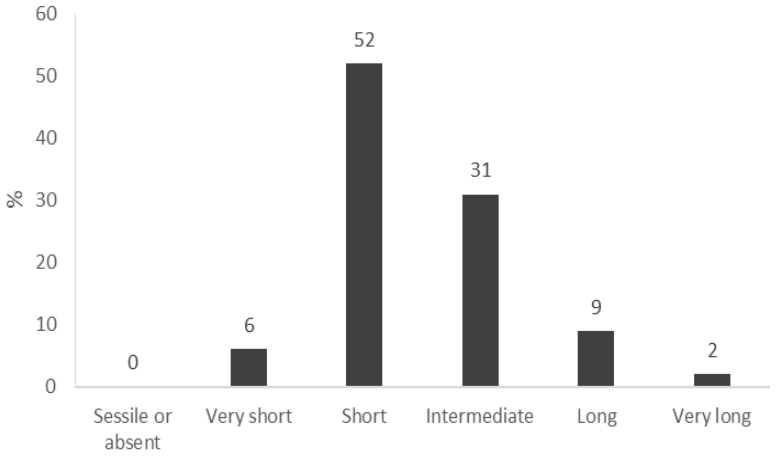
(24) Secondary flesh colour



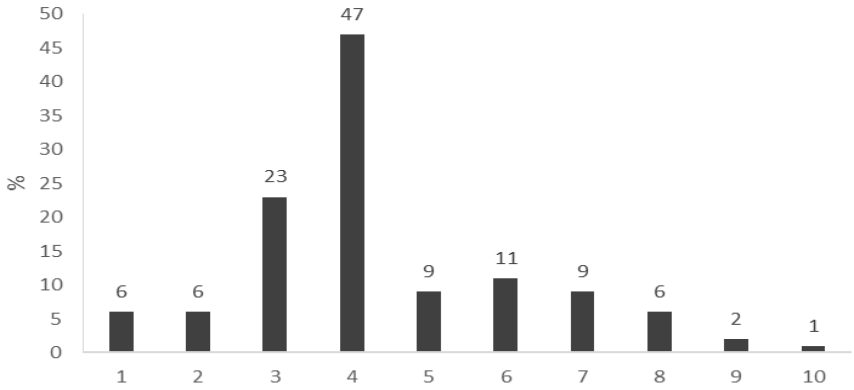
(25) Distribution of secondary skin colour



(26) Storage root formation



(27) Storage root stalk



(28) Number of storage roots per plant

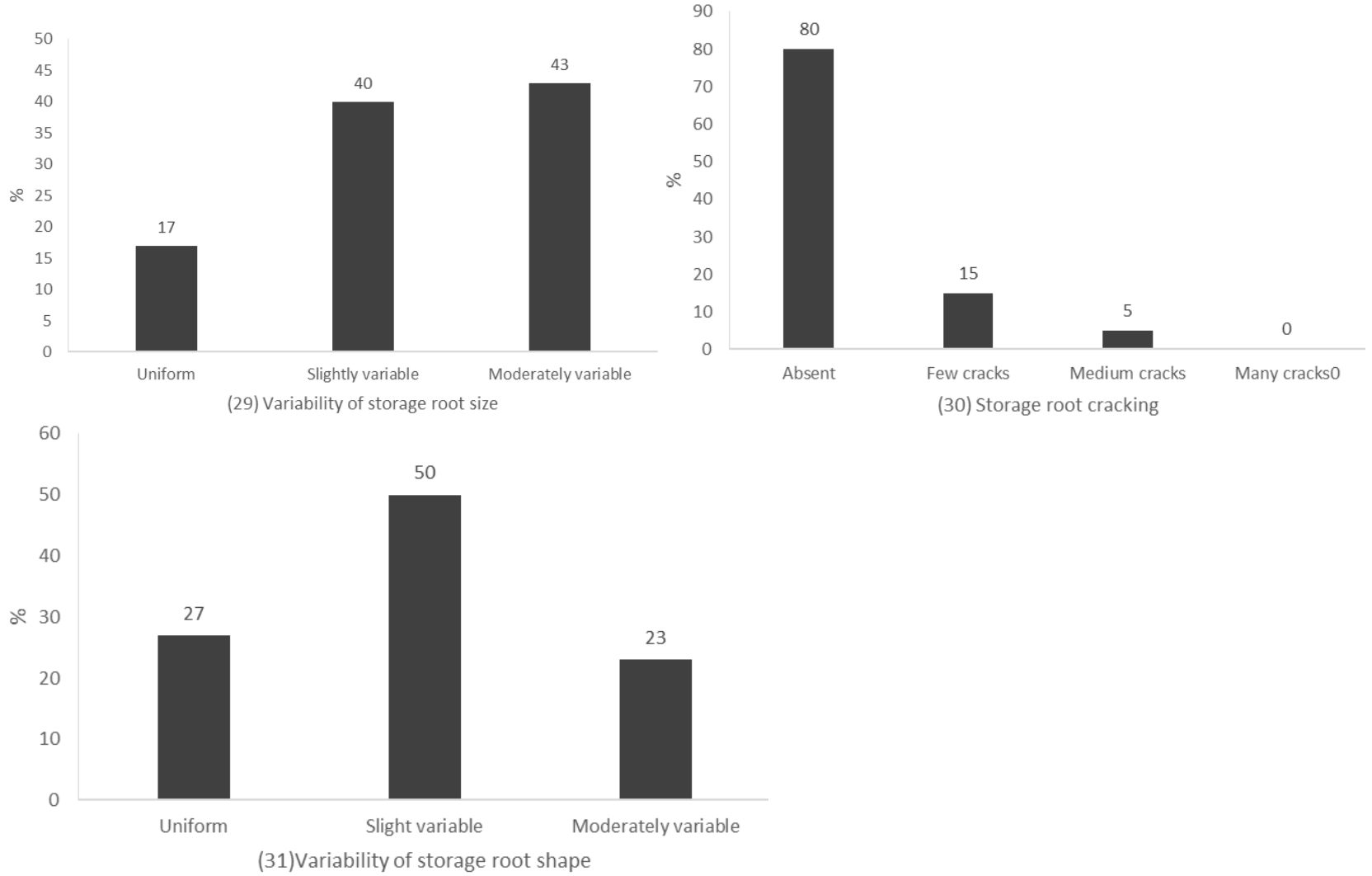


Figure 4.2. Morphological description of sweetpotato genotypes

4.4.2 Cluster analysis

Three distinct clusters were identified from the morphological character analysis (Figure 4.3, 4.4 and 4.5). There were 27, 58, 7 accessions for clusters 1, 2, and 3, respectively. Cluster 2 had two subgroups; 2a and 2b. Subgroup 2a contained 27 accessions (29.3%), while subgroup 2b contained 31 accessions (33.7%) (Table 4.2). The accessions were randomly clustered irrespective of where they were collected from. The following accessions were found to be duplicates: Unknown CA and Bosbook; Hwedza1 and Hwedza 5H; Birchenough and Muzvareshonga; Unknown 1 and Unknown 10T; Chidhumbe dhumbe and Chibikiravaenzi.

The attributes which were common between cluster 1 accessions are; semi-erect plant type, lobed and almost divided leaf shape, green immature and mature leaves, short internodes, thin internodes, 3-5 lobe numbers, medium (8-15 cm) mature leaf size, long elliptical and curved roots, and sparse root formation. While cluster 2a had erect to semi-erect plant types, intermediate internodes, lobed triangular mature leaf shape, 5 leaf lobe number, teethed central leaf lobe, open to dispersed root formation, and elliptic to ovate root shape. Cluster 2b had semi-compact to spreading plant type, green base, deep and very deep lobes, lanceolate central lobes, green and green with purple near leaf petiole, and very thin to thin root cortex thickness (Table 4.2).

Cluster 3 comprised 7 accessions (7%) related through unique attributes. Common attributes among them included; semi-erect plant type, thin vines, almost divided leaf shape, lanceolate, oblanceolate leaf shape, 7-9 lobe number, narrow central leaf lobe, obovate, elliptic storage root, a mixture of white, purple, cream, and pale orange flesh colours (Table 4.2.6). Clusters 1 and 2 had accessions with a characteristic of producing more than 6 roots per plant unlike cluster 3 which had genotypes bearing 5 or fewer roots per plant.

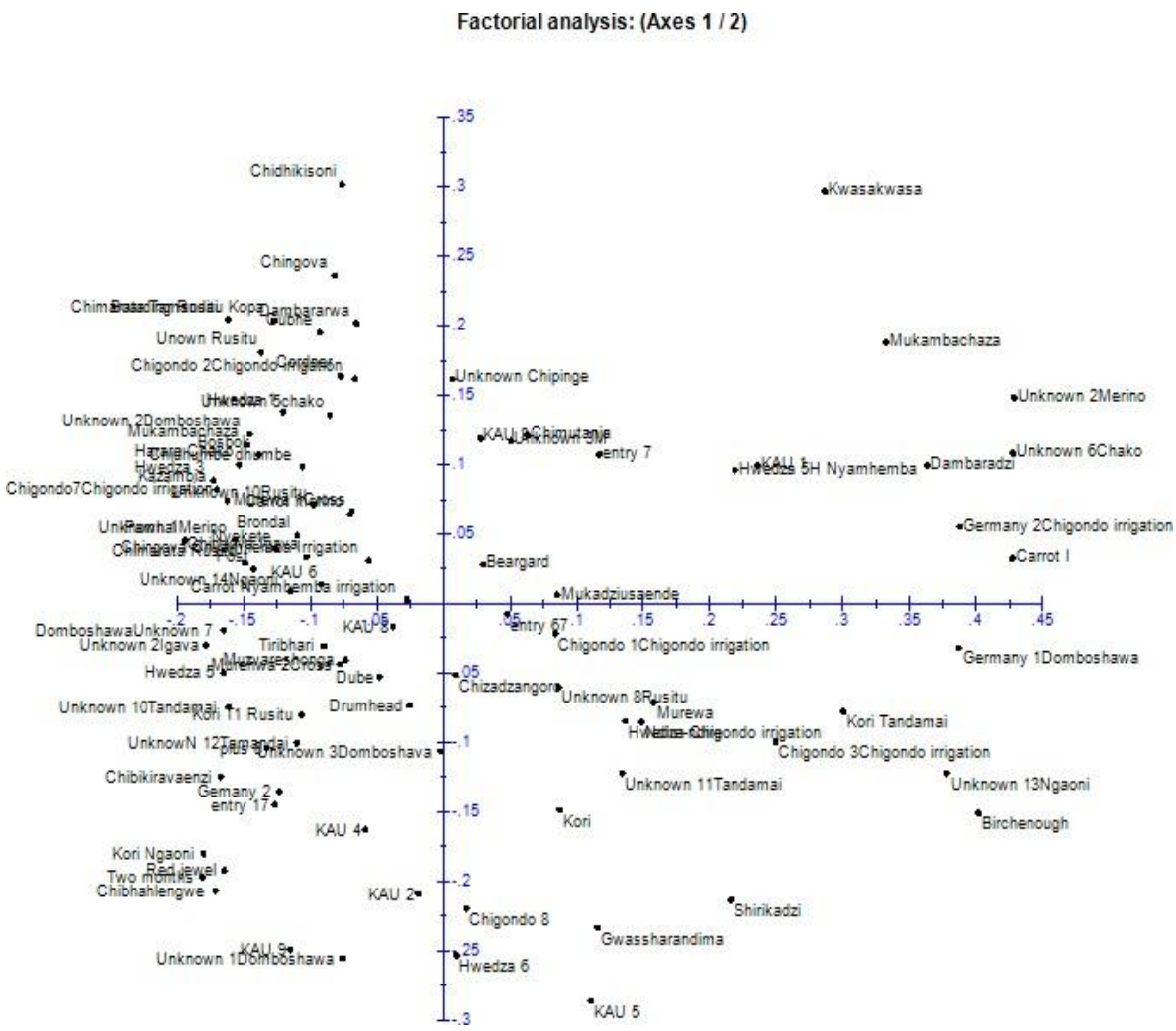


Figure 4.3. Factorial analysis of the 93 sweetpotato genotypes collected from across Zimbabwe

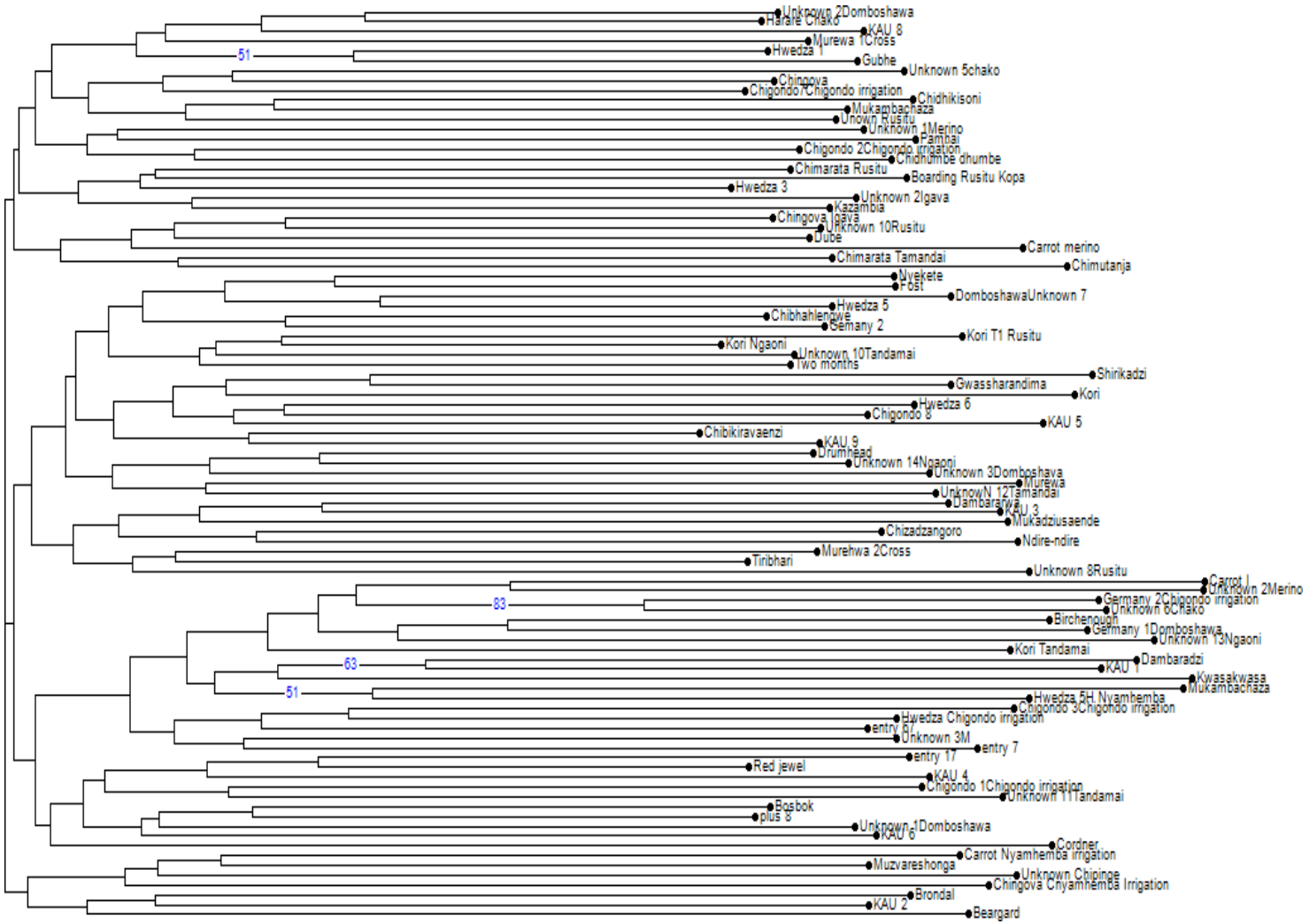


Figure 4.4. Hierarchical cluster analysis of the 93 genotypes collected from across Zimbabwe

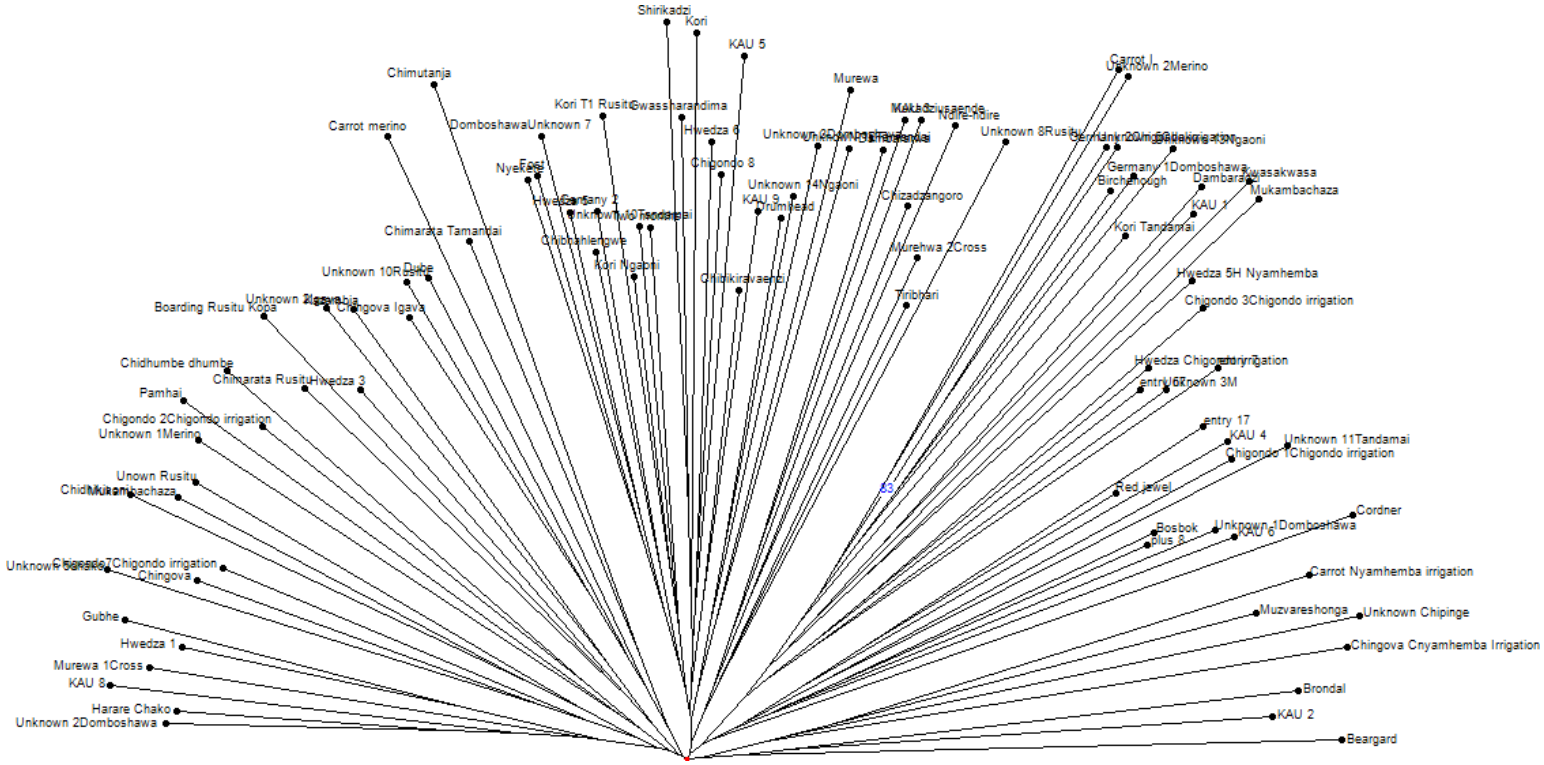


Figure 4.5. Radial tree view of 93 sweetpotato genotypes collected from across Zimbabwe based on 32 morphological attributes

Table 4.2. Main characteristics differentiating the clusters

Major groups	Sub-groups	Genotypes in that group	Major characteristics on those genotypes
1		KAU 8, Chingova, Gubhe, Unknown 5chako, Hwedza 3, Chidhikisoni, Dube, Kazambia, Carrot merino, Unknown Rusitu, Chingova Igava, Chidhumbedhumbe, Pamhai, Chimutanja, Hwedza 1, Unknown 2Domboshawa, Harare Chako, Murewa 1Cross, Unknown 1Chako, Boarding Rusitu Kopa, Chimarata Tamandai, Mukambachaza, Chimarata Rusitu, Unknown 10Rusitu, Chigondo7Chigondo irrigation, Chigondo 2Chigondo irrigation, Unknown 2Igava,	Semi-erect (75-15 cm) plant type, with green vine colour, lobed and almost divided leaf shape, short (3- 5 cm) internode length, thin (4-6 mm) mm) vine internodes. diameter absent/sparse vine tip pubescence, 3-5 lobe numbers, medium (8-15 cm) mature leaf size, green abaxial leaf vein pigmentation, green mature and immature leaf colour, short (10-20 cm) petiole length, green petiole pigmentation, long elliptic and curved roots, shallow horizontal constrictions and shallow longitudinal grooves, open root to very dispersed root formation, absent root cracking and secondary skin colour.
2	2 a	Hwedza Chigondo irrigation, Carrot 1, Unknown 2Merino, Kwasakwasa, KAU1, Entry 17 (Mafutha), Birchenough, Dambaradzi, [Entry 67 (Unknown)], Mukambachaza, Kori Tamandai, KAU 8, KAU7, KAU 4, Red Jewel, KAU6, Unknown 6Chako, Bosbok, Germany 2 Chigondo irrigation, Germany1 Domboshava, Cordner, Unknown 13Ngaoni, Hwedza 5H Nyamhemba, Chigondo 3 Chigondo irrigation, Chigondo 1Chigondo irrigation, Unknown 1Domboshawa, Unknown1 Tamandai	Erect (≤ 75 cm) to semi-erect (75-150 cm) plant type, short (3-5 cm) to intermediate (6-9 cm) internode length, sparse vine tip pubescence, triangular, lobed mature leaf shape, 5 leaf lobe number, teethed central leaf lobe, medium (8-15 cm) mature leaf size, white storage root flesh colour without secondary colour, open to dispersed storage root formation, elliptic to ovate storage root shape and without cracks on the storage root.
2	2 b	Drumhead, Kori Ngaoni, Shirikadzi, Two months, Ndirendire, KAU 3, Murewa, Gwasharandima, Kori	Semi-compact (75-150cm) to spreading plant type (151-250 cm) with green, mostly vine colour with green base, deep and very deep lobes,

Major groups	Sub-groups	Genotypes in that group	Major characteristics on those genotypes
		T1 Rusitu, Murehwa 2Cross, Tiribhari, Dambararwa, Chibikiravaenzi, Chizadzangoro, Unknown10Tandamai, Mukadziusaende, Unknown 14Ngaoni, Unknown8Rusitu, DomboshawaUnknown 7, Unknown 3Domboshava, Unknown N 12Tamandai. Kori, Nyekete, Fost, Hwedza 5, Germany 2, Chibhahlengwe, Hwedza 6, Chigondo 8, KAU5, KAU 9	lanceolate central lobes, green coloured abaxial leaf veins, mature leaf coloured green with green and purple near leaf petiole, long elliptic or curved roots, shallow horizontal constriction on storage root surface, very thin (1mm to thin (1-2 mm) root cortex thickness.
3		Carrot Nyamhemba Irrigation. Muzvareshonga, Unknown Chipinge, Chingova C Nyamhemba Irrigation, Brondal, KAU2, Beauregard.	Semi-erect (75-150 cm) plant type, thin (4-6 mm), green vine colour with purple spots, secondary vine colour with green tip and base, almost divided leaf shape, deep lobe type, 7 to 9 lobe number, lanceolate, oblanceolate, narrow central leaf lobe, medium (8-15) to large (16-25) green abaxial leaf vein pigmentation with main rib partially purple or mostly or totally purple, green mature leaf colour with few purple veins on the upper surface, green upper and purple lower, green immature leaf colour with short (10-20 cm) petiole length, green petiole pigmentation, green with purple near leaf, long elliptic or curved storage root shape, shallow horizontal constrictions storage root surface defects, very thin (1 mm) to thin (1-2 mm) storage rootcortex thickness, white, purple-red, cream storage root skin colour, pale orange, cream storage root flesh colour, cream, yellow, orange secondary flesh colour, obviate, elliptic variability of storage root shape, absent to few cracks on storage root.

4.5 Discussion

The findings of this study will serve as an important foundation in sweetpotato breeding in Zimbabwe. Many morphological characters were scored in this study. There was evidence of a wide range of phenotypic classes which is critical in future breeding efforts. This is supported by the observed 174 classes across all attributes though classes within an attribute ranged from 3 to 10.

The high variation in plant type, vine internode length and pigmentation, leaf lobe type and number, the shape of central lobe, mature leaf shape, abaxial leaf vein pigmentation, petiole pigmentation, petiole length, storage rootstalk length, storage root per plant, storage root formation, predominant flesh colour, secondary flesh colour, storage root skin colour, storage root shape and size, distribution of secondary skin colour, the intensity of predominant skin colour and predominant storage root skin colour could be exploited by breeders for developing new varieties. The huge variation could be a result of a response to environmental influences. These results validate what was observed by Alves et al. (2017)). In separate studies, Alves et al. (2017) reported that root surface defects, secondary pellicle skin colour and secondary flesh colour caused divergence in the grouping. However, in this study root surface defects did not contribute much variation among the evaluated accessions. Su et al. (2016) reported natural mutations as the force behind huge variability among sweetpotato accessions and this could be a contributing factor in the observed variations.

The attributes that contributed less variability were: mature leaf size, 75% of the genotypes had amedium size between 8-15 cm; mature leaf colour (69% green- coloured); immature leaf (76% green-coloured; secondary vine colour, from which 77% of the accessions had green tips, storage root surface defects of which 69% of the accessions had shallow horizontal constrictions, storage root cortex thickness, vine internode diameter, of which 78% of the accessions had thin (4-6 mm) vines, vine tip pubescence which had 69% of the accessions. These characters are not highly influenced by the environment thus why they exhibited less variation among the genotypes.

Fusco et al. (2010) indicated that the majority of attributes depict differences among the population under study. Yada et al. (2010) and Fongod et al. (2012) reported similar findings while working on sweetpotato accessions. Karuri et al. (2010) reported that for asexually propagated

species such as sweetpotato the differences are a result of somatic variation and due to selection by farmers. In addition, Lule (2012) and Soares et al. (2015) indicated that apart from genetic influences, differences in cultivated species could be caused by artificial selection in diverse geographical conditions. Farmers grow sweetpotato mainly for the storage roots which are of economic importance. The accessions significantly differed in terms of root shape, storage root skin, root size, and root flesh colour. These differences are important since they can be exploited as markers for breeding purposes. Most accessions had no root surface defects which is most preferred by farmers and consumers. Nwankwo et al. (2015) reported that smooth storage roots are easier to clean and peel than rough ones hence most favoured by consumers. In Zimbabwe, the majority of sweetpotato accessions are white and cream coloured and very few yellow and orange-fleshed genotypes. Constant selection by farmers for these varieties over time could have played a part. Sweetpotato farmers grow different varieties for different purposes and they derive different satisfaction from each of them.

The identified variation among the accessions can be useful to farmers, breeders and consumers. Different skin, vine and flesh colours, leaf shapes and leaf outlines are used by farmers and breeders to identify and or name sweetpotato genotypes. The observed variation is an opportunity for breeders to identify important attributes for crop improvement. In Zimbabwe, skin colour is very important because markets such as the Mbare market prefer white-skinned types yet the Bulawayo market favours purple-skinned sweetpotato. Gasura et al. (2008) reported that skin colour was very important because it has a bearing on market preference and individual buyers. Thomas-Sharma et al. (2016) indicated that the selection of parents of vegetative propagated crops is based on yield, resistance to diseases and insects, and root shape and size. Nair (2017) reported that orange and yellow-fleshed sweetpotato genotypes are renowned as reliable sources of carotene yet light-fleshed sweetpotato are good sources of Vitamin C. In addition, Ray et al. (2012) reported that purple-fleshed genotypes are important in the food industry due to their richness in anthocyanins. Toan et al. (2019) pointed that purple-coloured genotypes are very important in food processing industries as food colourants for purple flour and paste for bread, snacks and noodles consequently the observed variation in sweetpotato accessions can be of immense value in the confectionary industry of Zimbabwe. Leaves of sweetpotato are rich in lutein, another type of carotenoid importantfor the prevention of ageing Menelaou et al. (2006). Apart from making weaning food, sweetpotato roots are important in the preparation of pickles,

sauce, sweets and soft drinks in India (Zhang et al., 2018). The genotypes had different numbers of roots per plant–a characteristic that offers an opportunity of increasing the number of roots for genotypes that produce far fewer rootsbut have other beneficial attributes desired by farmers and the market.

There is a school of thought that sweetpotato storage root yield is a function of the number of storage roots per plant (Villordon et al., 2009). In this, study storage root yield was inversely related to the number of storage roots per plant. The fewer the number of storage roots the higher the storage root yield mainly because fewer storage roots grew bigger than those from numerous storage roots that were thinner. Root length also varied among the genotypes, which offers an opportunity for breeding for medium-sized roots which do not easily break-a desirable attribute by farmers andmarkets. Most genotypes exhibited a semi-erect and a few genotypes had spreading and erect growth habits. Genotypes with semi-erect growth habits might be more preferable for intercrop. Farmers may like few branches in intercropping since it would be ideal for smothering weeds. On the other hand, accessions with spreading growth habits could be ideal for commercial vine produces since more vines would be got within the shortest time possible. Gasura et al. (2008) reported that vine length and stem thickness were highly heritable and maternally inherited, hence their improvement was easy but should be done in line with farmer preferences. Genotypes with spreading growth habits might be beneficial as animal feed especially in drier areas.

4.5.1 Cluster analysis

Three distinct clusters were identified from the morphological character analysis, with Cluster 2 having two subgroups 2a and 2b. Of interest is that the genotypes were randomly clustered, thus accessions were grouped irrespective of where they were collected. Some genotypes bearing the same names clustered differently, an example being Chingova collected from Igava and Chingova from the Horticulture Research Centre fell into subgroup 2a, whereas Chingova from Nyamhemba irrigation scheme fell into Group 3. Another example was Kori T1 Rusitu, Kori Ngaoni and Kori from the Horticulture Research Centre grouped together in subgroup 2b, but Kori Tamandai fell into subgroup 2a. Yada et al. (2010) had similar observations of the absence of association between sweetpotato genotypes and places of collection in Uganda and this might be due to extensive exchanges of planting material among farmers and at marketing places. The results from this study are in agreement with the findings of Laurie et al. (2013) who failed to get any association

between accessions and their places of collection.

Some et al. (2014) indicated that duplicate samples could be a result of growing sweetpotato genotypes for a long time. In some cases, duplicates bear different names in different locations. Sharing of vines among farmers for a long period could also contribute to naming the same genotype with different names. Veasey et al. (2008) implicated a lack of structuring among genotypes and places of origin. This could also point to a common ancestry among the genotypes. noted that farmers identified sweetpotato genotypes through the shape of leaves,maturity time, root colour and flesh colour and taste after cooking. In this study, names of genotypes were influenced by the name of a person or organization that introduced the cultivar inthe particular area. An example was the cultivar Fost which derives its name from a local donor organisation; Gwasharandima and Kori bearing people's names. Informal naming of sweetpotato complicates the traceability of sweetpotato accessions. Surprisingly, only 51accessions had names out of 100 accessions. The current study revealed that one could not precisely identify sweetpotato genotypes without relating to morphological attributes. Elias et al. (2000) and Glato et al. (2017) made similar observations while working on sweetpotato and cassava, respectively.

4.6 Conclusion

The Zimbabwean sweetpotato diversity is structured by genetics and morphology and not by geography. Morphological analysis managed to identify duplicates thus enhancing conservation efforts in Zimbabwe. There is great variability among the Zimbabwean sweetpotato genotypes which can be beneficial for future sweetpotato breeding efforts. In all the three clusters, local accessions and some improved varieties grouped together and this confirms the presence of genetically distinct local accessions, which are closely similar to the improved varieties in their morphological traits.

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CHAPTER 5

POPULATION STRUCTURE AND GENETIC DIVERSITY ASSESSMENTOF INTRODUCED AND LOCAL SWEETPOTATO GERMPLASM IN ZIMBABWE

Abstract

Sweetpotato [*Ipomoea batatas* (L.) Lam] is a strategic staple crop in Zimbabwe, second to Irish potato. There has been no genetic diversity work done on the Zimbabwe collections that I worked with. Understanding sweetpotato diversity and population structure is thefoundation of breeding, and conservation initiatives. Ninety- eight sweetpotato genotypes consisting of introduced and local accessions from Zimbabwe were subjected to genotyping by sequencing. Two groups were inferred using both structure software and silhouette plots in RStudio. The smaller group had four individuals that are Bosbok, UnknownC4, Kwasakwasa C, and Kau7. These individuals had large Gower's genetic distances of 2.54, 2.37, 1.65, and 3.20, respectively, compared to others. Analysis of molecular variance showed a very low PhiPT value(equivalent to FST value) of -0.017 suggesting that these sub-populations could come from the same major population. The dendrogram produced can direct future breeding activities and conservation strategies for sweetpotato.

5.1 Introduction

Sweetpotato is an important staple crop for rural and urban Zimbabweans. Price rocketing of other staples such as maize, wheat, rice, and Irish potato has caused an increase in the importance of sweetpotato. (Mutandwa, 2008) reported that sweetpotato is considered a food security crop partly because of its reliable yields, ease of multiplication through vines and low input requirements. Eriksson et al. (2018) observed that even though there are some improved sweetpotato cultivars in sub-Saharan Africa most smallholder farmers are still dependent on unimproved sweetpotato cultivars.

In support of this proposition, (Zamir, 2001) noted that landraces have desirable genes for breeding hence the need for molecular characterization. Gasura et al. (2008) also stated that sweetpotato is endowed with high genetic variability which allows it to exploit diverse habitats. Emanuelli et al. (2013) raised the importance of both morphological and molecular characterization in isolation of duplicates, identification of unique attributes and population structure for conservation, thus economizing storage space.

Lammerts van Bueren et al. (2010) reported that molecular markers are ideal for plant characterization because they are stable against environmental influences. The discovery of contemporary molecular markers such as the single nucleotide polymorphism has made it possible to understand whole genomes, makes automation easier, and provides highly reproducible results (Semagn et al., 2006). Therefore, this studyaimed at assessing the sweetpotato population structure and genetic diversity of local and introduced cultivars in Zimbabwe through genotyping by sequencing approach.

5.2 Materials and Methods

5.2.1 Plant materials

Fresh, tender, two-week old leaves were sampled from field grown accessions. A leaf was placed on the cutting mat before collecting leaf disks by the leaf cutting punch rotated back and forth. The respective disks were removed from the punch by depressing the plunger on top of the punch. Ten leaf disks were collected for each accession. The leaf punch device was sterilized with 70% alcohol before punching the next leaf to prevent cross contamination.

Leaf fresh disks were placed in the oven without caps and dried overnight in a drying oven at 35^0C. Once leaf disks were completely dry to prevent fungal growth then the strips were covered with caps. Two 96-well plates were used in this study-the second well plate carrying only two accessions. The lids were secured using elastic band and placed in the sealed rack into the large sealable bag. Excess air was forced out of the bag and sealed tightly. The sealed bag was placed into the shipment kit box and shipped to BeCA-Hub-ILRI laboratories in Nairobi, Kenya. In this study, ninety-eight (98) sweetpotato accessions were used as described in Chapter 3. The samples were 100 in total but two samples were contaminated to the point that the results were considered unreliable.

5.2.2 Genotyping

DNA extraction was done with the modified Cetyl Trimethyl Ammonium Bromide (CTAB) method (Saghai-Maroof et al. 1984). Quality check for DNA was done using an agarose gel. Spectrophotometer was used to establish the quantity of DNA and this was followed by genotyping by sequencing (GBS) for single nucleotide polymorphism (SNP) marker discovery. The wild relative of sweetpotato (*Ipomoea trifida* L.) was used as the reference genome.

5.2.3 Data analysis

The number of groups among the sweetpotato accessions was established by the use of Structure software (Pritchard et al. 2000) with a burning length of 5000 and MCMC of 50 000 (Ana et al., 2014). The online genetic software Structure Harvester (Earl and vonHoldt, 2012) was used to visualize the results of the structure analysis following the Evanno approach. The bar plot showing the proportion of genomes in an individual coming from different populations was produced at K=2 since two groups were inferred.

The Silhouette plots were also produced in RStudio to determine the possible number of clusters present. The cluster analysis was done using RStudio software to show the inferred groups using the Gower's distance (Gower, 1971) and neighbour-joining algorithm. Two groups were suggested by the silhouette using RStudio like structure. The dendrogram was then sub-divided into two groups using the cut option of the RStudio (Team R, 2015). This was then followed by subjecting the genotypic data to the analysis of molecular variance (AMOVA) using GenAlEx software version 6.5 (Meirmans, 2012; Peakall and Smouse, 2012) with the assumption that there were two groups as shown by structure and silhouette plots.

5.3 Results

The Evanno method showed the highest peak for delta K at K=2 (Figure 5.1 and Table 5.1) and the silhouette plot suggested the existence of two groups as well (Figure 5.2). The two groups shared their genomes almost equally (Figure 5.3). Part of the genetic distances are shown in Table 5.2. The smaller group had four individuals out of a total of 98, and these individuals are Bosbok, UnknownC4, KwasakwasaC, and Kau7 (Figure 5.3). The four genotypes showed an average Gower's genetic distance from other genotypes which were larger 2.5, 2.37, 1.65, and 3.20, respectively (Table 5.3). After the analysis of molecular variance done for comparing the four genotypes to the rest of the genotypes, the percentage variance among the population came to zero resulting in 100 percent variation within populations (Table 5.4). Furthermore, the PhiPT value (equivalent to FST value) was very low-0.017.

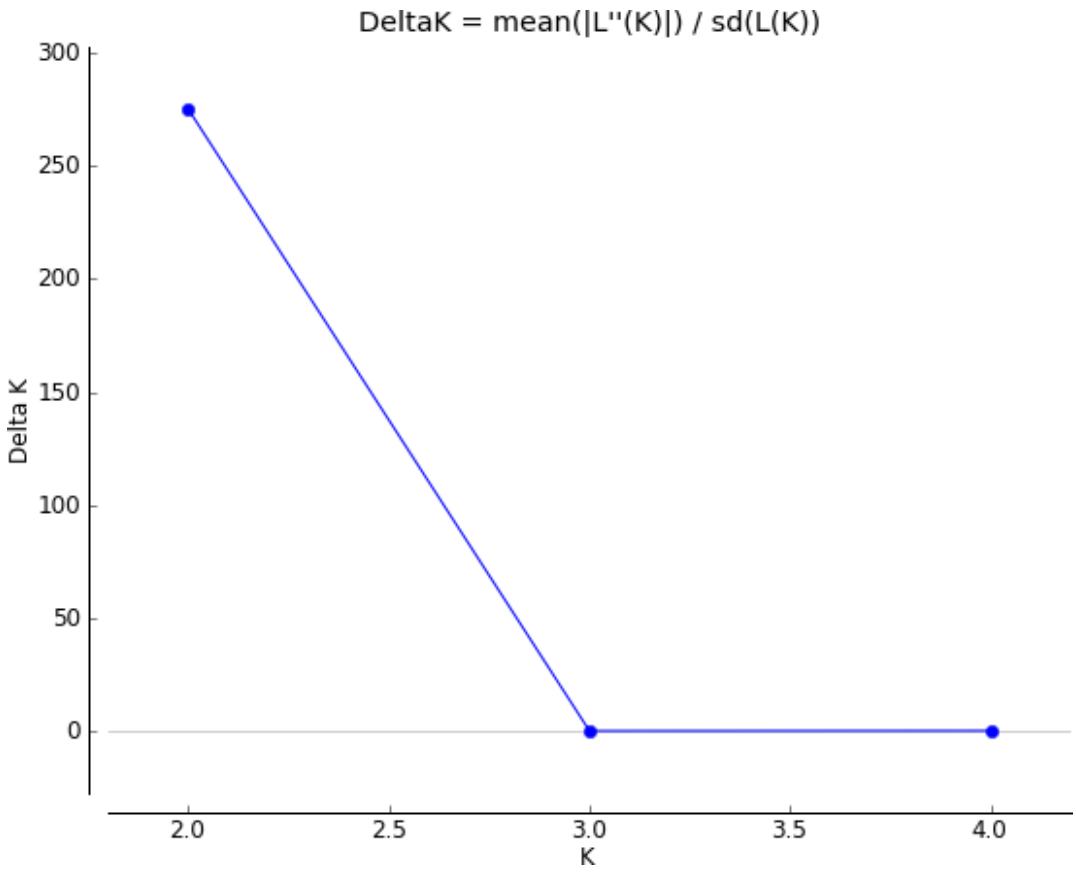

Figure 5.1. The ad hoc statistic for Δk computed for k varying from 1 to 5 from which the best k was selected at 2.

Table 5.1. Absolute values of the ad hoc statistic for Δk computed for k varying from 1 to 5 from which the best k was selected at k=2.

K	Reps	Mean LnP(K)	Stdev LnP(K)	Ln'(K)	|Ln''(K)|	Delta K
1	3	-503136.233333	528.814810	—	—	—
2	3	-493569.700000	30582.381666	9566.533333	8414263.733333	275.134351
3	3	-8898266.900000	14083044.548697	-8404697.200000	303651.066667	0.021561
4	3	-17606615.166667	15569811.831051	-8708348.266667	1329526.033333	0.085391
5	2	-24985437.400000	34325418.374961	-7378822.233333	—	—

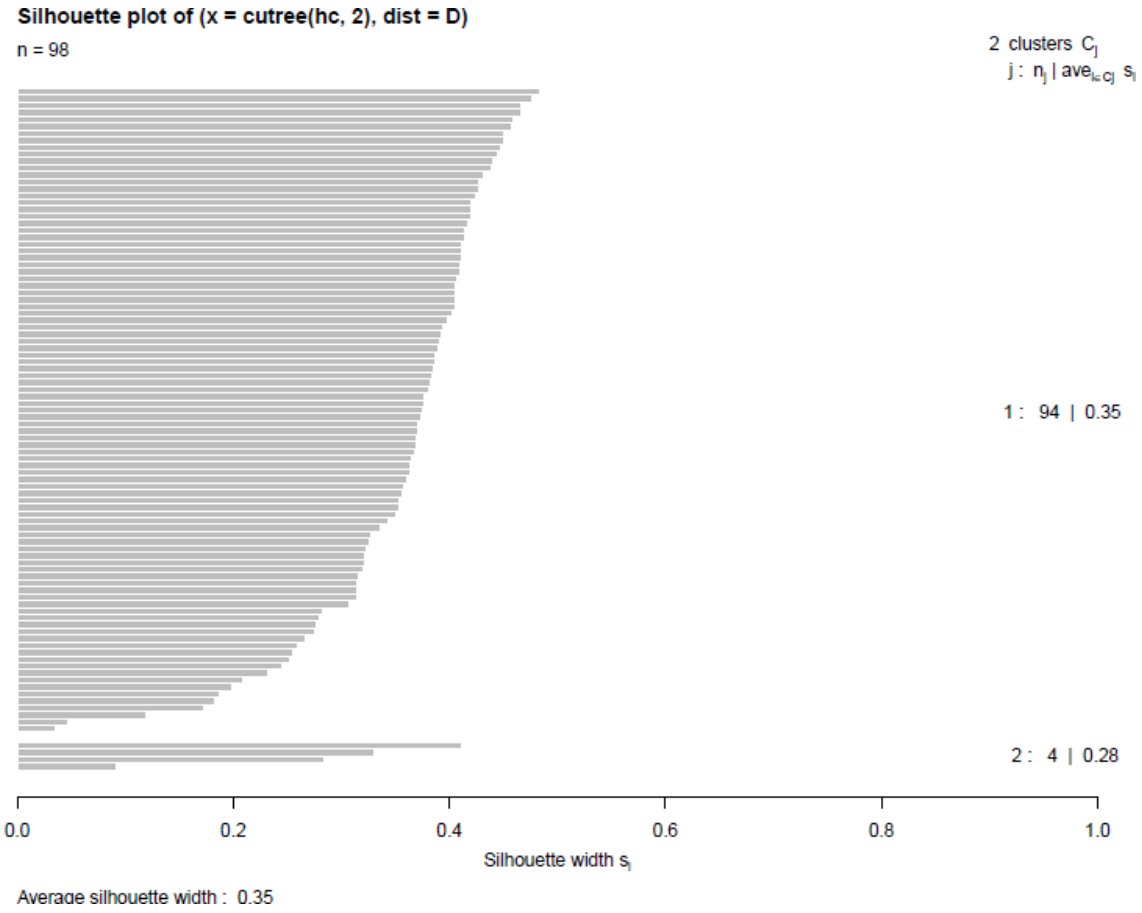

Figure 5.2. Silhouette plot shows that two groups are possible according to RSoftware

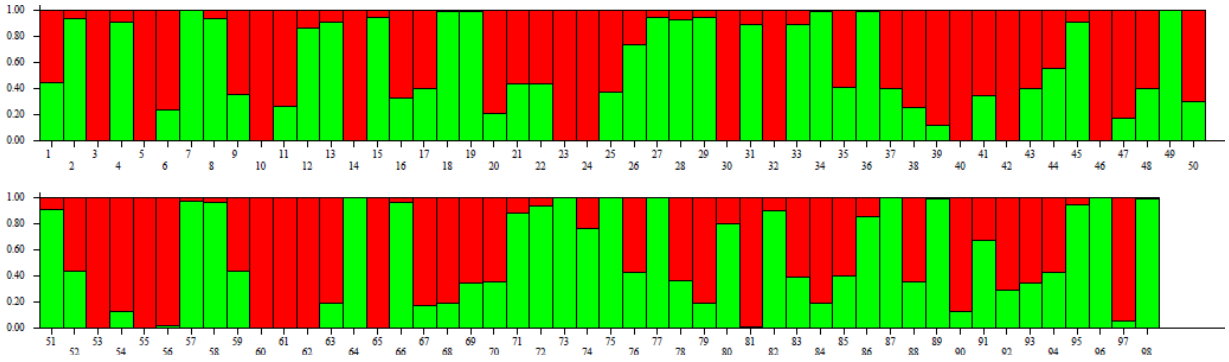

Figure 5.3. Bar plot of model-based quantitative clustering showing proportion of genome of individual genotypes for 98 sweetpotato accessions at K=2 used for genetic diversity studies with thousands of SNP markers

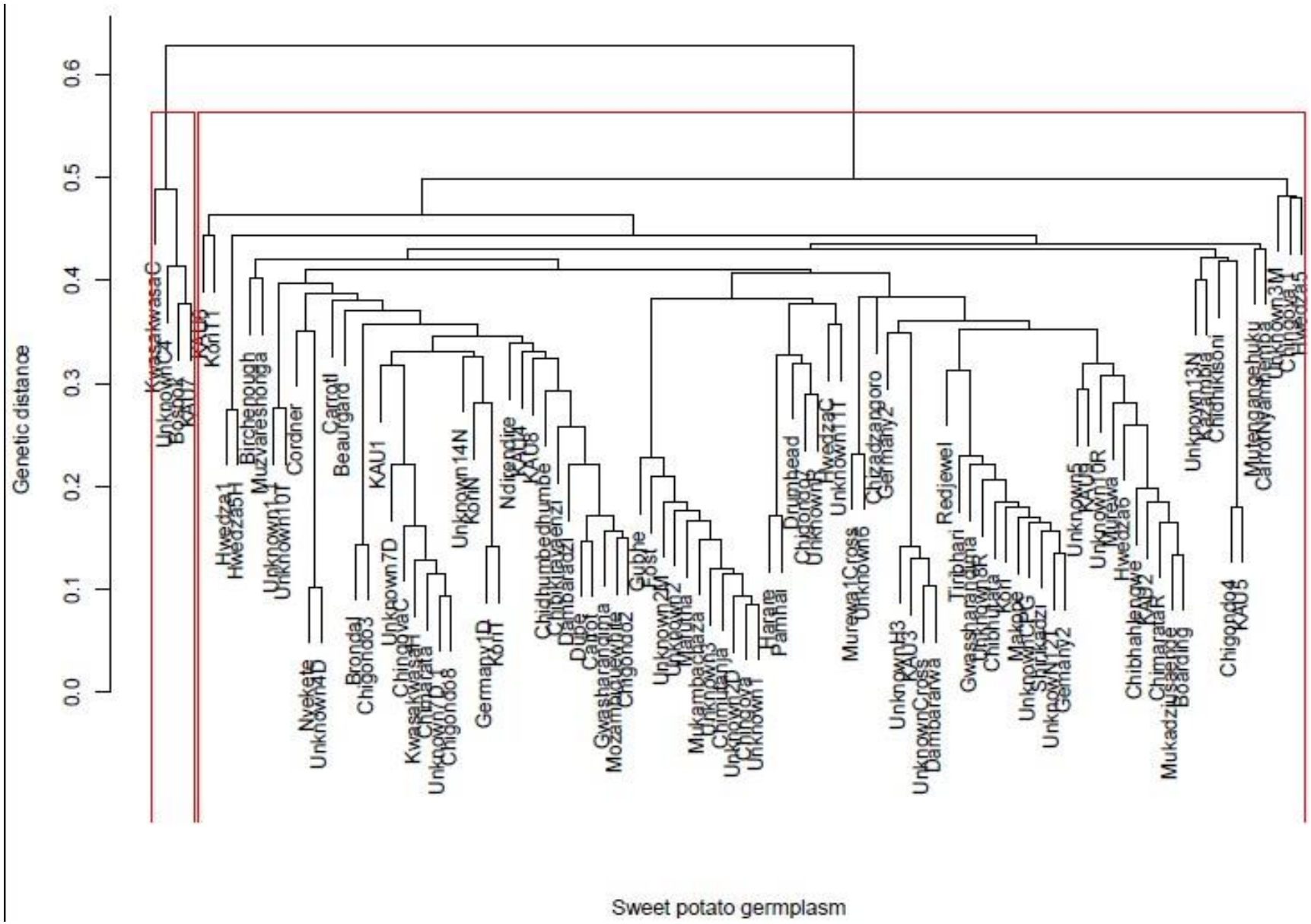

Figure 5.4. Dendrogram showing relationship among the 98 sweetpotato accessions

Table 5.2. A portion of the distance matrix showing eight out of the 98 sweetpotato genotypes evaluated

	KAU6	Tiribhari	Unknown5	Birchenough	UnknownH3	Chingova	Chimarata	Kori
KAU6	0	1.301308	0.938554	0.945988	1.33509	1.53994	1.540638	1.466568
Tiribhari	1.301308	0	0.908192	0.897737	0.80201	1.133146	0.890782	0.407831
Unknown5	0.938554	0.908192	0	0.83179	1.017982	1.364399	1.250488	1.079206
Birchenough	0.945988	0.897737	0.83179	0	0.877417	1.142132	1.090251	1.002636
UnknownH3	1.33509	0.80201	1.017982	0.877417	0	0.992806	0.921124	0.803817
Chingova	1.53994	1.133146	1.364399	1.142132	0.992806	0	1.189948	1.139159
Chimarata	1.540638	0.890782	1.250488	1.090251	0.921124	1.189948	0	0.821801
Kori	1.466568	0.407831	1.079206	1.002636	0.803817	1.139159	0.821801	0
Chizadzangoro	0.970093	0.848414	0.64024	0.746296	0.811794	1.164376	1.07976	0.974335
Unknown3M	0.819092	1.396992	1.02533	1.102814	1.490369	1.638511	1.813757	1.593631
Gubhe	1.205507	1.056334	1.100044	0.929765	0.975363	0.519335	1.207178	1.140718
Unknown2M	1.343513	1.058619	1.206326	0.998549	0.938762	0.358807	1.165201	1.100598
Dube	1.232649	1.043457	1.253586	0.999923	1.102243	1.274642	0.817741	1.070192
KAU9	0.9923	0.938548	0.443503	0.878294	1.029731	1.404977	1.240177	1.08947

Table 5.3. Estimated genetic distances among genotypes with emphasis given to the four individuals that belong to a separate cluster

	Bosbok	Muzvareshonga	Shirikadzi	Chingova.1	Fost	Unknown C 4	Hwedza5H	KwasakwasaC	Pamhai	KAU7	Dambararwa	Dambaradzi	Gemany2	Carrot	Average in current genotypes	Average in all genotypes
Bosbok	0.00	2.39	2.98	1.49	2.60	0.68	1.87	1.24	2.60	0.90	2.85	2.51	3.02	2.77	**1.99**	**2.54**
Muzvareshonga	2.39	0.00	0.99	1.18	0.92	2.22	0.88	1.43	0.66	3.08	0.91	0.87	1.02	0.97	1.25	0.91
Shirikadzi	2.98	0.99	0.00	1.75	1.19	2.81	1.46	2.02	0.93	3.65	0.82	1.22	0.26	1.18	1.52	1.04
Chingova.1	1.49	1.18	1.75	0.00	1.46	1.34	0.89	0.80	1.42	2.15	1.61	1.41	1.79	1.63	1.35	1.43
Fost	2.60	0.92	1.19	1.46	0.00	2.40	1.20	1.67	0.92	3.27	1.01	1.17	1.17	1.19	1.44	1.06
Unknown C4	0.68	2.22	2.81	1.34	2.40	0.00	1.73	1.12	2.42	1.08	2.62	2.35	2.84	2.62	**1.87**	**2.37**
Hwedza5H	1.87	0.88	1.46	0.89	1.20	1.73	0.00	1.03	1.06	2.53	1.37	1.11	1.50	1.32	1.28	1.21
KwasakwasaC	1.24	1.43	2.02	0.80	1.67	1.12	1.03	0.00	1.66	1.86	1.88	1.58	2.06	1.83	**1.44**	**1.65**
Pamhai	2.60	0.66	0.93	1.42	0.92	2.42	1.06	1.66	0.00	3.28	0.80	1.00	0.93	1.03	1.34	0.94
KAU7	0.90	3.08	3.65	2.15	3.27	1.08	2.53	1.86	3.28	0.00	3.52	3.17	3.69	3.45	**2.55**	**3.20**
Dambararwa	2.85	0.91	0.82	1.61	1.01	2.62	1.37	1.88	0.80	3.52	0.00	1.20	0.80	1.18	1.47	1.00
Dambaradzi	2.51	0.87	1.22	1.41	1.17	2.35	1.11	1.58	1.00	3.17	1.20	0.00	1.27	0.43	1.38	1.04
Gemany2	3.02	1.02	0.26	1.79	1.17	2.84	1.50	2.06	0.93	3.69	0.80	1.27	0.00	1.22	1.54	1.06
Carrot	2.77	0.97	1.18	1.63	1.19	2.62	1.32	1.83	1.03	3.45	1.18	0.43	1.22	0.00	1.49	1.07
	1.99	1.25	1.52	1.35	1.44	1.87	1.28	1.44	1.34	2.55	1.47	1.38	1.54	1.49	1.56	2.54

Table 5.4. Analysis of molecular variance comparing the two groups inferred by structure and silhouette plots

Source	Degrees of Freedom	Mean square	Estimated Variance	% Variance
Among populations	1	2857.095	0.000	0%
Within Populations	96	3277.549	3277.549	100%
Total	97		3277.549	100%

5.4 Discussion

Population structure and genetic diversity assessment offer a huge opportunity in guiding germplasm utilization (Egea et al., 2017). The current results showed that there is a huge variation within the populations than among the population variation suggesting possible rapid mutations. Continuous selection by farmers can also result in more homogenous populations leading to a single bigger group and a smaller group with very few individuals. When a comparison is done between the four genotypes and the 94 genotypes, they become maskedsuggesting the absence of among-population variation.

The existence of one large population with constant gene and genotypic frequencies is expected (Kitchen and Allaby, 2012). Sweetpotato is an outcrossing heterozygous species with 100% self-incompatibility (Rodriguez-Bonilla et al., 2014). Therefore,new variation arises from random mating among the genotypes.

The existence of large variation within this population offers a huge potential for sweetpotato utilization (Gasura et al., 2008). For example, sweetpotato conservation would require capturing a set of genotypes that are related and also unrelated. The related individuals form abasis of breeding where most traits are to be conserved but only a few have to be altered. However, the conservation of a diverse set of accessions is critical when sweetpotato breeding should accommodate diverse uses and is also focused on diverse traits. The farming conditions found in sub-Saharan Africa are quite diverse (Low et al., 2020) thus making it possible to conserve diverse sweetpotato accessions that could adapt to those diverse conditions. In the yield trialsfrom this thesis, the genotype x environment was significant suggesting that one way of dealingwith it is to grow cultivars that are adapted to specific growing conditions and this implies conserving diverse germplasm. (Kudadjie, 2006) noted that farmers prefer local accessions mainly because they have built pest and disease tolerance over time.

The development of molecular markers (Mercati and Sunseri, 2020) was very instrumental in identifying duplicates. A core collection of sweetpotato can be conserved and this requires selecting un-related individuals. Such information is available in the dendrogram and could guide the conservation strategy and future breeding efforts in the region.

5.5 Conclusion

Two groups were inferred from structure and silhouette plots. The smaller group had four individuals; Bosbok, UnknownC4, KwasakwasaC, and Kau7. These individuals have large Gower's genetic distances of 2.54, 2.37, 1.65 and 3.20 compared to one another. Analysis of molecular variance showed a very low PhiPT value (equivalent to F_{ST} value) of -0.017 suggesting the populations were not divergent, maybe they come from the same major population. The dendrogram produced can direct future breeding activities and conservation strategies.

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CHAPTER 6

GENOTYPE X ENVIRONMENT INTERACTION AND STABILITY ANALYSIS OF ZIMBABWEAN SWEETPOTATO GENOTYPES FROM FOR FRESH ROOT YIELD

Abstract

Current sweetpotato recommendations in Zimbabwe are not based on the understanding of the existence or nonexistence of genotype x environment interaction in growing areas. This can compromise the profitability of sweetpotato enterprises mainly because of a mismatch between the genotype and the environment. As a result, one hundred sweetpotato genotypes collected from across Zimbabwe were evaluated in four environments. The experiments were laid as a 10 x 10 alpha-lattice design with two replications for all sites. Significant ($p<0.001$) genotypic, environmental and genotype x environment interaction effects on storage root yield were observed. Chiredzi had a yield of 15.213 t ha^{-1}, Shamva (11.539 t ha^{-1}), Africa University (6.594 t ha^{-1}), and Harare (4.876 t ha^{-1}). The mean yield ranged from 0.84 t ha^{-1} to 8.25 t ha^{-1}. Forty-seven percent of the sweetpotato genotypeswere above the mean yield (5.19 t ha^{-1}) with G87 (Mukambachaza), G100 (Beauregard), G13 (Germany 2), and G96 (Drumhead) having the top yields of 8.25, 8.17, 7.74 and 7.69 t ha^{-1}, respectively. Genotypes G11 (Red Jewel) and G 40 (Unknown13Ngaoni) had low yields below 1.0 t ha^{-1}. Genotype ranking across environments were non-consistent. Genotype 94 (Murewa2Cross) won in Shamva, while genotypes G100 (Beauregard) and G28 (Chidhumbe dhumbe) won in the other locations. The GEI variance component (1.3% of total variance) forroot yield was smaller than the variance of the genotypes (2.33%). Among the test environments,Chiredzi was the most representative and discriminating site, while Harare was the most unfavourable site for sweetpotato fresh root yield evaluations. The genotype designated G53 (Unknown6Chako) was the most stable genotype. The two principal components (PCs)explained 85.39% of the variance. The two principal components: PC1 and PC2 accounted for56.92% and 28% of the variation, respectively. Genetic correlation revealed that marketable yield, non-marketable yield, and total yield were significantly correlated (R^2=0.9999). Phenotypic correlations revealed that total root yield was highly correlated to marketable rootyield (R^2 =0.8338), and non-marketable root yield (R^2=0.755). However, the number of roots per plant was not correlated to yield (R^2=0.334). The results showed that there is potential to initiate a strong sweetpotato breeding program in Zimbabwe through exploiting the variation within the collection and ideal production sites for the betterment of farmers.

Keywords: sweetpotato, genotype x environment interactions, fresh root yield, stability analysis, ideal testing environment, biplots

6.1 Introduction

Sweetpotato (*Ipomoea batatas* [L] Lam.) is a strategic crop within Southern African Development Community (SADC), which is grown mainly for food and as a source of income. Ngailo et al. (2015) reported that sweetpotato is rich in vitamins A and C, carbohydrates, fibre, and minerals. It is a crop of choice for smallholder farmers since it is a low input crop. According to Yada et al. (2017), sweetpotato gives good yields under soils of marginal fertility. Ngailo et al. (2019b) reported that sweetpotato was occupying an area of 3.7 million hectares yearly in sub-Saharan Africa. However, Mohammed et al. (2015) indicated that sweetpotato yields are still low ranging between 4.0 -10.0 tonnes per hectare. In Zimbabwe, the average sweetpotato yield per hectare ranges from 3. 5 to 8 tonnes per hectare. Low yields are partly a result of monocropping, the use of unimproved plantlets, and the prevalence of pests and diseases (Kamutando et al., 2013).

The huge demand for sweetpotato as food in Zimbabwe has resulted in farmers from different agro-ecological zones buying any sweetpotato cultivar or genotype available. These cultivars need to be evaluated for specific and wide adaptation in order to provide farmers with research-based recommendations. (Yan and Tinker, 2005) defined a genotype as an individual's genetic makeup while an environment refers to a set of non-genetic factors that affect the phenotypic value associated with a cultivar. Southern Africa was demarcated into two mega-environments by the International Maize and Wheat Improvement Centre. Areas within a mega environment share similar conditions. According to Crop et al. (2012), Zimbabwe has different agro-ecological zones as a result it was divided into natural regions with different crop production potentials.

Zimbabwe has five natural regions demarcated on the basis of the amount of rainfall received and soil types. Sweetpotato is adaptable to all five natural regions. However, sweetpotato is mainly grown in regions I.II, and III. Setimela et al. (2005) reported that the main sweetpotato production areas are found in Mashonaland Central, Mashonaland East, Mashonaland West, Manicaland, Masvingo, and the Midlands provinces. Sweetpotato favours loose soils such as sandy to sandy loamy soils. Therefore, adaptability trials would be critical for the identification of cultivars that can grow best to specific or across sites. Kamutando et al. (2013) pointed that variety trials provide important information that enables the selection and recommendation of crop cultivars. Several trials revealed the plasticity of sweetpotato across geographical sites (Glato et al., 2017b). Mekonnen et al. (2015) reported a highly significant interaction between sweetpotato genotypes and environment on storage root yield. This finding was also reported

by Gurmu et al. 2014) when evaluated orange-fleshed sweetpotato accessions in Ethiopia.

The confounding effect of significant interaction on the selection of high performing genotypes has been reported by Dudley and Moll (1969), de Souza Gonçalves et al. (2003). Jalata Zerihun (2011) highlighted that a significant interaction would mean that selections from one environment may perform poorly in another environment. A change of order in the genotypes is defined as cross-over interactions (Rodrigues et al., 2011; Gasura et al., 2015). Ding et al. (2008) defined yield stability as a measure of the ability of a genotype to maintain relative performance across a wide range of environments. Stability has been shown to be eitherstatic or dynamic. Static stability results in the performance of the genotype not changing evenwhen the environmental conditions change. Kamutando et al. (2013) indicated that an appropriate stable cultivar is capable of utilizing resources that are available in high yield environments while maintaining above average in all other environments. This would call for breeding for specific adaptation. Kamutando et al. (2013) also pointed that significant interaction means difficulties in predicting response to selection, thus complicating the process of selecting genotypes with superior performance. In addition, Mustamu et al. (2018) reported multi-environment trials to assist in the identification of production environments that best suit certain genotypes. Kamutando et al. (2013) indicated that plant genotypes show wide variations in their yielding ability when grown over varied environments or agro-climatic zones. Poland et al. (2012) reported that each genotype might be adaptable to a specific environment for its maximum performance, but successful new cultivars must show high performance for yield and other important agronomic attributes, and their superiority should be consistent over a wide range of environments. Lastly, Ding et al. (2008) reported that plant breeders desire stable cultivars with good performance under all conditions within the targetedproduction region.

There are several ways of investigating genotype-by-environment interaction with the aim of making recommendations for specific or across-site adaptation. (Mcdermott and Centre, 2012) revealed that regression models are some of the tools used by breeders in assessing yield stability. However, Cooper et al. (2008) reported that breeders are mostly using the additive main effects and multiplicative interaction analysis (AMMI). This method is used in complementarity with the genotype + genotype x environment interaction. (Yan and Tinker, 2006) pointed thatgenotype main effect (G) plus genotype x environment interaction (GEI) are the sources of variation. (Yan and Tinker, 2006; Snedecor, 1946) described this as a tool that allows a visual appreciation of the variables at play. Gauch et al. (2008) and Gasura et al. (2008) reported that bi-plots allow the researcher to concentrate on the part of the multi-environment

trial data that is most useful to genotype selection. The other methods include analysis of variance (ANOVA) (Ngailo et al., 2019), and principal component analysis (PCA) (Mukoyi et al., 2018). The advantages and disadvantages of AMMI and GGE bi-plots analyses are dealt within detail by Kamutando et al. (2013). The main difference between the two ways of analysis isthat in AMMI bi-plots the genotype main effect is included as a multiplicative effect and not as an additive main effect (Yan and Tinker, 2005; Yan and Tinker, 2006; Kamutando et al., 2013; Gasura et al., 2015). This study used the AMMI and GGE bi-plot analyses.

6.2 Material and Methods

6.2.1 Study areas

The trials were conducted at Harare Research Institute, Shamva (Panmure Research Institute), Africa University and Chiredzi Research Institute. These sites were selected because they represent the main sweetpotato-growing regions in Zimbabwe. Table 9 no Table 9 (one of the cases of referring to tables or figured that doesn't exist shows the characteristics of the respective sites. The locations represent all the three velds found in Zimbabwe namely, low, middle, and high veld.

Table 6.1. Characteristics of the testing locations in Zimbabwe

Location name	Agro-ecological Region	Altitude (m.a.s.l)	Rainfall (mm/ annum).	Temperature Ranges (°C)	Soil type
Shamva (Panmure)	2b	1149	750-1000	15-28	Sandy loam.
Africa University	2b	1.13	750-1200	18 -32	Red clay
Harare	2a	1,506	750-1, 200	18- 35	Red clay.
Chiredzi Research series.	5	429	400-450	10-35	P Triangle

6.2.2 Trial design and management

Ridges were made using hoes at all sites as the common practice by smallholder farmers. The trial was laid as a 10 x 10 alpha lattice with two replications. One hundred sweetpotato genotypes were randomly assigned to the plots. Each plot had a single three-metre ridge with 0.3 m width and height. Ten vines with 3 to 4 nodes each were planted at 0.3 m depth covering 2/3 of the vine. All vines were spaced at 0.3 m within a ridge. The ridges were spaced at 0.9 m. Compound S (7:21:8 ratio of NPK) was the basal fertilizer applied at 300 kg per hectare. Top dressing was done with ammonium nitrate fertilizer (34.5% N) three weeks after transplanting at a rate of 150 kg per hectare. Hand weeding was done once at 3 weeks after planting before top dressing at all locations. Leaf chewing and sap-sucking insects were controlled by spraying 30 g of carbaryl/ 15 litres of water; while 30 g of copper-oxychloride / 15 litres of water was used for fungal and bacterial diseases control. Irrigation was applied at 18 mm per week during the first two weeks to ensure good establishment and at 25 mm of water per week at mid-season for adequate storage root enlargement at all locations.

6.2.3 Data collection

The genotype x environment interaction analysis was done on storage root yield. Mature sweetpotato roots were carefully harvested at physiological maturity using hand hoes after planting at all locations. The storage roots were graded according to how good they were for the market.Fresh weights were taken using a scale. Weight for each plot was then converted to tonnes perhectare and this was done for each genotype and for all the 4 locations. Five plants positioned at the centre of the ridge were considered as the data plants.

6.2.4 Data Analysis

An analysis of variance was done on root yield. The genotype plus genotype x environment interaction and biplot analysis and variance component calculations were done with genotype plus genotype by environment interaction (GGE) biplot analysis and the variance component calculations were conducted using Genstat version 14 (Gauch et al., 2008; Hongyu et al., 2014). The analysis of variance was done using the model:

$$Yijk = gi + Ek + rj(Ek) + giEk + eijk,$$

where Yijk is the effect of the ith genotype evaluated in the jth replication within the kth environment, Ek is the effect of the kth environment, rj(Ekrj) is the effect of the jth replication within the kth environment, giEk is the interaction effect of the ith genotype and the kth environment, and eijk is the residual term associated with the random error.

The respective F-tests were obtained by dividing mean squares for error into the respective means squares of the replicates, genotypes, environments, and genotype x environment as recommended by Gasura et al. (2015) and Yan and Tinker (2006). The variances of genotypes, genotype x environment interaction, and error complied with the mixed model as recommended by (Feng et al. 2014) as the variance of the genotypes or genotype x environmentinteraction minus the error variance divided by the total number of observations which is 100 for genotypic variance and three for the interaction variance component. The broad-sense heritability was approximated as the genotypic variance divided by phenotypic variance; where phenotypic variance is the sum of genotypic variance, the variance of interaction, and variancecomponents of error.

The appropriate number of principal components to retain for the genotype+genotype x environment biplot analysis was reached through a postdictive evaluation for model fitting, using the Gollob's (1968) F-test as recommended by Hassani et al. (2018). Genstat Software version18 was used to do a GGE analysis. A genotype, genotype x environment-2 biplot analysis was done on the adjusted means across environments as recommended by Ding et al. (2008). Mukoyi et al. (2018) and Yan et al. (2007) described the GGE biplot as:

$$Yij - \mu - \beta j = k\sum l = 1\ \lambda l\ \xi il\ \eta jl + €ij,$$

where Yij is the mean yield of the ith genotype in the j^{th} environment, μ is the grand mean, βj is the main effect of the environment j, ϖI is the singular value of the I^{th} principal component and K=2 in this case, ςil is the eigenvector of the genotype i for PC li, ϖIj is the eigenvector of environment j for PC l, €ij is the residual associated with genotype i in the environment j.

Based on this model, the results of all biplots presented in this work are environment centred. Biplots for which-won-where, sites, and genotype were constructed by observing the singular value partitioning method. For the scatter biplot, the polygon depicting the which-won-where was developed through linking genotype indicators at the furthest distance from the biplot origin. The dissections of the resultant polygon passed through the origin of the biplot. The mean and stability analysis of the genotypes preceding a genotype biplot was obtained by describing an average environment coordinate as a small circle. The vectors of the locations were constructed from the origin of the biplot to the indicators of the location.

6.5 Results

6.5.1 Analysis of Variance

The storage root yield was significantly ($p<0.001$) influenced by genotype, environment, and genotype x environment interaction (Table 10). The environment accounted for 87.48% of the variation. However, genotypes and genotype x environment interaction explained 2.33%, and 1.3% of the variation respectively. The error variation was the least (0.43%) (Table 10) not table 10. The genotype x environment interaction variance (1.3%) for root yield was smaller than the variance of the genotypes (2.33%). However, the variance of the error (0.43%) was smaller thanthat of the genotype x environment interaction (Table 10). Heritability for the storage root yieldwas 54%.

The average root yield ranged from 0.84 - 8.25 tonnes per hectare for G87 and G11 respectively. The experimental mean was 5.19 tonnes per hectare (not shown in the table). Forty-seven (47%) percent of the genotypes were well above the mean. The genotypes G87 (Mukambachaza), G100 (Beauregard), G13 (Germany 2), and G96 (Drumhead) registered the top root yields of 8.25, 8.17, 7.74 and 7.69 t ha^{-1}, respectively. Genotypes G11 (Red Jewel) and G 40 (Unknown13Ngaoni) had low yields below 1.0 t ha^{-1}. G87 (Mukambachaza) from Domboshawa out yielded improved varieties from the Horticulture research centre. The test sites- Harare, Africa University, Shamva (Panmure), and Chiredzi significantly differed ($p< 0.001$). Chiredzi had 15.213 tonnes per hectare seconded by Shamva (11.539 tonnes per hectare), Africa University (6.594 tonnes per hectare) and Harare (4.876 tonnes per hectare) (not shown in the table).

Table 6.2. Analysis of variance for sweetpotato root yield evaluated across four locations during the 2017/18

Source of variation	Degrees of freedom	Mean square values	F-probability	Variance component	variance component as % of total variance
Total	799	39.8			
Gen *Environ	399	65.0	<0.001	4.14	3.16
Genotypes	99	47.9	<0.001	3.05	2.33
Environments	3	4440.6	<0.001	114.75	87.48
Block	4	38.7	0.0447	2.47	1.88
Interactions	293	26.9	<0.001	1.71	1.30
IPCA 1	101	47.5	<0.001	3.03	2.31
IPCA 2	99	22.9	<0.001	1.46	1.11
Residuals	93	8.8	0.0067	0.56	0.43

6.5.2 Which-won-where patterns for sweetpotato genotypes

According to the Gollob (1968) F-test, the two principal components significantly explained much of the variation (85.39%). The first principal component (PC1) accounted for 56.92% and PC2 explained 28% of the variation (Figure 21) no figure 21. Figure 21 displayed a 7-sided polygon with nine sectors. Sector 2 had G94 (Murewa2Cross) as the winning genotype and one test environment (Shamva) fell in this sector. Sector 4 had genotypes G100 (Beauregard) and G28(Chidhumbe dhumbe) as the winning genotypes and included the rest of the environments: Africa University, Chiredzi, and Harare (Figure 21). Sectors 1, 3, 5, 6, 7, 8, and 9 had no environments in them but contained genotypes. The biplot had one mega-environment.

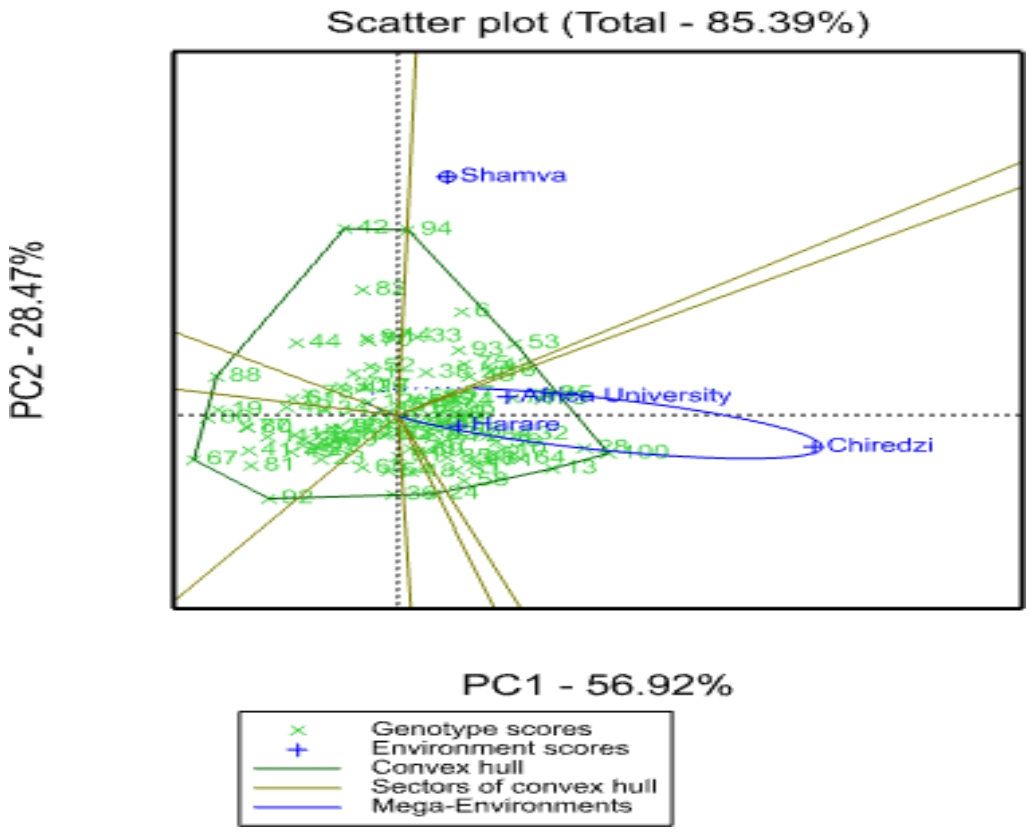

Figure 6.1. The which-won–where and delineation bi-plot for mega-environments

6.5.3 Biplot analysis of sweetpotato genotypes

There was a significant genotype x environment interaction warranting the need for stability analysis. Genotype 53 was the most stable genotype found in the inner most circle (Figure 6.2).

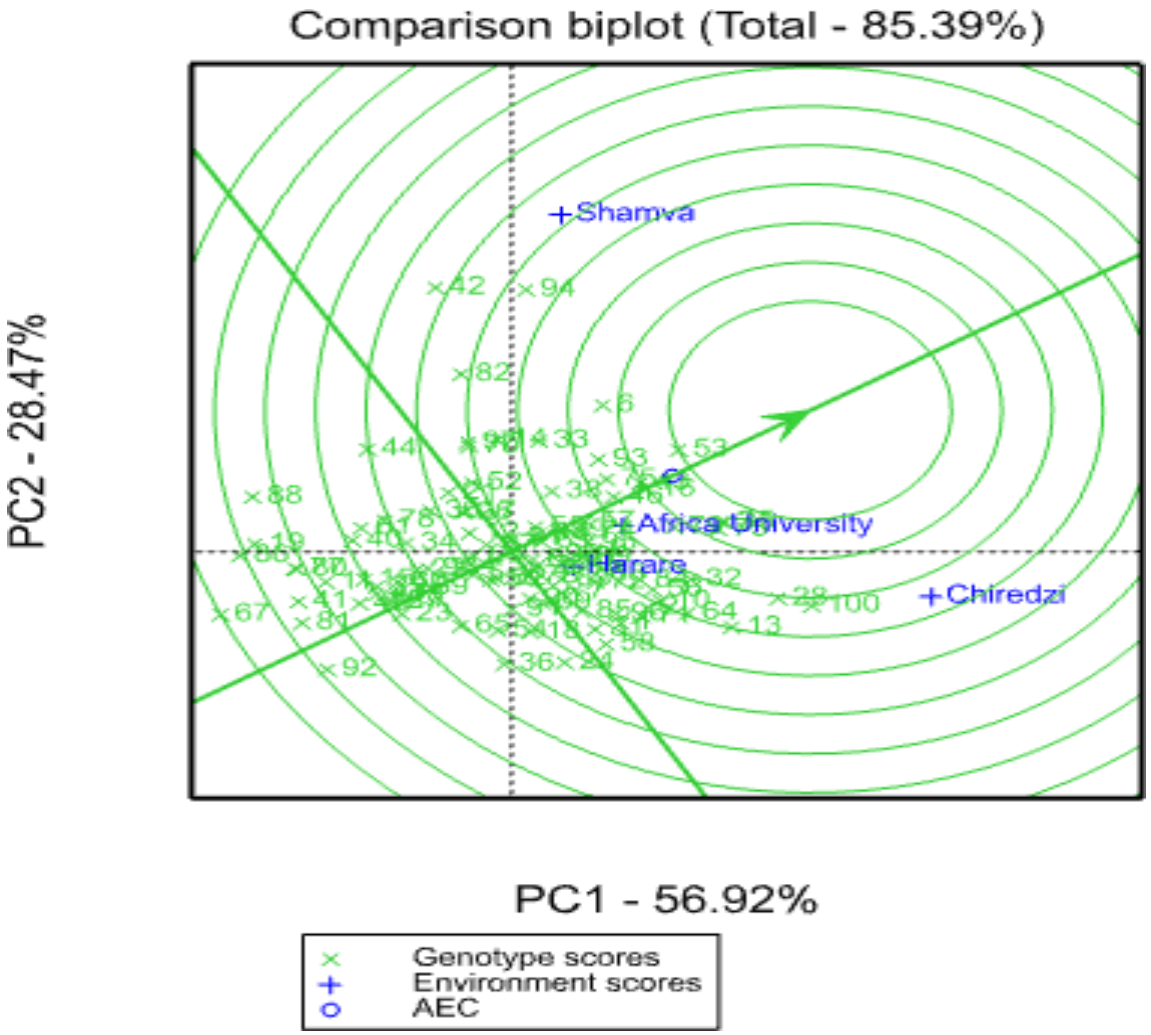

Figure 6.2. Biplot analysis for identification of best performing sweetpotato genotypes across four sites in Zimbabwe

6.5.4 Test location evaluation

Chiredzi was the most representative site since it is located in the innermost concentric circle (Figure 6.3). The sites were ranked as Chiredzi> Shamva>Africa University > Harare according to suitability for sweetpotato production. Chiredzi had the highest yield of 15.213

tonnes per hectare, seconded by Shamva (11.539 tonnes per hectare) while Africa University posted (6.594 tonnes per hectare) and Harare with (4.876 tonnes per hectare).

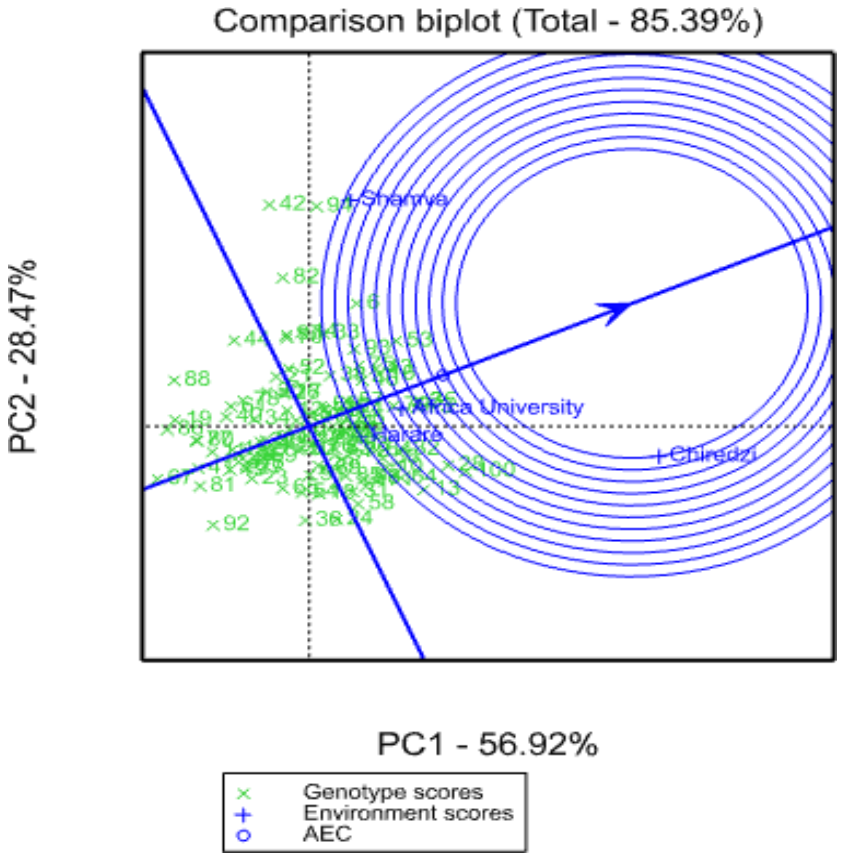

Figure 6.3. GGE biplot based on storage root yield (t ha^{-1}) for four locations based on location correlation and most representativeness.

6.5.5 Discriminating Environments

A single mega–environment was observed warranting the identification of the best testing environments. Chiredzi was the most discriminating site with the longest environment vector from the biplot origin and along the first axis (Figure 6.4).

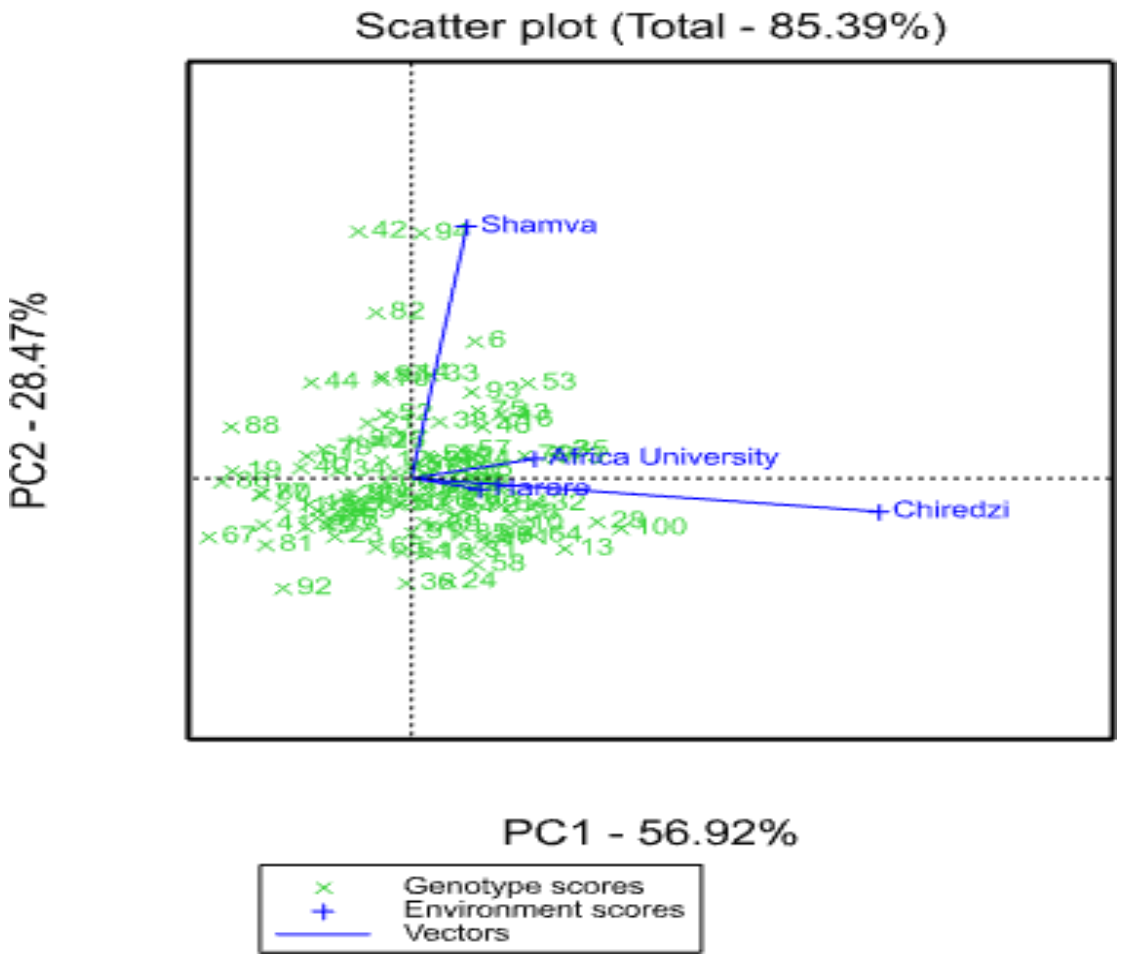

Figure 6.4. GGE biplot based on storage root yield (t ha^{-1}) for four environments showing the relationship amongst the test locations

6.5.6 Genetic correlation

Marketable root yield, non-marketable yield and total yield were highly correlated R^2=0.9999). None of those parameters were correlated to number of roots per plant (Figure 6.5).

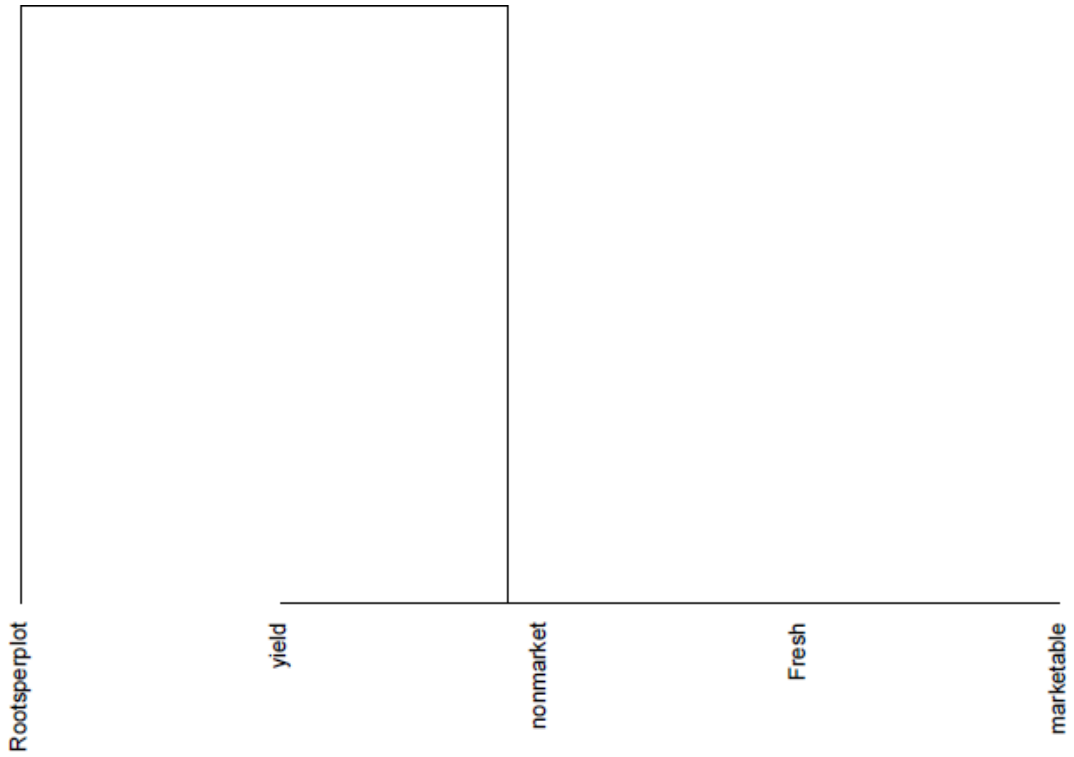

Figure 6.5. Correlation analysis of root per plot vs yield, non-market, fresh weight and marketability

A matrix presentation of correlation of variables will give better insight than a dendrogram, because there will be values and the correlation coefficient (R^2) can be shown.

6.5.7 Phenotypic correlations

Total root yield was highly correlated to marketable root yield (R^2 **=0.8338**) and non-marketable root yield (R^2 **=0.755**). However, storage root number was not correlated to storage root yield (R^2**=0.334**) (Figure 6.6).

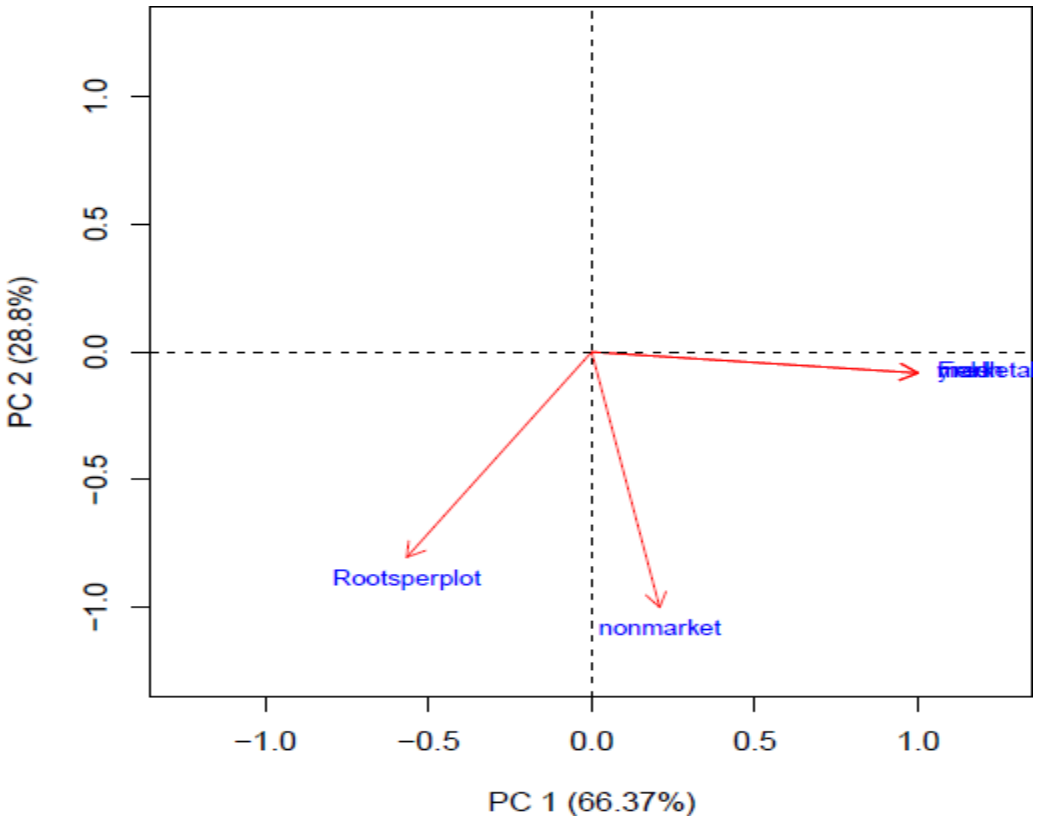

Figure 6.6. Correlation analysis of number of storage roots to storage root yield

6.6 Discussion

6.6.1 Variance components analysis

There was evidence of a significant genotype x environment interaction effect on storage root yield. The test sites varied greatly with the effect of environment accounting for 87. 39%. Mustamu et al. (2018) reported that a large variance component as a result of the environment alone justifies the need to use the genotype + genotype x environment interaction biplot. Singh et al. (1999) and Zakir (2011) indicated that Zimbabwe is sub-divided into five natural agro-ecological zones based on crop production potential. In these agro-ecological zones, there is huge variability in predictable factors (soil characteristics) and unpredictable factors (temperature and rainfall). Basing on sweetpotato root yield from the study sites, the sites could be ranked as Chiredzi > Shamva >Africa University > Harare. Very little rainfall was received countrywide during this growing season. Chiredzi and Shamva had more reliable irrigation systems than Africa University and Harare. Chiredzi and Shamva are warmer than Africa University and Harare.

6.6.2 The implication of a significant genotype x environment interaction

A large genotype x environment interaction (GE) shows that genotype ranking changes with environment/location, thus complicating selection. Singh et al. (1999) reported that genotype x environment interactions are prevalent and complicate interpretation of results slowing down plant breeding efforts. Gurmu et al. (2014) reported that significant GE impedes the speed at which desirable cultivars are made. Kang (1998) revealed that changes in cultivar ranks across environments make it difficult to recommend a single best genotype for all environments based on evaluations from a single site. Furthermore, this GE was of crossover-type as based on the Simon-Gail test (Hölker et al., 2019). Crossover GE reflects a situation; whereby different sweetpotato genotypes are wining in different environments (Zobel et al., 1988). Significant interaction masks the contribution of main effects. (Sharifi and Ebadi (2018) advised not to ignore large genotype x environment interaction. This was also supported by (Sharifi and Ebadi (2018) who advocated for the identification of the causes of large interaction and their redress. The variation experienced in this study could be a result of soil fertility, temperature differences for the respective locations, and management practices. Farmers can come in with organic and inorganic fertilizers to improve soil fertility and also employ irrigation to manage drought conditions. However, this will tend to increase variable costs for the resource-poor farmers. Mulugeta et al. (2014) reported a significant genotype x environment interaction on total root yield, dry matter content, and mineral characteristics. However, Zhang et al. (2018) highlighted that an ideal genotype must be high yielding with strong stability across environments.

6.6.3 The which-won-were analysis

The study was guided by Gollob's F-test where the first 2 principal components explained much of the variation. Zhang et al. (2018) recommended that the first two principal components were the most significant in the explanation of variation from a biplot. Yan et al. (2007) advised that once GE is greater than genotype main effects one cannot ignore probing the causes of the interaction. Yan and Tinker (2006) highlighted that use of the GGE-2 biplot is suitable when the GE captures at least 60%; while the genotypes capture at least 5% of the variation. In this study, the two principal components (PCs) explained about 85.39% of the total variation observed, of which PC1 and PC2 explained 56.92 and 28% of the total variation,respectively. Finlay and Wilkinson (1963) reported that such complicated situations arecommon in multi-environment trials. Yan and Tinker (2006) and Yan et al. (2007) reported that once different genotypes win in different environments it suggests the existence of different mega-environments. In this study, only a single mega-environment was picked. This

means that the sweetpotato breeding program should not concentrate on breeding for specific adaptation; instead, the program should focus on breeding for wide adaptation. Matova and Gasura (2018) reported that once there is one mega-environment, the strategy is to select varieties based on mean performance and stability using MET data for production across this mega-environment.

6.6.4 Test Environments analysis

Chiredzi was the most ideal testing site as shown by the longest vector. Ullah et al. (2012) reported that the vector length of the biplot approximates the standard deviation within each location and is a measure of the discriminating power. Feng et al. (2018) cited that environmental analysis was essential because it helps in understanding test locations better and might lower evaluation costs.

Identification of Chiredzi, a high potential location as the most ideal testing environment in this study (Figure 6.4) concurs with Jalata Zerihun (2011) who reported that high potential environments were more representative and discriminating than the low potential environments. The presence of a single mega-environment means that variety evaluation will not necessarily need all testing environments. Therefore, a few locations could be chosen for variety evaluation and these will represent the rest of the mega-environment (Laurie et al., 2015).

6.6.5 Storage root yield stability

Genotype G53 (Unknown6Chako) was the most stable genotype as it was found within the innermost circle of the GGE biplot. Haruna et al. (2017)reported that ideal genotypesmust be high-yielding and stable across all test sites. Yan and Hunt (2001) pointed that genotype by environment interactions were the main cause of yield differences among genotypes. Genotypes 94 (Murewa2Cross), G100 (Beauregard), and G28 (Chidhumbe dhumbe) were the highest yielders and sensitive genotypes. Yan and Hunt (2001) indicated that best-performing genotypes are found at the vertices of the polygon. In addition, Yan and Hunt (2001) reported that environment- specific adapted varieties have the attribute of responding to environmental changes compared to widely-adapted (stable) and non-responsive) varieties.

6.7 Conclusion

Sweetpotato genotypes from Zimbabwe responded differently across test sites. There was evidence of a significant genotype x environment interaction. Chiredzi was the most ideal sweetpotato production and testing site. G53 (Unknown6Chako) was the only stable and high-yielding genotype. Chiredzi had the highest mean yield (15.213 t ha^{-1}) and Harare had the lowest mean yield (4.876 t ha^{-1}). These test sites can be regarded as good examples of favourable and unfavourable testing environments respectively.

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CHAPTER 7

GENOME WIDE ASSOCIATION STUDY OF SWEETPOTATO STORAGE ROOT TRAITS

Abstract

Sweetpotato breeding has been lagging in the Southern African region, yet sweetpotato is faced with many challenges that include low yield and poor quality. Young leaves from the tip were sampled, dried overnight in a drying oven at 35^0C and were sent to BecA- ILRI Hub Nairobi, Kenya in 2 by 96 well microtiters for genotyping using a genotype by sequencing approach. The objective was to identify markers (SNPs) for agronomic and quality attributes in sweetpotato using Genome-Wide Association Study (GWAS). At LOD score of 3, flesh colour and root formation traits had markers at unidentified chromosomepositions. Chromosome 10 had more influence on root traits. A total of 19 145 SNP markers used were densely distributed across the sweetpotato genome suggesting that the markers covered possible mutations and linkage disequilibrium that exist between the markers and phenotypes. The markers also showed good quality since the frequency of heterozygous markers was low. The MLM used in the study fitted the data well as shown by a Q-Q plot that was almost a straight line. An appreciation of single nucleotide polymorphism markers associated with root quality traits that include flesh colour, intensity of flesh colour and secondary flesh colour and agronomic attributes such as root yield would go a long way in enhancing sweetpotato marker assisted breeding in Zimbabwe.

Keywords: sweetpotato, genotype by sequencing, single nucleotide polymorphism, molecular markers

7.1 Introduction

Sweetpotato productivity is mainly limited by socio-economic, abiotic, and biotic factors. Kapinga et al. (2007) and Chandrasekara and Josheph Kumar (2016) identified poor post-harvesting and storage facilities, absence of processing skills, lack of improved planting material as important socio-economic factors affecting sweetpotato production and productivity in developing countries. Laurie et al. (2005) and Murugan et al. (2012) reported that weevils, nematodes weeds, and diseases as major factors affecting sweetpotato productivity. In their study, Gurmu et al. (2014) reported that low sweetpotato productivity in the countries of the Southern African Development Community (SADC) region was due to the use of diseased planting material. These observations are in agreement with Ezin et al. (2018) who implicated a lack of clean planting material as a major constraint in African countries.

Knowledge of genetic variations and how they are structured within and among populations is important for plant improvement. A molecular marker is a Deoxyribonucleic acid (DNA) sequence in association with a target gene or attribute. Nadeem et al. (2018) classified markers as classical and molecular. Mondini et al. (2009) gave examples of classical markers as morphological, biochemical, and cytoplasmic makers, and they are less favoured by breeders because they are affected by environmental factors. Examples of molecular markers as reported by Jiang et al. (2016) are Restriction Fragment Length Polymorphism (RFLP), Amplified Fragment Length Polymorphism (AFLP), Simple Sequence Repeats (SSR), Single Nucleotide Polymorphism (SNP) and Diversity Array Technology (DArT).

Single Nucleotide Polymorphism are the most ideal markers partly because of being co-dominant, uniformly distributed throughout the population, have high repeatability, and are highly polymorphic Mondini et al. (2009). The Genome-Wide Association Study (GWAS) is a technique used to detect associations between genetic variants and traits in samples from populations mainly based on SNP markers (Xiao et al., 2017a). This technique has led to recent advancements in the arena of genotyping and sequencing; therefore, it is a very important method for the study of natural variation and target traits (Xiao et al., 2017b).

Sweetpotato breeding has been lagging in the Southern African region, yet sweetpotato is faced with many challenges that include low yield and poor quality. Furthermore, the breeding tools for sweetpotato have remained traditional and heavily dependent on field phenotyping. Field phenotyping is time-consuming, costly, and associated with many errors, highly influenced by environmental effects, and thus is less reliable. Therefore, the objectives of this study were

to identify markers (SNPs) for GWAS of agronomic and quality traits in sweetpotato. The benefits of identifying SNP markers associated with agronomic and quality attributes in sweetpotato can help to speed up the breeding process. Molecular markers are becoming cheaper compared to phenotyping, and are more reliable. Molecular markers have been successfully used in cereal species such as maize and rice and would thus offer a huge opportunity in fast-tracking the breeding process of sweetpotato.

7.2 Materials and Methods

7.2.1 Plant materials and phenotypic data

The plant materials are as described in (Chapter 4 and 5) while the data used for association was obtained as means across the environments as described in Table 6.2 of Chapter 6. The across sites means are given in Table 6.2 of Chapter 6.

7.2.2 Genotyping and data analysis

Fresh, tender, two-week old leaves were sampled from field grown accessions. A leaf was placed on the cutting mat before collecting leaf disks by the leaf cutting punch rotated back and forth. The respective disks were removed from the punch by depressing the plunger on top of the punch. Ten leaf disks were collected for each accession. The leaf punch device was sterilized with 70% alcohol before punching the next leaf to prevent cross contamination.

Leaf fresh disks were placed in the oven without caps and dried overnight in a drying oven at 35^0C. Once leaf disks were completely dry to prevent fungal growth then the strips were covered with caps. The lids were secured using elastic band and placed in the sealed rack into the large sealable bag. Excess air was forced out of the bag and sealed tightly. The sealed bag was placed into the shipment kit box and shipped to BeCA-Hub-ILRI laboratories in Nairobi, Kenya. Two 96-well plates were used in this study-the second well plate carrying only two accessions. In this study, ninety-eight (98) sweetpotato accessions were used as described in Chapter 3. The samples were 100 in total but two samples were contaminated to the point that the results were considered unreliable.

7.2.3 Genotyping

DNA extraction was done with the modified Cetyl Trimethyl Ammonium Bromide (CTAB) method (Saghai-Maroof et al. 1984). Quality check for DNA was done using an agarose gel. Spectrophotometer was used to establish the quantity of DNA and this was followed by

genotyping by sequencing (GBS) for single nucleotidepolymorphism (SNP) marker discovery. A total of 19145 SNP markers were used following the mixed linear model. The wild relative of sweetpotato (*Ipomoea trifida*) was used as the reference genome. The purity, integrity, and quality checks of the isolated DNA samples were done for the presence of high concentrations of compounds such as polyphenols, polysaccharides, and proteins determined by a NanoDrop 2000 spectrophotometer. The GWAS was done using the GAPIT program in R studio.

7.3 Results

Figure 7.1 and 7.2 shows the distribution of the markers across the genome while Figure 7.3, or 7.2 shows the frequency of heterozygous calculated for both individuals and markers. Considering a LOD score of 3, flesh colour and root formation traits have markers at unidentified chromosome positions. However, the intensity of skin colour, roots, secondary flesh colour, and size variability 2, 10, 10, and 15 respectively (Figure 7.4 to Figure 7.9). Chromosome 10 has more influence on root quality traits. However, for other traits studied, there were no strong associations of traits and SNP markers used (Figure 7.10 to Figure 7.23).

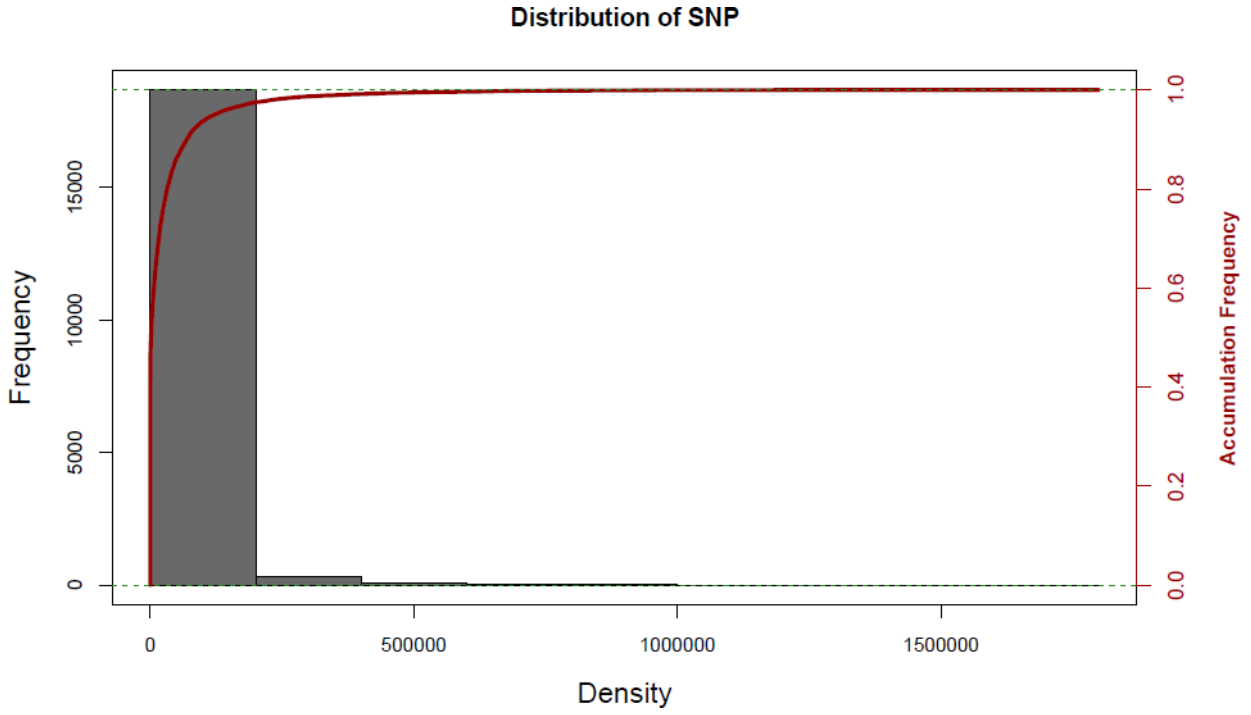

Figure 7.1 Frequency and accumulation frequency of marker density.

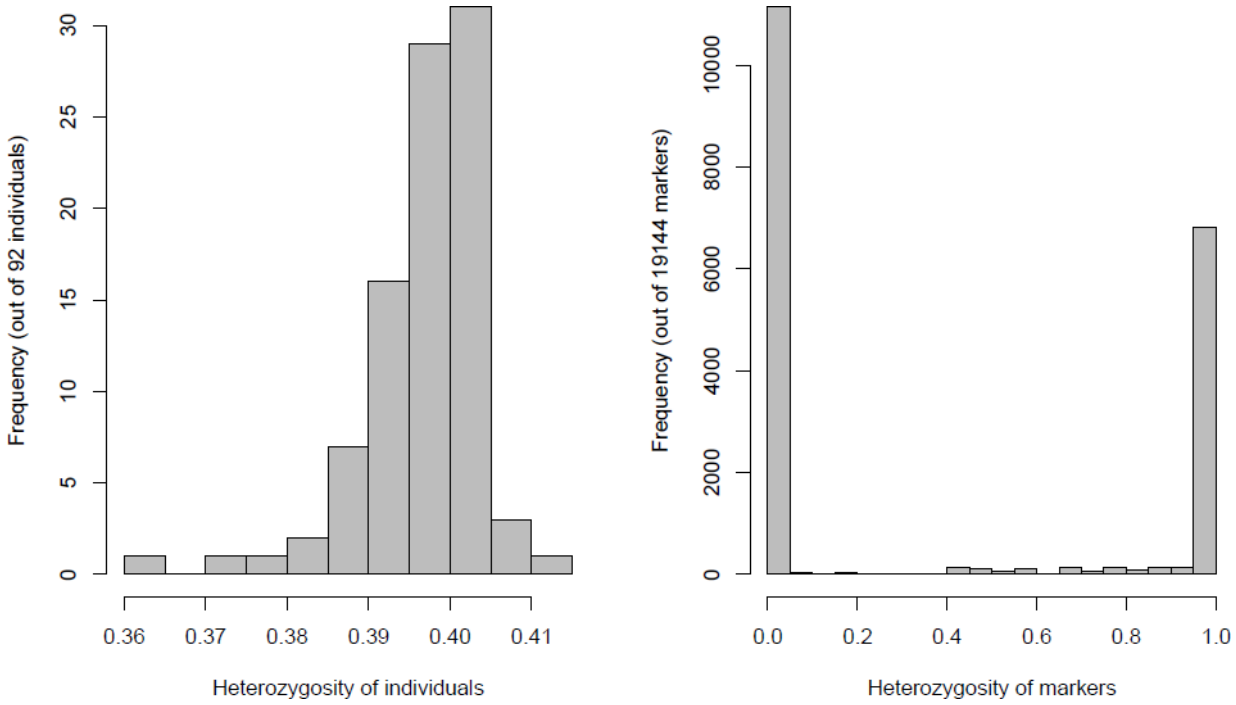

Figure 7.2. The frequency of heterozygous calculated for individuals and markers.

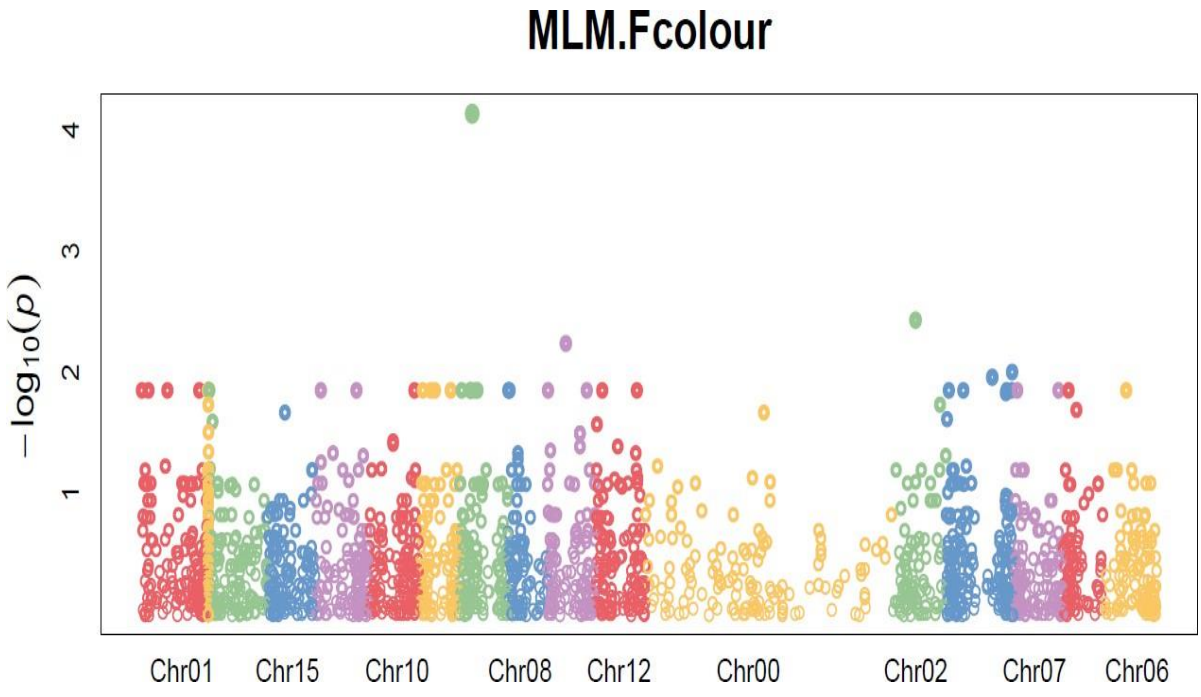

Figure 7.3. Manhattan plot for flesh colour shows a marker at an unidentified chromosome

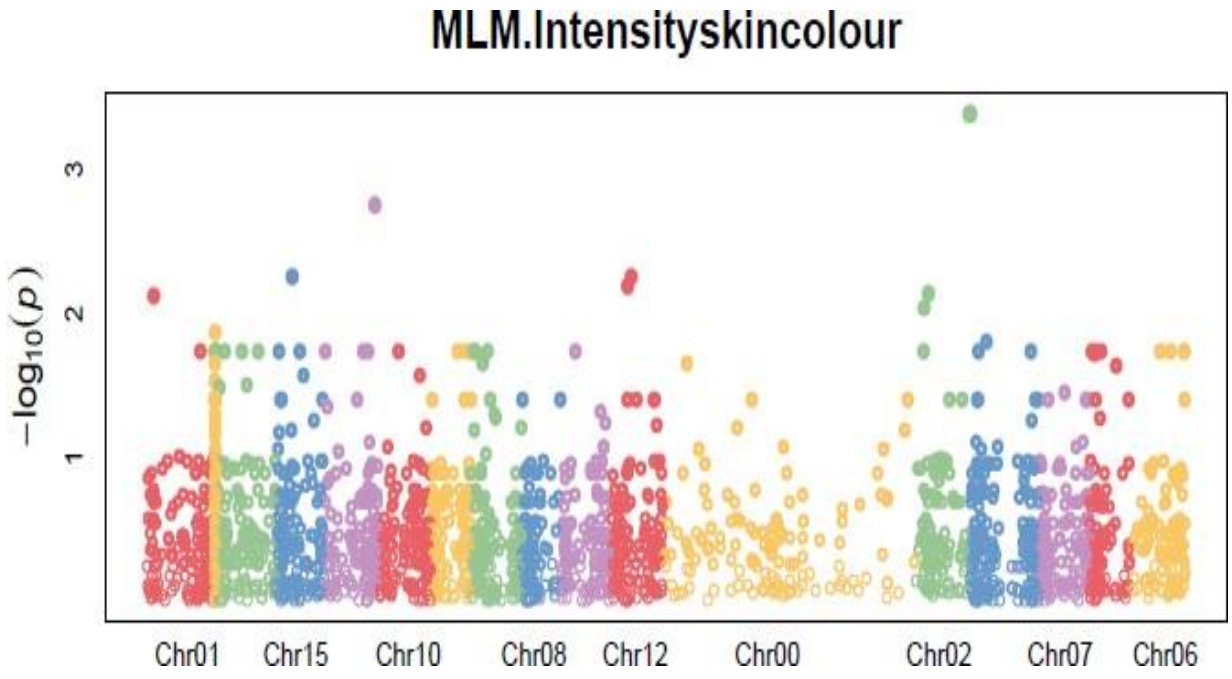

Figure 7.4. Manhattan plot for intensity of skin colour shows a marker at chromosome number 2

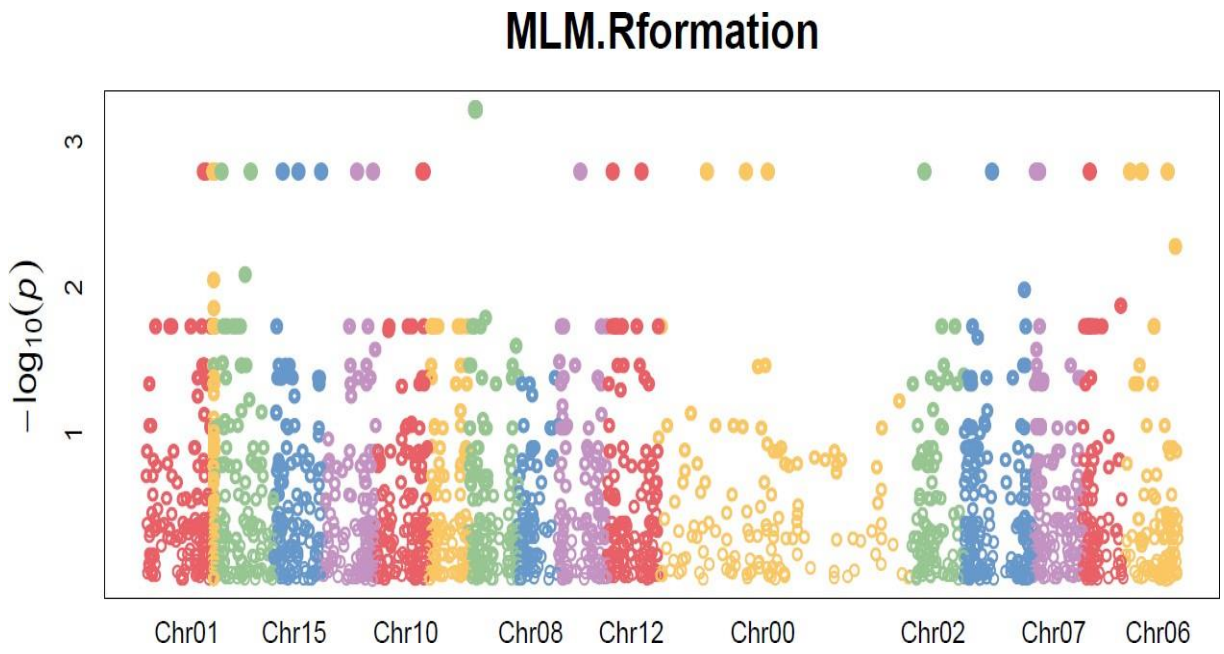

Figure 7.5. Manhattan plot for storage root formation shows a marker at an unidentified chromosome

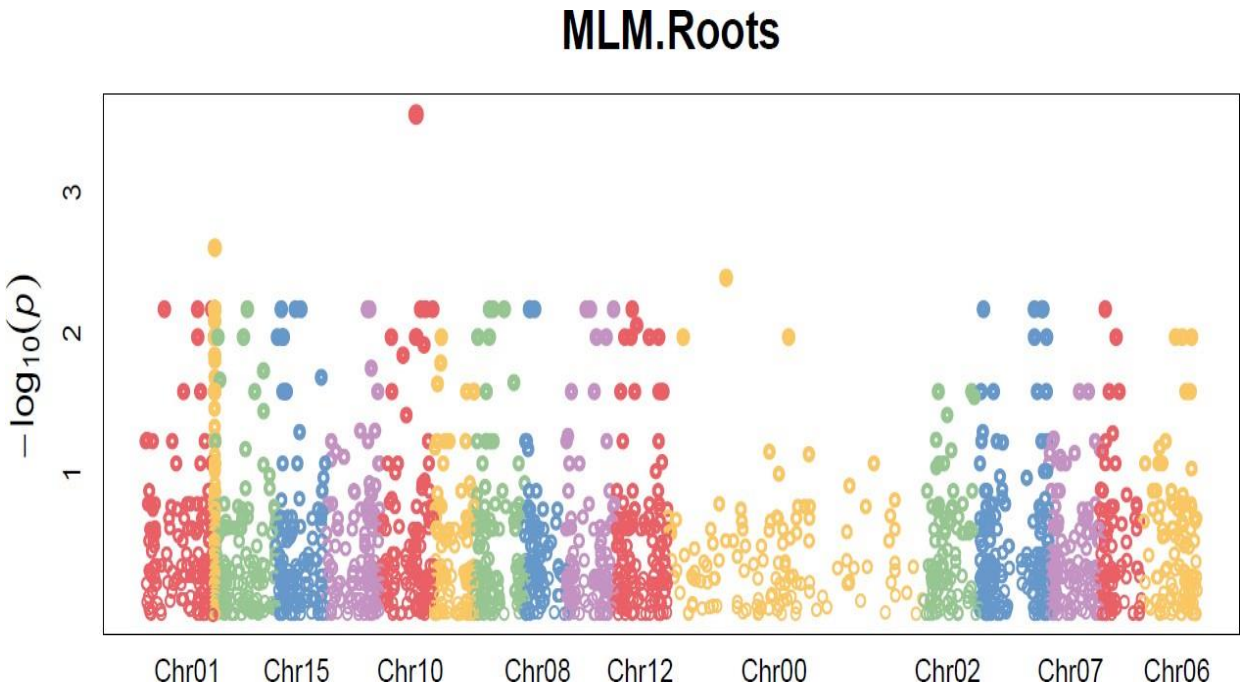

Figure 7.6. Manhattan plot for roots shows a marker at chromosome number 10

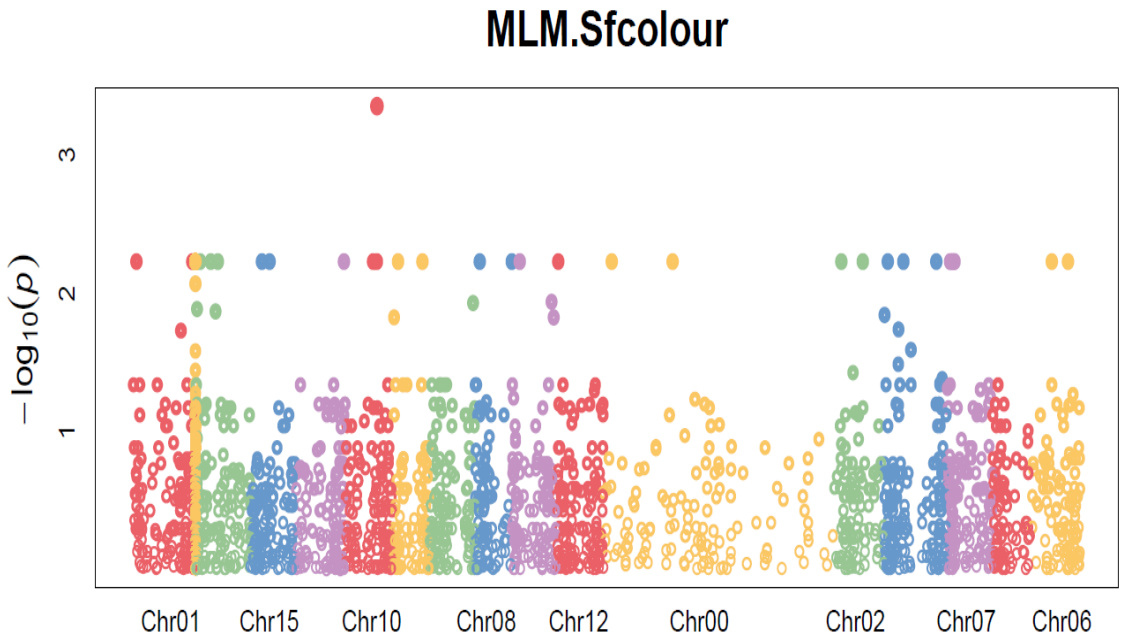

Figure 7.7. Manhattan plot for secondary flesh colour shows a marker at chromosome number 10

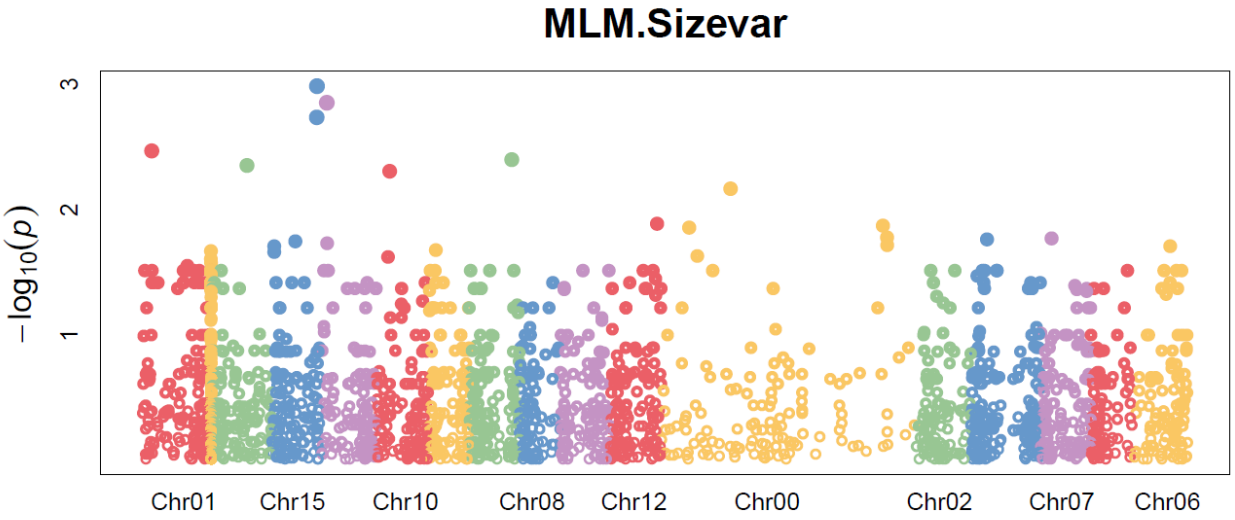

Figure 7.8 Manhattan plot for root size variability shows a marker at chromosome number 15

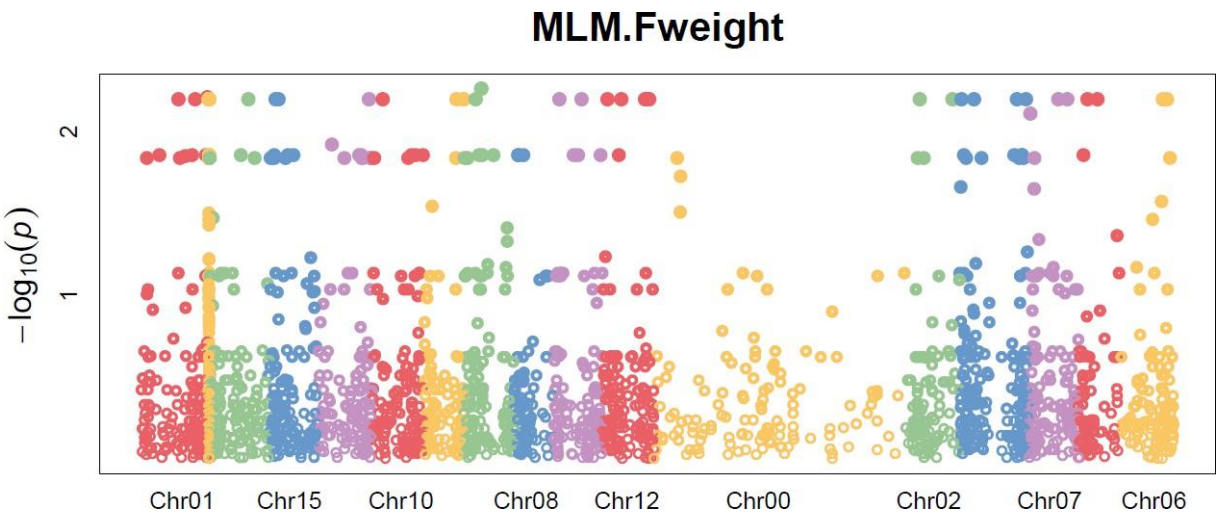

Figure 7.9. A Manhattan plot for variability in root size

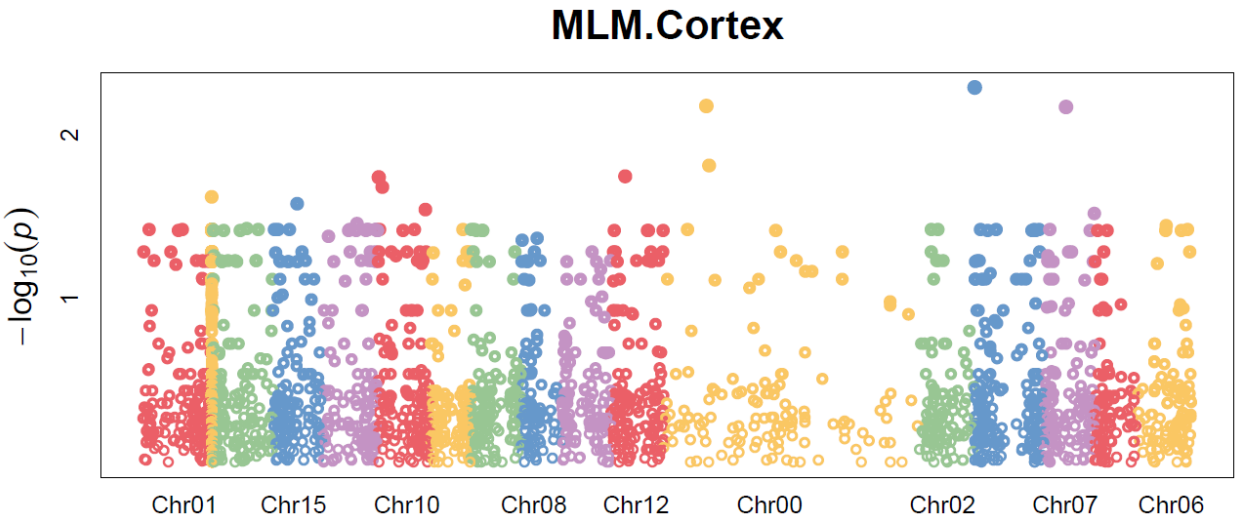

Figure.7.10. A Manhattan plot for root cortex thickness

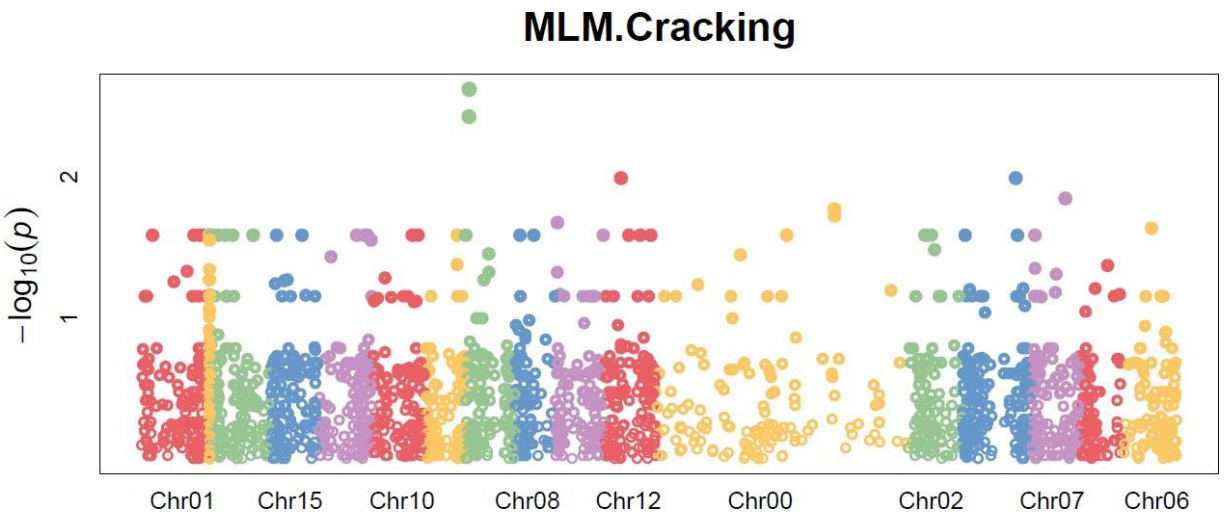

Figure 7.11. A Manhattan plot for root cracking

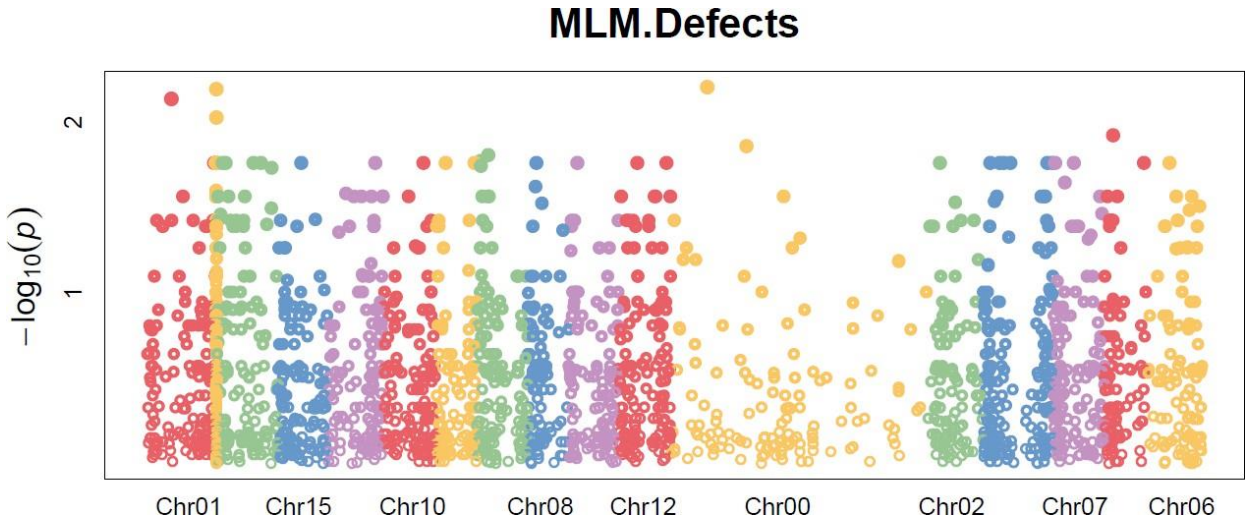

Figure 7.12. Figure. A Manhattan plot for root defects

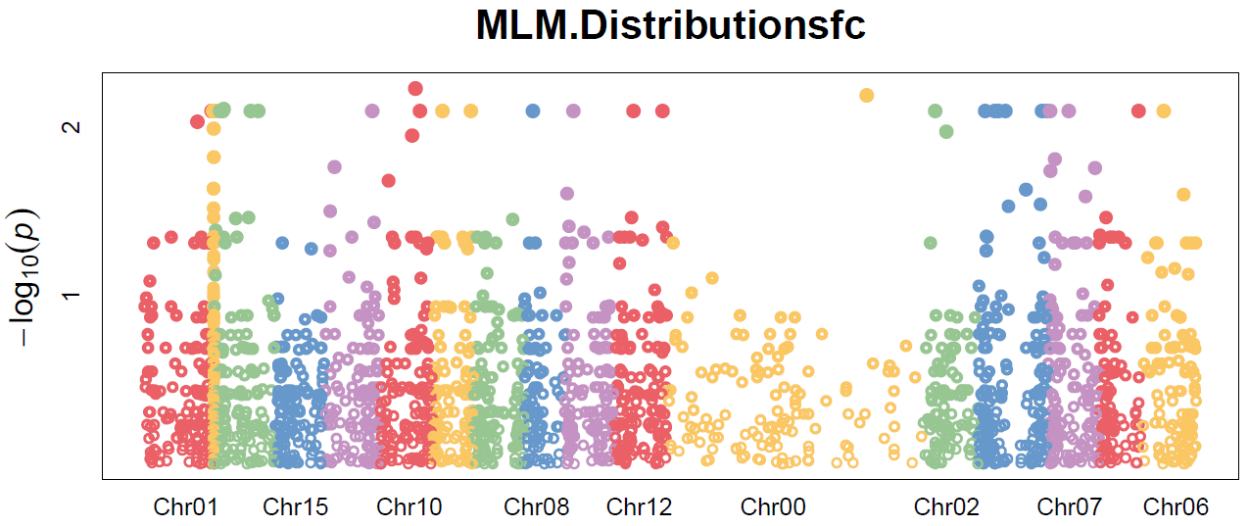

Figure 7.13. A Manhattan plot for distribution of flesh colour

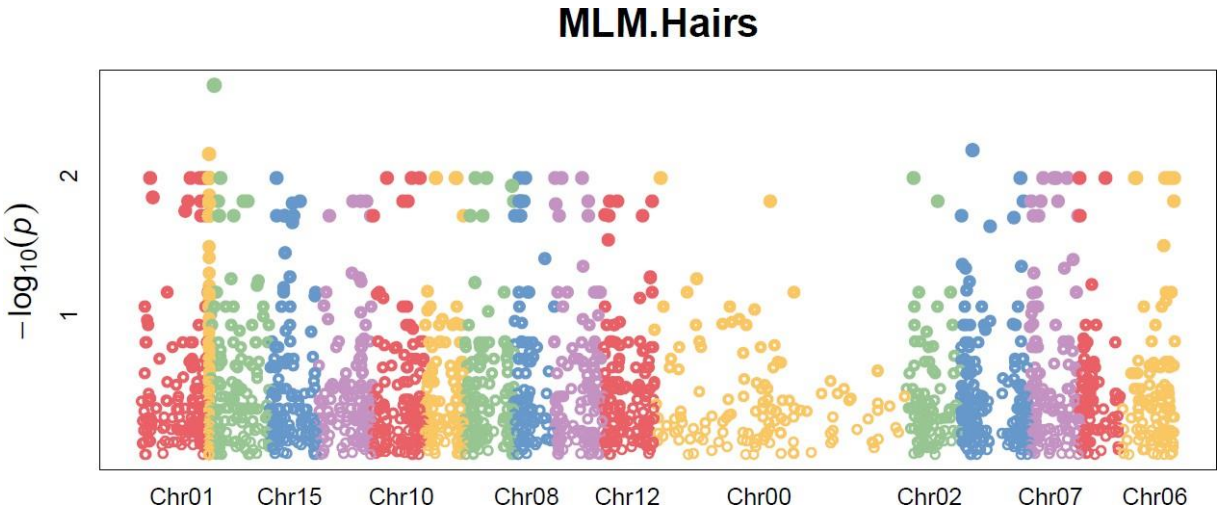

Figure 7.14. A Manhattan plot for vine tip pubescence

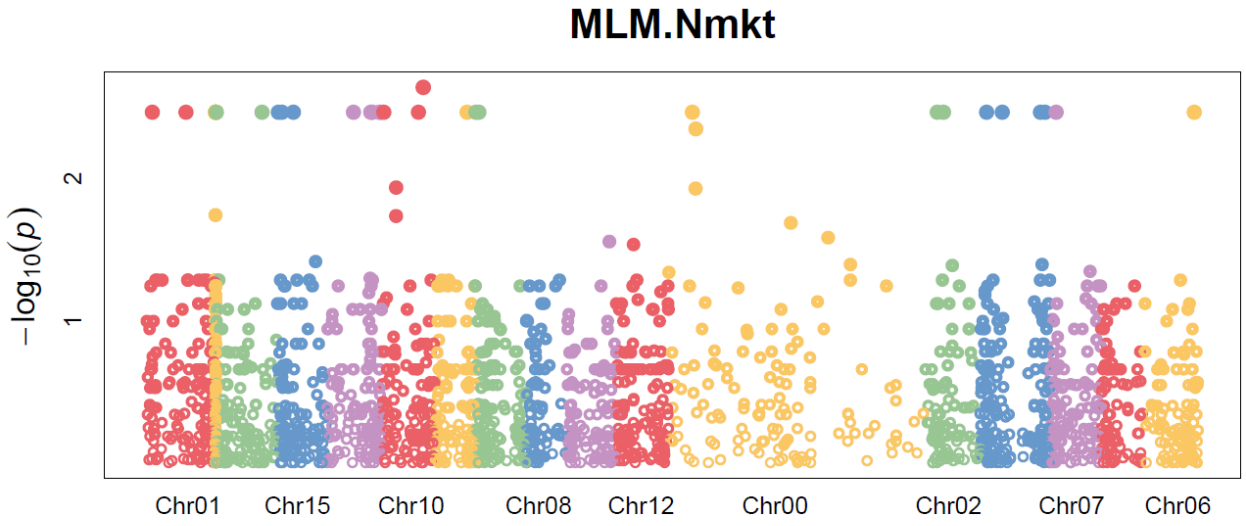

Figure 7.15. A Manhattan plot for number of marketable tubers

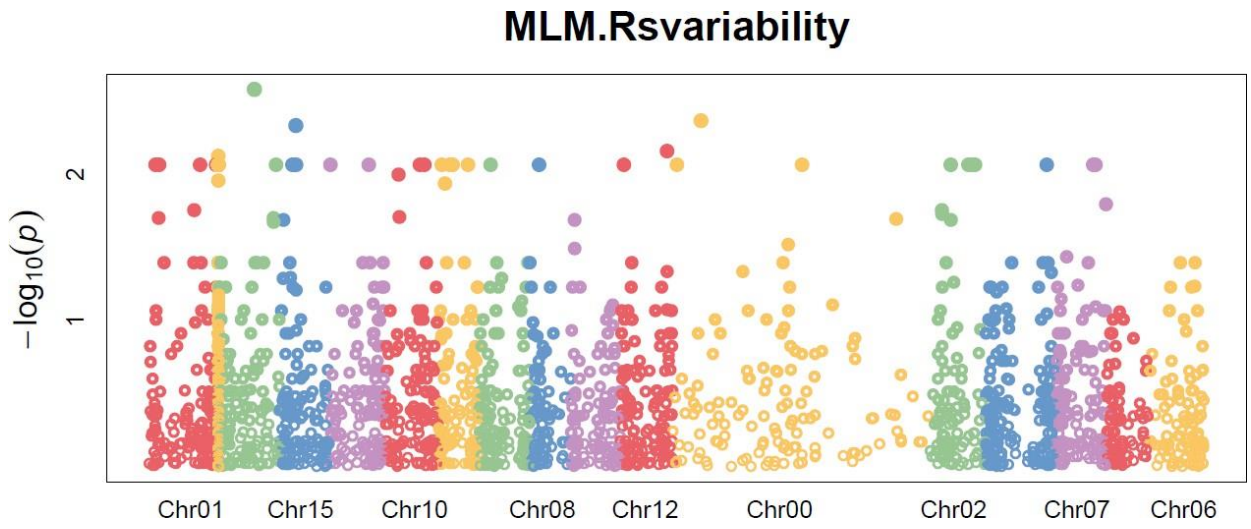

Figure 7.16. A Manhattan plot for variability in root size

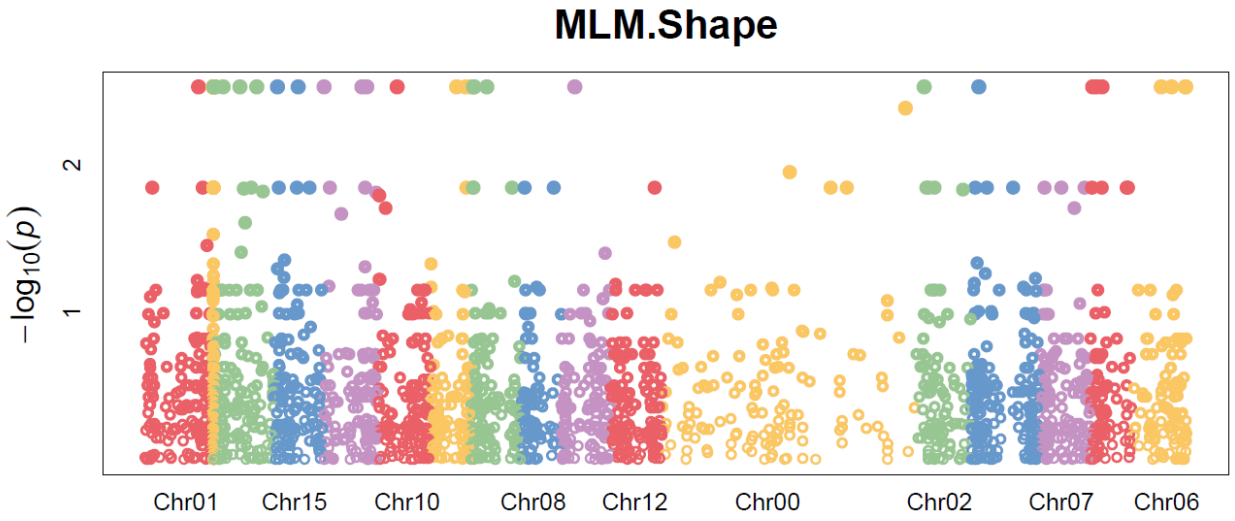

Figure 7.17. A Manhattan plot for root shape

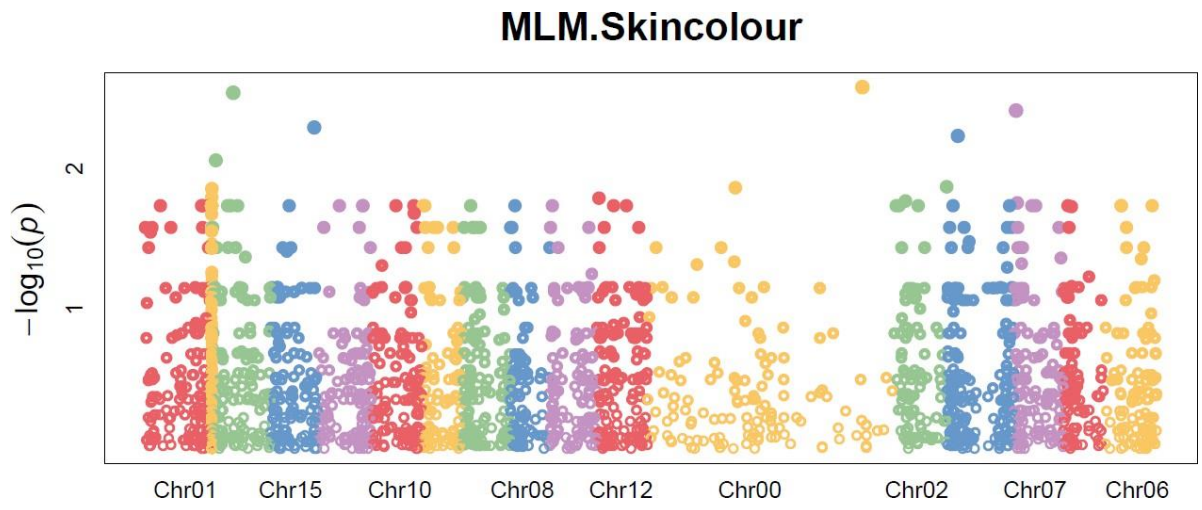

Figure 7.18. A Manhattan plot for skin colour

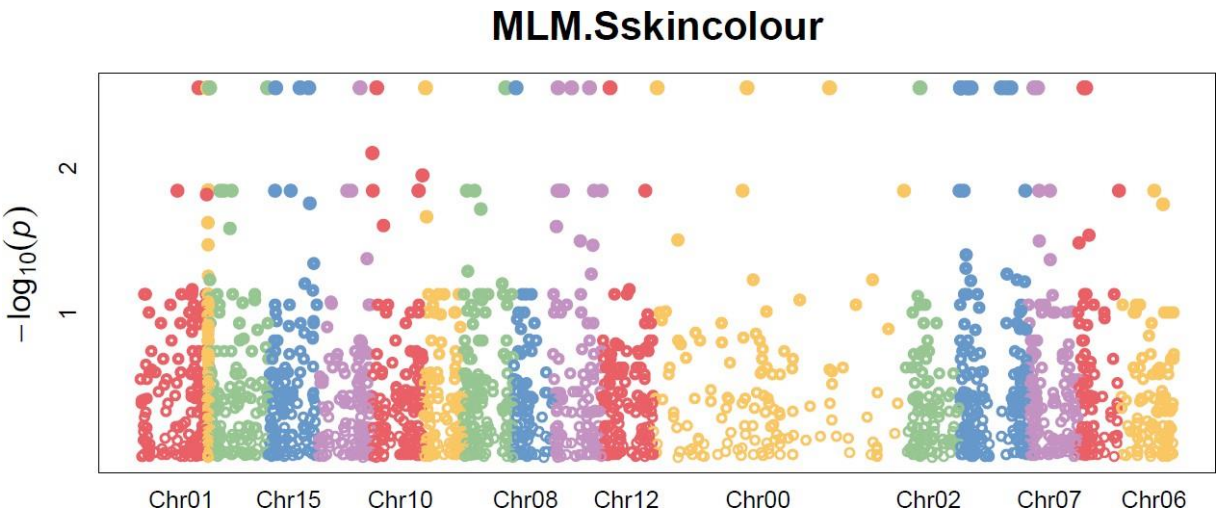

Figure 7.19. A Manhattan plot for secondary skin colour

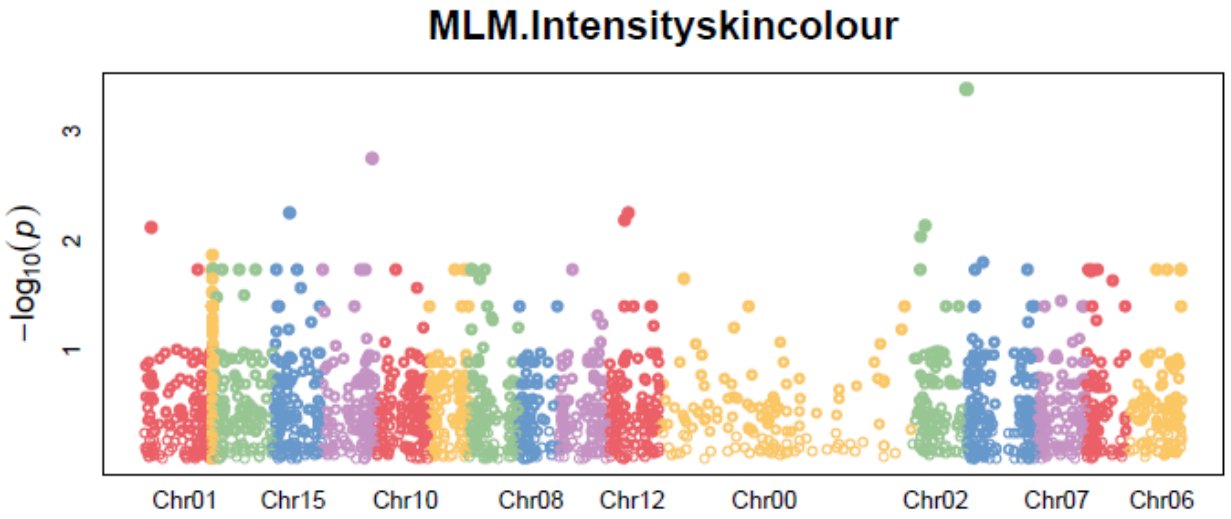

Figure 7.20. Manhattan plot for intensity of skin colour shows a marker at chromosome number

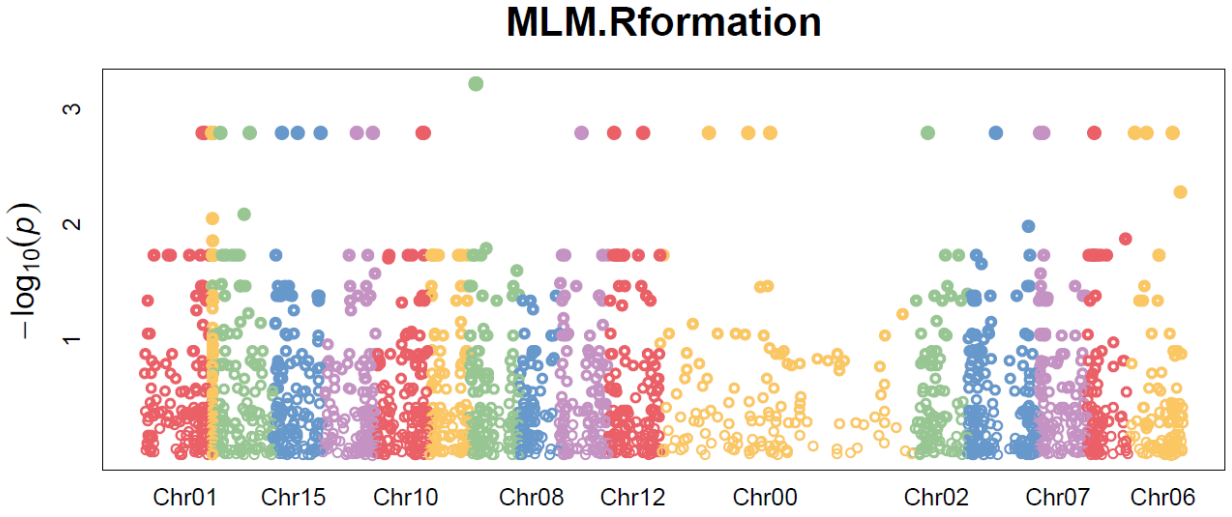

Figure 7.21. Manhattan plot for storage root formation shows a marker at an unidentified chromosome

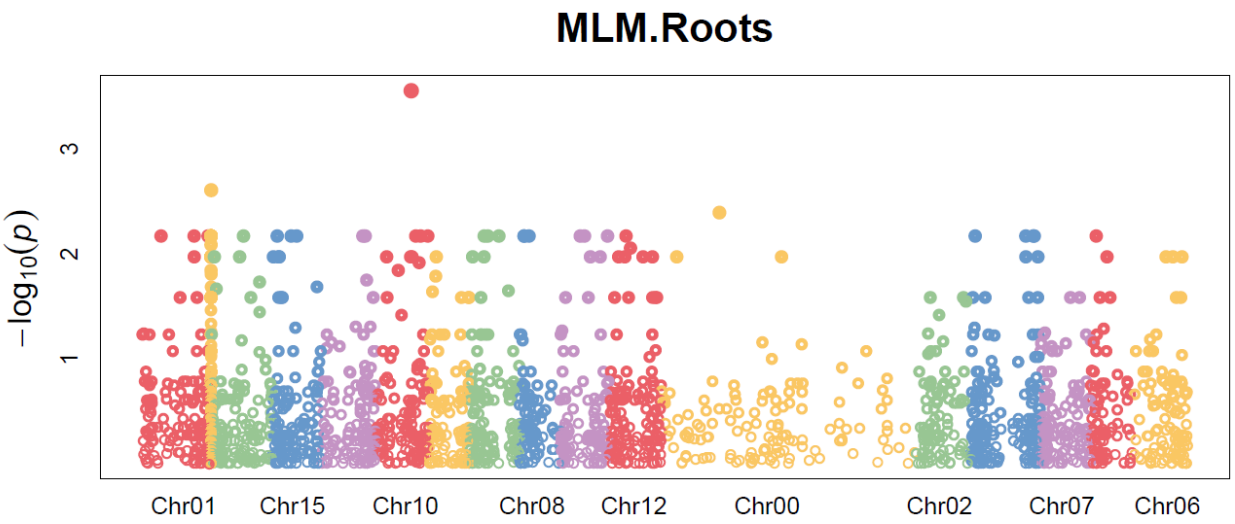

Figure 7.22. Manhattan plot for roots shows a marker at chromosome number 10

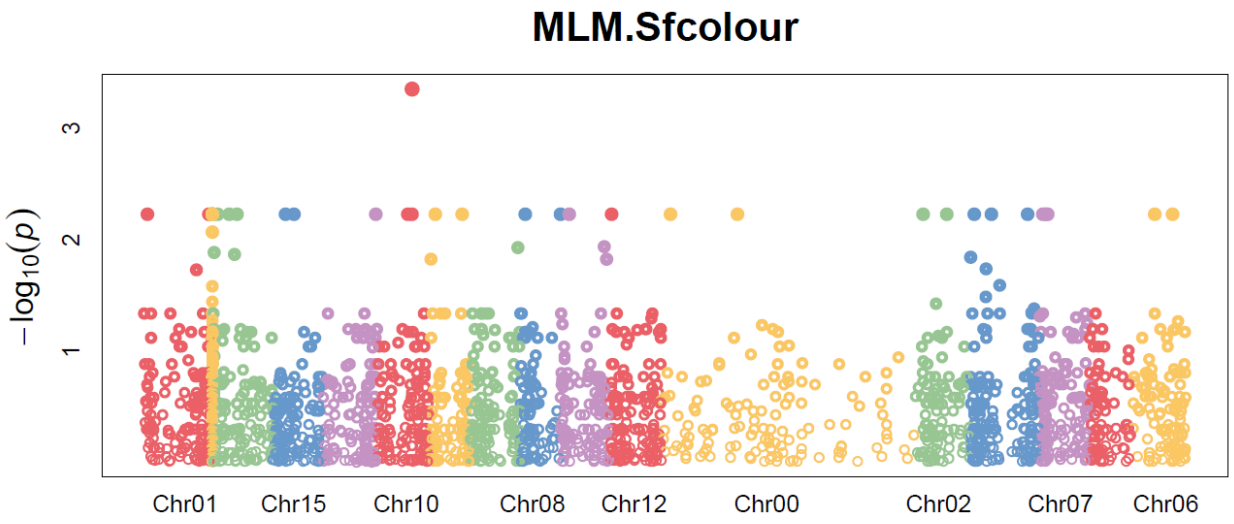

Figure 7.23. Manhattan plot for secondary flesh colour shows a marker at chromosome number 10

7.4 Discussion

A total of 19145 SNP markers used in this study were densely distributed across the sweetpotato genome suggesting that the markers covered possible mutations and linkage disequilibrium that exist between the markers and phenotypes. The markers also showed good quality since the frequency of heterozygous markers was low. The MLM used in the study fitted the data well as shown by a Q-Q plot that was almost a straight line. (Sun-Joo-Cho, 2021) pointed the benefitsof Genome wide association study as facilitation of greater resolution, ability to discern haplotype blocks small in size which are significantly correlated with quantitative trait variations and is a very economical method with high throughput (Sun-Joo-Cho, 2021). Genome-Wide association study was successfully conducted in cereals such as maize, rice, sorghum and millet (Thilakarathna et al., 2021).

The identified SNP markers are a huge opportunity presented for breeding. These markers include 100067303|F|0-13:A>C-13:A>C for flesh colour located on an unidentified chromosome, 7552141|F|0-33:C>A-33:C>A for intensity of flesh colour located on chromosome 2, 7631353|F|0-38:T>G-38:T>G located on chromosome 10, but linked to both root yield and secondary flesh colour while 11823423|F|0-11:A>T-11:A>T is associated with root formation but not on a specified chromosome. Markers-assisted breeding has shown to have several advantages that include early selection and also markers arestable and not affected by the environment since the heritability of a marker is a unity. Marker-assisted breeding has proved to be cheaper especially for quantitative traits that would requirephenotyping at multi-

locations to get a fair estimate of the phenotypic value of a genotype. Furthermore, the genomic prediction approach can be used with markers of important traits included in the genotype. This can improve the efficiency of genomic prediction. Furthermore,the increase in genotyping throughput and reduction in cost per data point offers a huge opportunity for marker-assisted breeding especially for clonally propagated crops like sweetpotato.

The Zimbabwe sweetpotato breeding program is at its infancy, and would require both infrastructural and technical support to effectively exploit marker assisted breeding. However, the identified markers could provide an excellent starting position for marker-assisted breeding in sweetpotato but verification of these markers would be required.

7.5 Conclusions

At LOD score of 3, flesh colour and root formation traits have markers at unidentified chromosome positions. However, the intensity of skin colour, roots, secondary flesh colour and size variability 2, 10, 10, and 15 respectively. Chromosome 10 has more influence on root traits. Competitive allele specific primers (KASP markers) can be developed from the identified markers following some validations using huge phenotypic data sets for these sweetpotato genotypes.

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CHAPTER 8

GENERAL DISCUSSION, CONCLUSION ANDRECOMMENDATIONS

8.1 Introduction

This chapter gives an overview of the study. It covers highlights of the main findings and their implications. The research was focused on identifying farmers' preferred sweetpotato genotypes, constraints, coping strategies, and exploring the level of sweetpotato genetic diversity in Zimbabwe, with the object of informing future breeding efforts. The first step towards formulating effective breeding strategies was to understand the genetic variability. The highly variable environments in Zimbabwe make the investigation of yield stability an important factor in the breeding programs. This research focus was used to formulate the objectives of the study and the following hypotheses were tested:

1. Smallholder farmers select sweetpotato cultivars to retain for production and utilization.
2. Diversity in agro-morphological traits exists among the sampled sweetpotato genotypes.
3. Diversity at the DNA level exists among the collected sweetpotato genotypes.
4. Variability in adaptation to different agro-ecological areas exists among sweetpotato genotypes collected in Zimbabwe.
5. Single Nucleotide polymorphism (SNP) markers are correlated to agronomic and quality attributes of sweetpotato storage roots.

8.2 Implications of the findings in increasing sweetpotato productivity and way forward

Results of the PRA and focused group discussions highlighted the importance of sweetpotato from a food security and income generation standpoint. Farmers preferred genotypes that can survive dry conditions, have higher yielding capacity, good taste, early maturity, resistance to diseaseand insect pests, market demand, long shelf life, cookability, and high dry matter. From this study, it was evident that local landraces are still featuring the most than improved varieties.

From this study, it was evident that local genotypes had reasonable yield potential and adaptable to local conditions. Efforts should be directed towards improved conservation and addressing production and marketing constraints that may be contributing to low yields; otherwise, increased yields will be unachievable.

Farmers indicated that the most production and marketing constraints were: low prices

(31.55%), insect pests (25%), diseases (20.83%), shortage of clean planting materials (14.29%), heat and drought (7.14%), shortage of labour (0.6%) and frost (0.6%). About (90%) of the farmers singled out weevils and moles as major pests of sweetpotato. Some of these constraints can be addressed through breeding and some by best agronomic practices. For example, breeding for drought-tolerant varieties is possible. Breeders can develop sweetpotato varieties adapted to low soil fertility and in this process farmers' desired characteristics such as high dry matter and taste could be incorporated.

The study found that farmers were using retained planting material, which is diseased and resulted in the loss of productivity. The results showed that it was not easy to run a viable sweetpotato enterprise partly because of depressed prices and middlemen creaming off the profits. Post-harvest losses were high due to the absence of a proper cold chain. Therefore, developmental efforts should prioritize infrastructure such as cold rooms, tissue culture laboratories in order to reduce the losses and also avail clean planting material for enhanced productivity. Most farmers used fertilizers, but the quantities and types of fertilisers were wrong in most cases. Extension support is thus vital in this respect, to assist the farmers in making right, informed decisions in their crop production. It was evident in the study that there is a need for more technical skills in sweetpotato production as well as increasing the extension: farmer ratio.

In Zimbabwe, there is a severe shortage of improved sweetpotato varieties. Although the farmers indicated their willingness to grow clean, improved sweetpotato varieties, they madeit clear that easy access to the material is still a big challenge. Shortage of clean planting material also leads to exorbitant prices. The way forward is for public institutions such asthe Horticulture research centre to scale up the production of tissue-cultured planting materialfor the benefit of sweetpotato farmers. As long as the farmers perceive no advantage in adopting improved varieties, they will not adopt them.

Another important trait that the farmers mentioned was early maturity. The farmers are aware that they can evade disease, drought, and frost by planting early. This is another opportunityfor breeders to breed for early maturing varieties, which can assist the farmers to sell their crop before gluts and also escape hunger.

The second objective was to assess the diversity of sweetpotato genotypes from Zimbabwe through an analysis of morphological attributes. This is the first study which combines morphological characterisation and use of molecular markers of *Ipomoea batatas* in

Zimbabwe. As a result, the gained knowledge will go a long way in extending the frontiers of crop breeding in Zimbabwe. The study revealed significant morphological variability. This offers an opportunity for strengthening sweetpotato breeding and conservation activities in Zimbabwe. Dendrograms which were used to establish the relationships between accessions are very important in future breeding efforts since breeders are now able to identify closely as well as distantly related accessions for crossing and coming up with desirable sweetpotato varieties. Closely related accessions which were considered to be duplicates were also implicated through use of dendrograms. These duplicates will not be considered for developing new sweetpotato varieties and will be discarded thus saving resources on conservation initiatives.

The focus of the third objective was to establish sweetpotato diversity at the molecular level from the collection of sweetpotato genotypes within Zimbabwe. Bosbok, UnknownC4, KwasakwasaC, and Kau7 are the four elements ofthe smallest set. These elements have large Gower's genetic distances of 2.54, 2.37, 1.65, and 3.20 respectively, compared to others. Analysis of molecular variance showed a very low PhiPT value (equivalent to FST value) of -0.017 suggesting panmixis and absence of among- population variance which might suggest close descendancy. The dendrogram produced can direct future breeding activities and conservation strategies for sweetpotato.

The morphological characterization identified three groups with sub-clusters while the molecular one identified 2 groups with one group containing only four genotypes. The morphological characterisation helped to identify genotypes with biological meaning such as based on some agronomic and quality traits. Morphological variation is usually more useful since it is an expression of genes while molecular variation could also include neutral variation that may not have significance in direct utilization or breeding. However, both tools sometimes complement each other and should be used jointly in breeding programmes.

The fourth objective was to assess the interactive effect of genotype and test environment on storage root and establish genotypes adapted to specific or across different agro-production areas of Zimbabwe. The study also identified genotypes that performed well across or in specific environments. Genotype G53 was stable and relatively high-yielding, and clearly showed that it performs well across a number of environments; therefore, it can be used for wide adaptation. Genotypes 94 (Murewa2Cross), G100 (Beauregard), G28 (Chidhumbe dhumbe), G87 (Mukambachaza), G13 (Germany 2), and G96 (Drumhead) were identified by AMMI and GGE biplot analyses as unstable but high yielding. Genotype 94 (Murewa2Cross)

won at Shamva, while genotypes G100 (Beauregard) and G28 (Chidhumbe dhumbe) won in the other locations and are therefore suitable for specific adaptation. Chiredzi was the most representative and discriminating site. Identification of only one mega-environment also means that variety evaluation will not necessarily have to be conducted in allpopulations of testing environments studied. A few locations can be chosen for variety evaluation and these will represent the rest of the mega-environment (Schwarz et al., 2014). The findings from this objective have significant practical implications for farmers who may unknowingly use sweetpotato genotypes better suited to a particular environment. Theperformance of genotypes adapted to specific environments may be significantly compromised when grown in nonadaptable areas. The best approach is to breed for niche genotypes that perform best in specific environments. However, the identified ideal test location Chiredzi, will require verification since this was based on a single season data. Zimbabwe has five agro-ecological regions, and the ideal testing location for sweetpotato will need to be ascertained based on multiple years data.

The fifth objective was to identify markers (SNPs) for agronomic and quality attributes in sweetpotato using Genome-Wide Association Study (GWAS). Thousands of markers used in this study were densely distributed across the sweetpotato genome suggesting that the markers covered possible mutations and linkage disequilibrium that exist between the markers and phenotypes. The markers also showed good quality since the frequency of heterozygous markers was low. The MLM used in the study fitted the data well as shown by a Q-Q plot that was almost a straight line. Genome-wide association study facilitates greater resolution, ability to scrutinize the haplotype blocks small in size which is significantly correlated with quantitative trait variations and is a very economical method with high throughput (Mohammadi et al., 2020). The identified SNP markers can speed up the breeding process through rapid identification of desirable attributes in different accessions. Marker-assisted breeding has proved to be cheaper especially for quantitative traits that would require testing at multi-locations to get a fair estimate of the phenotypic value of a genotype. Furthermore, the genomic prediction approach can be used with markers of important traits included in the genotype. This can improve the efficiency of genomic prediction. Furthermore, the increase in genotyping throughput and reduction in cost per data point offers a huge opportunity for marker-assisted breeding especially for clonally propagated crops like sweetpotato.

8.4 Conclusions

Zimbabwe has diverse sweetpotato genotypes which can be exploited in furthering sweetpotato

breeding efforts. However, for sound commercialization of sweetpotato in Zimbabwe,there is a need to overcome socio-economic, biotic, and abiotic challenges experienced by farmers. The following conclusions can be made from the findings of the study:

- Sweetpotato breeding programs need to be strategized to address the specific needs of farmers and consumers.
- Sweetpotato attributes preferred by farmers differed according to the region and use.
- Characteristics of sweetpotato cultivars preferred by the farmers included: high yieldingcapacity, taste, days to maturity, resistance to diseases and insect pests, market demand, long shelf life, cookability, and high dry matter.
- Interventions including access to means of transport, clean planting material, access to market information, and availability of reliable markets will increase sweetpotato production and productivity.
- Women play a significant role in the conservation of sweetpotato diversity in Zimbabwe.
- There was significant genotype by environment interaction on sweetpotato genotypes ofZimbabwe necessitating the formation of separate breeding schemes for distinct environments. However, genotype G53 showed stability across test environments and can be recommended for wide adaptation.
- Among the test environments, Chiredzi was the most representative and discriminating site while Harare was the most unfavourable site for sweetpotato fresh root yield evaluations.
- In conclusion, the extent of genetic variation in environmental sensitivity for sweetpotatostorage root yield is sufficient to warrant breeding for specific and wide adaptation.
- The thousands of the markers used were densely distributed across the sweetpotato genome suggesting that the markers covered possible mutations and linkage disequilibrium that exist between the markers and phenotypes.
- The markers also showed good quality since the frequency of heterozygous markers waslow. The MLM used in the study fitted the data well as shown by a Q-Q plot that was almost a straight line.
- The identified as SNP markers are a huge opportunity presented for breeding.
- Marker-assisted breeding has proved to be cheaper especially for quantitative traits that would require to be assessed at multi-locations to get a fair estimate of the phenotypicvalue of a genotype.

- Finally, genotyping-by-sequencing (GBS) and morphological analysis were successful in revealing the diversity of sweetpotato genotypes in Zimbabwe.

8.5 Overall recommendations

The main thrust of the study was to assess the genetic diversity of sweetpotato genotypes from Zimbabwe. However, there are several areas for further research:

1. There is need for scheduled collection expeditions which cover the whole country so that a wider genome coverage is achieved. Scheduling collection expeditions is critical because new accessions are continuously added from other countries such as Mozambique.
2. Sweetpotato breeders should establish well-characterized sweetpotato germplasm observing gene bank requirements.
3. Future studies should also consider sweetpotato landraces from neighbouring countries such as Mozambique, Zambia and Malawi in order to compare them with those in Zimbabwe so as to assess genetic diversity.
4. Concerted efforts by all sweetpotato value chain actors are required in order to ensure sustainability in sweetpotato production.

8.6 Further areas of study

1. Trials need to be repeated in a range of localities or alternatively by growing plants in a controlled environment since morphological characteristics are known to be susceptibleto environmental influences (Schwarz et al., 2014).
2. There is a need to conduct genetic mapping so that only genotypes with important traitsare conserved.
3. Investigations on how improvements in the sweetpotato marketing system can result inthe viability of sweetpotato growing are needed.

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Appendix 1. Sweetpotato collections from different regions of Zimbabwe

Genotype Code	Genotype name	Collection site	Coordinates	Skin colour	Flesh colour
G1	KAU1	Africa University	458013.74m E 7910545.58m S	White	White
G2	KAU2	Africa University	458013.74m E 7910545.58m S	Purple-red	Cream
G3	KAU3	Africa University	458013.74m E 7910545.58m S	Purple-red	White
G4	KAU4	Africa University	458013.74m E 7910545.58m S	Pink	Cream
G5	KAU5	Africa University	458013.74m E 7910545.58m S	Purple-red	Cream
G6	KAU6	Africa University	458013.74m E 7910545.58m S	Purple-red	Cream
G7	KAU7	Africa University	458013.74m E 7910545.58m S	Cream	Pale yellow
G8	KAU8	Africa University	458013.74m E 7910545.58m S	White	White
G9	KAU9	Africa University	458013.74m E 7910545.58m S	Purple-red	Cream
G10	Chingova	Horticulture Research Centre	312920.7 E 181246.3 S	White	White
G11	Red Jewel	Horticulture Research Centre	312920.7 E 181246.3 S	White	Cream
G12	Brondal	Horticulture Research Centre	312920.7 E 181246.3 S	Purple-red	White
G13	Germany 2	Horticulture Research Centre	312920.7 E 181246.3 S	Purple-red	White

G14	Dube	Horticulture Research Centre	312920.7 E 181246.3 S	Cream	Cream
G15	Ndirendire	Horticulture Research Centre	312920.7 E 181246.3 S	Cream	White
G16	Mozambique White	Horticulture Research Centre	312920.7 E 181246.3 S	Red	White
G17	Mafutha	Chiredzi	351731.56M E 7675051.94m S	Pink	Cream
G18	Pamhai	Chiredzi	351731.56M E 7675051.94m S	White	White
G19	Cordner	Chiredzi	351731.56M E 7675051.94m S	Orange	Pale-Orange
G20	Kazambia	Karoi	294132.00 E 294125.00 m S	Purple-Red	Cream
G21	Mukadziusaende	Chiredzi	351731.56M E 7675051.94m S	Cream	White
G22	Bosbok	Chiredzi	351731.56M E 7675051.94m S	Purple-Red	White
G23	Unknown Chipinge	Chipinge	323712.12.00 E 20120.00 S	White	Pale-Orange
G24	Chimutanja	Rusitu	485011.35m E 7782979.25m S	Cream	Pale-Orange

G25	Boarding Rusitu	Rusitu/ Kopa	484536.98 m E 7783002.96 mS	White	White
G26	Two Months	Cherutombo	313248 .00 E 181123.00 S	Cream	Cream
G27	Unknown 12Tamandai	Tamandai	483969.02 m E 7755429.98 m S	Cream	White
28	Chidhumbedhumbe	Rusitu	433515.20 m E 7716186.39 m S	Dark-Purple	White
G29	Unknown 10 Rusitu	Rusitu	433515.20 m E 7716186.39 m S	Cream	Cream
G30	Unknown 11Tamandai	Tamandai	483969.02 m E 7755429.98 m S	Purple-Red	White
G31	Unknown 5 Chako	Chako	463957.64 m E 7752044.26m S	White	White
G32	Carrot Merino	Merino	464109.87m E 7737514.56m S	Purple-Red	Pale-Orange
G33	Kori Tamandai	Tamandai	483969.02 m E 7755429.98 m S	Purple-Red	White
G34	Kori Ngaoni	Ngaoni	456396.96m E 7787557.01m S	Purple-Red	Cream
G35	Kori T1 Rusitu	Rusitu	486407.02m E 7782644.98 m	Purple-Red	Cream

			S		
G36	Tiribhari	Rusitu	486407.02m E 7782644.98 m S	Red	White
G37	Mutenganehuku	Merino	464109.87m E 7737514.56m S	Purple-red	White
G38	Chizadzangoro	Merino	464109.87m E 7737514.56m S	White	Cream
G39	Gwasharandima	Rusitu	486407.02m E 7782644.98 m S	White	White
G40	Unknown 13	Ngaoni	456396.96m E 7787557.01m S	Cream	Pale-Yellow
G41	Unknown 14	Ngaoni	456396.96m E 7787557.01m S	Brownish-Orange	White
G42	Unknown 10 Tamandai	Tamandai	482795.37 m E 7754879.93m S	Cream	Pale-Orange
G43	Chibhahlengwe	Tamandai	482795.37 m E 7754879.93m S	Purple-red	White
G44	Chimarata Tamandai	Tamandai	482795.37 m E 7754879.93m S	Cream	Pale-Orange

G45	Kori	Tamandai	482795.37 m E 7754879.93m S	Pink	Cream
G46	Unknown Rusitu	Rusitu	486407.02m E 7782644.98 m S	White	Pale-Yellow
G47	Chimarata Rusitu	Rusitu	486407.02m E 7782644.98 m S	White	Cream
G48	Gwasharandima	Rusitu	486407.02m E 7782644.98 m S	White	White
G49	Unknown 8R	Rusitu	486407.02m E 7782644.98 m S	Cream	White
G50	Dambaradzi	Rusitu	486407.02m E 7782644.98 m S	Purple-red	White
G51	Unknown 2Merrino	Merino	464109.87m E 7737514.56m S	Cream	White
G52	Gubhe	Merino	464109.87m E 7737514.56m S	Pink	White
G53	Unknown 1	Chako	463957.64 m E 7752044.26m S	Cream	White
G54	Unknown 7	Chako	463957.64 m E 7752044.26m	N/A	N/A

			S		
G55	Unknown 6	Chako	463957.64 m E 7752044.26m S	White	White
G56	Unknown CPG	Chipinge urban	-	Purple-Red	White
G57	Harare	Merino	463581.70m E 7737906.97m S	White	Cream
G58	Fost	Merino	463581.70m E 7737906.97m S	Purple-red	Cream
G59	Chibikiravaenzi	Merino		Purple-red	Cream
G60	Unknown 3 Merino	Merino	463581.70m E 7737906.97m S	Cream	White
G61	Chibhutata	Merino	463581.70m E 7737906.97m S	White	White
G62	Hwedza 1	Hwedza	-	White	Cream
G63	Muzvareshonga	Hwedza Irrigation	-	Purple-red	White
G64	Hwedza 5	Nyamhemba Irrigation	-	White	Cream
G65	Carrot Nyamhemba	Nyamhemba Irrigation	-	Cream	Cream
G66	Hwedza 8	Chigondo Irrigation	369361.32. m E 7923873.56m S	White	Cream
G67	Unknown	Hwedza	-	N/A	N/A
G68	Kwasa Kwasa H	Chigondo Irrigation	369361.32. m E 7923873.56m S	White	Pale-Orange
G69	Chingova C	Chigondo Irrigation	369361.32. m E 7923873.56m S	Cream	Cream
G70	Hwedza C	Chigondo Irrigation	369361.32. m E 7923873.56m S	Cream	Cream
G71	Hwedza 6	Nyamhemba Irrigation	374116.47 m E 7927938.52 m S	Cream	Cream

G72	Hwedza 5H	Chigondo Irrigation	369361.32. m E 7923873.56m S	Cream	White
G73	Chigondo 2	Chigondo Irrigation	369361.32. m E 7923873.56m S	Purple-red	White
G74	Chigondo 1	Chigondo Irrigation	369361.32. m E 7923873.56m S	Cream	Cream
G75	Chigondo 3	Chigondo Irrigation	369361.32. m E 7923873.56m S	Purple	White
G76	Chigondo 4	Chigondo Irrigation	369361.32. m E 7923873.56m S	Cream	White
G77	Chigondo 7	Chigondo Irrigation	369361.32. m E 7923873.56m S	White	White
G78	Kwasakwasa	Chigondo Irrigation	369361.32. m E 7923873.56m S	Cream	White
G79	Germany 2 Domboshawa	Domboshawa	302984.00m E 8051797.53m S	Purple-Red	White
G80	Unknown 3Domboshawa	Domboshawa	308721.28m E 8057651.84m S	Purple-Red	White
G81					
G82	Makope	Domboshawa	302984.00m E 8051797.53 m S	Purple-Red	White
G83	Unknown 2 D	Domboshawa	302984.00m E 8051797.53 m S	White	White
G84	Unknown 1	Domboshawa	302984.00m E 8051797.53 m S	Purple-Red	Cream
G85	Germany 1	Domboshawa	302984.00m E 8051797.53 m S	Purple-Red	White
G86	Unknown 4Domboshawa	Domboshawa	302984.00m E 8051797.53 m S	White	Cream
G87	Mukambachaza	Domboshawa	307529.41 m E 8056157.29 m S	White	Cream
G88	Dmbararwa	Domboshawa	307529.41 m E 8056157.29 m S	Red	White

G89	Chidhikisoni	Domboshawa	307529.41 m E 8056157.29 m S	White	White
G90	Unknown 2	Igava	374116.47 m E 7927938.52 m S	Purple-red	Cream
G91	Chingova	Igava	374116.47 m E 7927938.52 m S	White	Cream
G92	Shirikadzi	Igava	374116.47 m E 7927938.52 m S	Purple-Red	White
G93	Murewa Cross	Cross Murewa	414233.00m E 8052487.00 m S	Purple-red	White
G94	Unknown Cross	Murewa	370941.10 m E 8048103.08 m S	White	White
G95	Murewa	Murewa	370941.10 m E 8048103.08 m S	Cream	White
G96	Drumhead	Igava	374116.47 m E 7927938.52 m S	Dark-Purple	White
G97	Birchenough	Igava	374116.47 m E 7927938.52 m S	Purple-Red	White
G98	Carrot 1	Igava	374116.47 m E 7927938.52 m S	White	White
G99	Nyekete	Igava	374116.47 m E 7927938.52 m S	White	White
G100	Beauregard	Chihota	312405m E 183121 m S	Cream	Pale-Orange

Appendix 2. Questionnaire on assessing farmers' perceptions on preferred sweetpotato attributes, constraints, and farmers' coping strategies in Zimbabwe.

Date: ……/……/…….

Name of interviewee: …… Cell number: ……

Section A: Administration

Province

Location

District

Ward

Latitude

Altitude

GPS coordinates

Germplasm collection site

Section B: Demographic profile of interviewee

1. Gender of respondent: a) Male □ b) Female □
2. Gender of household head: a) Male □ b) Female □
3. Age of respondent: a) 16-19yrs □ b) 20-29yrs □ c) 30-49yrs □

   d) 50-60yrs □ e) ≥60yrs □
4. Education level of household head

   a) No formal education □ b) Primary education □

   c) Secondary education□ d) Tertiary Education □
5. Which varieties do you grow and why?

Variety Reasons for growing (select from key below) Desired improvements in current varieties (select from key below)

1. Early maturing 2) disease resistance 3) highly yielding 4) pest-resistant

5) Consumer demand 6) cooking quality 7) storage quality 8) Taste

6. Did you ever formally train in sweetpotato cultivation?

a) Yes □ b) No □

7. If yes, specify

a) Research □ b) extension workers □ c) Donor community□ d) Private sector□ e) Friend □

Section C. Sweetpotato production

8. How many seasons have you been actively producing sweetpotato?

a) 1year □ b) 2 years □ c) 3 years □ d) more than 3years □

9. What production system do you use for sweetpotato?

a) Irrigation □ b) Dryland □

10. Where do you grow sweetpotatoes?

a) Rainfed field □ b) garden □ c) homestead □ d) other(s)…….

11. Do you apply fertilizer to your sweetpotato? a) Yes □ b) No □

12. If yes, please specify the type of fertilizer you use.

a) Organic only □ b) Inorganic only □ c) both organic and inorganic

(Please name the fertilizers eg Compound S)…….

13. What method do you use for land preparation? (Multiple answers)

a) Hand hoeing □ b) Animal plough □
c) Tractor drawn plough □ d) Others (specify)……..

14. Which cultivation system do you use?

a) Flat □ b) Ridges □ c) Mounds □ d) Furrows□ e) Beds□

15. Why do you use that method of planting--?

What spacing do you use for the crop? -

16. Do you weed the crop? Yes/No

17. If "Yes" how many times do you weed before harvesting?

18. Which method of weeding do you use?

a) Hand pulling □ b) Hoeing □ c) Herbicide □ d) Others (specify)……………….…..

19. Do you use agricultural inputs for sweetpotato? Yes/No?

20. From the list of inputs below, which one is most expensive in sweetpotato production? (tick one)

a) Labor □ b) Planting material □ c) Fertilizers □

d) Pesticides□ e) Irrigation □ g) Others (specify)…………………………

21. Do you practice intercropping with sweetpotatoes? a) Yes □ b) No □

22. Do you rotate sweetpotato with other crops? a) Yes□ b) No □ 23. If your answers to 20 and21 above are yes, tick (√) the respective crop(s) you rotate or intercrop with.

Crop Rotation (√) Intercropping (√)

Maize

Finger millet

Groundnuts

Sorghum

Others (specify)

Section D. Diversity and characterization

24. How do you classify the sweetpotatoes grown in the area (multiple responses)?

a) By skin and flesh colour of tuber □ b) by the shape of leaves □ c) by colour of stems □ d) colour of leaves □ e) other specify……..

25. Which characteristics best describe the type of sweetpotato tubers you grow

Sweetpotato characteristic Tick (√)

White fleshed Red skin colour

Orange fleshed yellow skin colour

White fleshed white skin colour

Red uneven shape

Other (specify)

Section 4: The role of sweetpotato in livelihoods

26.What is your major livelihood/source of income? (on-farm)

a) Dryland crop production □ b) Horticulture □ c) livestock production □ d) poultry production □ e) rain-fed crop production□ f) rain-fed sweetpotato crop production □ Other(specify)

g) Others (specify)……

27. What is your main source of livelihood?

a) Formal employment □ b) cross border trading □ c) buying and selling □

d) Remittances □ e) brick moulding □ d) others (specify)……...

28. Rank the benefits of growing sweetpotatoes (from 1 to 7) Where 1 is the most important and 5 is the least important?

a) Tradition □ b) Food security □ c) Ideal climate □

d) Availability of good soils □ e) Income generation □ f) crop rotation □

g) Others specify……

29. Rank only 5 crops below according to importance. Ranking (1 - 5). Where 1 is the most important and 5 is the least important.

Crop Food Cash

Grain crops

Irish potatoes

Sweetpotato

Fruits

Vegetables

Others (specify)

Others (specify)

30. What is the average cost of a bucket of sweetpotatoes during the peak season?

31. What is the average cost of a bucket of sweetpotatoes during the off-season?

32. Where do you sell excess produce?

a) Neighbours □ b) Door to door □ c) Local market □

d) Fresh produce market □ e) Others (specify) ……

33. What is your average monthly income from sweetpotatoes?

a) Less than $50 □ b) 51-100 □ c) 101-200 □ d) 201 – 300 □ e) more than $300 □

34. Contribution of income from sweetpotato to household expenditure School fees %

Food

Medication

Transport

Others (specify)

Total 100

35. How often do you consume sweetpotatoes during the growing season?

a) less than once per week □ b) once per week □ c) Twice per week □

d) 3-5 per week □ e) Daily □

36. In which form do you consume sweetpotatoes?

a) As vegetable in main meal □ b) Boiled with tea □ c) Leaves as vegetables □ d) Chips □ e) Baking products □

Germplasm: planting material

37. Indicate your source of planting material

a) Own □ b) Relatives □ c) Neighbours/ Friends □

d) Shop □ e) Registered nurseries □ f) others (specify)……..

IF NOT GROWING OWN MATERIAL

38. Is it easy to get hold of planting material? a) Yes □ b) No □

If not, give the reason

39. Do you know of any farmers who produce and sell sweetpotato cuttings? Yes □ No □

40. If you grow your own material, how do you preserve your material

41.

42. (during winter time)?

Greenhouse □ b) Mulching □ c) Overwintering the tubers □

d) Others (specify)…….

43. Did you ever receive any formal training in making sweetpotato planting material?

a) Yes □ b) No □

44. If yes, from whom did you receive the training?

a) Research □ b) Extension workers □ c) Donor community□

d) Private sector□ e) Friend □ f) Others (specify) ..... 43. Which pest and disease control measures do you use (multiple)?

a) Rotation □ b) Disinfecting vines □ c) Chemical control □ d) All the above □

e) Others (*specify*)……

G. Constraints and opportunities in sweetpotato production

44. What are the major problems encountered in sweetpotato production? (Please tick one appropriate)

a) Access to clean planting materials □ b) Pest and diseases □ c) Drought □

d) Others ……..

45. Are you aware of climate change?

a) Yes □ b) No □

46 What is the major climatic challenge affecting sweetpotato production (please tick only one)?

Indicator	Tick where applicable
Late rainfall	
Long dry spells	
Erratic rainfall	
Shortened rainy season	
Increased frequency of droughts	
Shortened cold season	
Increased frequency of floods	
Others (*specify*)	

44. Does climate change affect production of sweetpotatoes yes □ no □ Explain why?

…….

45. Does climate change affect availability of planting vines yes □ no □ Explain why……

46. Do you agree that sweetpotato contributes to food and nutrition security during dry

seasons?

a) Not at all □ b) Agree □ c) Strongly agree □

47. Do you have any other information with regards to Sweetpotato germplasm that you might want to share? …….

Name of interviewer …….

Signature ……

Appendix 3. Agronomic and quality traits used in genome-wide association studies (GWAS)

Genotype	FreshWeight kgperPlant	Makertable per Ha	NonMakertable perHa	Roots Per plot	TotalYield t_Ha	Vinetip pubescence	Storage root shape	Storageroot surface defects	Storage root cortex thickness	Storage Root skin colour
KAU 6	0.14	4.53	0.82	7.31	5.35	5	2	2	3	8
Tiribhari	0.17	4.83	1.35	10.59	6.18	3	8	3	1	7
Unknown 5chako	0.14	3.84	1.22	6.30	5.05	0	8	3	1	1
Birchenough	0.16	5.17	0.83	5.34	6.01	3	9	3	3	8
Hwedza 3	0.16	4.98	0.88	6.77	5.86	3	8	3	1	1
Chingova Igava	0.13	3.82	1.12	3.20	4.94	3	8	3	3	1
Chimarata Tamandai	0.09	2.47	0.43	4.97	3.40	3	8	3	3	2
Kori	0.11	3.78	0.29	6.39	4.07	0	8	3	3	6
Chizadzangoro	0.14	4.14	1.05	5.50	5.19	3	8	2	3	1
Unknown 3M	0.07	1.98	0.61	9.64	2.60	0	3	0	3	8
Gubhe	0.17	5.07	1.40	5.80	6.46	3	9	3	3	6
Unknown 2Merino	0.10	3.22	0.44	6.24	3.66	3	9	5	1	2
Dube	0.15	3.33	2.16	5.00	5.50	3	9	5	1	2
KAU 9	0.50	5.24	1.30	3.71	6.54	3	8	3	1	8
Drumhead	0.21	5.49	2.20	5.95	7.69	3	8	3	1	9
Unknown 14Ngaoni	0.05	1.54	0.47	5.25	2.01	3	8	3	1	5
Red jewel	0.02	0.37	0.47	1.48	0.84	0	9	3	1	1

Genotype	FreshWeight kgperPlant	Makertable per Ha	NonMakertable perHa	Roots Per plot	TotalYield t_Ha	Vinetip pubescence	Storage root shape	Storageroot surface defects	Storage root cortex thickness	Storage Root skin colour
Bosbok	0.09	2.14	1.01	8.32	3.46	3	3	3	3	8
Muzvareshonga	0.14	4.70	0.43	6.49	5.10	0	8	3	3	1
Shirikadzi	0.15	4.78	0.77	5.65	5.55	2	3	3	3	8
Chingova	0.19	5.82	1.29	5.40	7.11	3	8	3	1	1
Fost	0.19	5.91	1.28	6.74	7.19	0	8	3	3	8
Chigondo 7Chigondo irrigation	0.17	5.47	0.96	6.50	6.43	0	8	3	1	2
KAU 2	0.20	5.37	1.95	5.70	7.32	2	9	3	2	8
Germany 1Domboshawa	0.19	5.93	1.17	6.00	7.11	3	2	3	3	8
Brondal	0.18	5.18	1.53	5.42	6.71	2	3	3	1	8
Kori T1 Rusitu	0.08	2.39	0.76	4.39	3.15	0	9	0	3	8
Chimarata Rusitu	0.16	5.40	0.66	4.40	6.05	3	8	3	3	1
Murewa 1Cross	0.16	4.21	1.58	4.90	5.79	3	9	3	3	8
Chimutanja	0.12	3.69	0.82	2.88	4.52	3	2	3	3	2
Chigondo 4Chigondo irrigation	0.16	4.58	1.16	6.50	5.74	3	8	3	1	8
Mutengangehuku	0.19	5.71	1.37	5.50	7.08		8	3	3	1
Unknown 2Igava	0.11	3.68	0.34	4.18	4.01	3	8	3	3	8

Genotype	FreshWeight kgperPlant	Makertable per Ha	NonMakertable perHa	Roots Per plot	TotalYield t_Ha	Vinetip pubescence	Storage root shape	Storageroot surface defects	Storage root cortex thickness	Storage Root skin colour
Cordner	0.04	1.48	0.71	6.90	2.18	3	3	5	1	4
Kori Ngaoni	0.09	4.26	0.94	2.13	3.26	0	8	0	3	8
Chibhutata	0.12	3.74	0.77	5.25	4.51	3	8	3		2
Germany 2Chigondo irrigation	0.13	4.30	0.55	4.75	4.85	3	3	3	1	2
Chigondo 3Chigondo irrigation	0.14	4.50	0.85	7.10	5.35	3	9	3	3	2
Unknown 1Merino	0.15	4.86	0.84	6.38	5.70	0	2	5	1	8
Hwedza 1	0.10	2.69	0.93	6.68	3.62	3	9	3	3	1
Chidhumbedhumbe	0.13	4.16	0.58	3.00	4.74	3	8	2	1	9
Chidhikisoni	0.12	3.58	0.68	5.13	4.26	3	2	3	1	1
Murehwa2Cross	0.06	1.36	0.81	5.00	2.17	3	9	3	5	1
MozambiqueWhite	0.10	2.80	1.03	4.14	3.83	7	9	3	3	7
Chingova Cnyamhemba Irrigation	0.17	4.34	1.77	5.75	6.11	5	8	3	1	1
Murewa	0.15	4.62	0.88	1.50	5.51	3	9	5	1	2

Genotype	FreshWeight kgperPlant	Makertable per Ha	NonMakertable perHa	Roots Per plot	TotalYield t_Ha	Vinetip pubescence	Storage root shape	Storageroot surface defects	Storage root cortex thickness	Storage Root skin colour
Unknown Chipinge	0.11	3.53	0.51	6.43	4.06	3	8	3	3	1
Carrot I	0.11	3.00	1.11	6.40	4.11	3	3	5	1	1
Nyekete	0.15	4.16	1.37	5.75	5.54	3	8	5	3	1
Hwedza Chigondo irrigation	0.12	4.06	0.44	5.78	4.49	3	3	3	3	2
Gwassharandima	0.10	3.01	0.61	5.28	3.62	3	9	3	2	8
Harare Chako	0.12	3.39	0.90	5.38	4.29	3	9	3	3	1
Hwedza 5H Nyamhemba	0.10	2.78	0.88	6.47	3.66	3	9	0	2	2
Unown Rusitu	0.10	2.84	1.02	5.80	3.86	3	8	3	1	1
Unknown 12Tamandai	0.12	3.89	0.55	4.84	4.43	0	9	3	1	2
Kwasakwasa	0.19	5.61	1.46	6.38	7.07	3	3	5	1	1
Pamhai	0.12	3.53	0.99	7.65	4.51	0	2	5	5	1
Kau 7						3	8	0	3	2
Dambararwa	0.06	0.96	1.26	4.34	2.21	3	3	3	3	7
Dambaradzi	0.12	4.04	0.30	5.00	4.34	5	3	0	3	8
Gemany 2	0.21	5.63	2.11	3.68	7.74	.	8	3	3	8
KAU 8	0.19	5.85	1.03	5.25	6.89	3	9	3	3	1

Genotype	FreshWeight kgperPlant	Makertable per Ha	NonMakertable perHa	Roots Per plot	TotalYield t_Ha	Vinetip pubescence	Storage root shape	Storageroot surface defects	Storage root cortex thickness	Storage Root skin colour
Unknown 4Domboshawa	0.19	3.50	0.36	3.08	3.86	3				
Carrot merino	0.43	2.34	0.60	5.75	2.94	3	8	5	3	8
Unknown 1Domboshawa	0.13	3.56	1.23	8.17	4.83	3	9	3	3	8
Mukadziusaende	0.15	3.85	1.54	8.34	5.40	3	3	3	1	2
Carrot Nyamhemba irrigation	0.19	5.64	1.46	7.50	7.10	0	8	3	3	1
Chibhahlengwe	0.15	5.09	0.59	7.39	5.68	0	3	3	3	8
Beargard	0.22	6.47	1.70	6.82	8.17	3	1	2	3	2
Hwedza 5	0.18	5.59	0.65	6.40	6.74	0	2	3	3	8
Unknown 10Rusitu	0.11	2.99	1.23	6.78	4.22	3	8	3	3	2
Kori Tandamai	0.14	4.05	1.28	4.80	5.33	3	8	0	3	8
Chibikiravaenzi	0.18	5.47	1.15	5.31	6.62	3	8	3	1	1
Unknown 2Domboshawa	0.13	5.18	2.07	5.17	4.85	3	2	3	3	1
KAU 1	0.15	4.63	1.07	6.75	5.69	7	8	3	3	1
Unknown 10Tandamai	0.14	4.01	1.04	7.09	5.05	0	9	3	1	2
Ndire-ndire	0.13	3.55	1.17	6.50	4.72	3	3	2	3	2

Genotype	FreshWeight kgperPlant	Makertable per Ha	NonMakertable perHa	Roots Per plot	TotalYield t_Ha	Vinetip pubescence	Storage root shape	Storageroot surface defects	Storage root cortex thickness	Storage Root skin colour
KAU 5	0.15	4.98	0.63	5.70	5.61	3	8	3	2	8
Chigondo 8	0.09	2.71	0.71	7.59	3.42	3	9	3	3	2
KAU 4	0.18	6.39	0.35	3.39	6.74	0	8	2	3	6
Chigondo 2Chigondo irrigation	0.17	3.86	2.36	4.61	6.23	3	2	0	3	2
Unknown 8Rusitu	0.11	3.28	0.92	5.78	4.20	0	9	3	5	2
Mukambachaza	0.36	1.32	0.56	6.74	1.52	3	8	3	3	8
KAU 3	0.16	4.61	1.44	4.75	6.05	3	3	3	3	8
Unknown 6Chako	0.17	5.40	0.88	6.08	6.28	3	8	0	1	2
Unknown 3Domboshava	0.17	5.38	0.75	6.75	6.13	0	8	3	1	8
Unknown 13Ngaoni	0.02	0.46	0.44	3.00	0.90	3	9	0	3	2
Boarding Rusitu Kopa	0.13	3.54	1.09	4.63	4.63	5	8	5	3	1
Kazambia	0.13	3.85	0.95	4.50	4.80	3	8	3	3	8
Hwedza 6	0.07	2.26	0.46	9.30	2.72	3	9	3	3	2
Mukambachaza	0.22	6.70	1.55	8.34	8.25	3	2	5	2	1
Unknown 11Tandamai	0.08	2.62	0.49	5.35	3.11	0	3	0	3	8

Genotype	FreshWeight kgperPlant	Makertable per Ha	NonMakertable perHa	Roots Per plot	TotalYield t_Ha	Vinetip pubescence	Storage root shape	Storageroot surface defects	Storage root cortex thickness	Storage Root skin colour
KAU 6	2	0	2	4	8	1	3	5	7	0
Tiribhari	3	0	1	0	0	7	7	5	7	0
Unknown 5chako	1	0	1	2	8	7	1	5	3	0
Birchenough	3	0	1	0	0	7	3	5	5	0
Hwedza 3	1	0	2	5	9	3	3	7	7	0
Chingova Igava	1	0	2	1	9	3	3	5	5	3
Chimarata Tamandai	1	6	4	2	1	7	7	3	7	3
Kori	3	0	2	1	3	5	3	5	7	0
Chizadzangoro	1	0	1	0	0	5	5	5	7	0
Unknown 3M	1	0	2	1	3	7	3	3	5	0
Gubhe	6	0	1	2	3	7	9	5	5	3
Unknown 2Merino	2	0	1	3	9	7	3	5	5	3
Dube	2	0	2	3	8	5	3	5	7	0
KAU 9	3	0	2	0	0	5	3	5	7	0
Drumhead	3	0	1	0	0	3	3	5	5	0
Unknown 14Ngaoni	1	0	1	0	0	3	5	3	3	0

Genotype	FreshWeight kgperPlant	Makertable per Ha	NonMakertable perHa	Roots Per plot	TotalYield t_Ha	Vinetip pubescence	Storage root shape	Storageroot surface defects	Storage root cortex thickness	Storage Root skin colour
Red jewel	1	0	2	0	0	3	3	7	7	0
Bosbok	2	6	1	2	8	3	3	3	3	0
Muzvareshonga	1	0	2	3	8	3	5	5	7	0
Shirikadzi	2	0	1	0	0	5	3	5	7	0
Chingova	1	0	1	2	8	7	5	5	5	0
Fost	2	6	1	0	0	7	5	5	5	0
Chigondo7C Chigondo irrigation	3	0	1	2	8	7	3	3	5	0
KAU 2	2	0	2	0	0	7	3	5	3	0
Germany 1Domboshawa	3	1	1	0	0	7	3	5	5	0
Brondal	1	7	1	2	3	3	3	3	3	0
Kori T1 Rusitu	3	0	2	0	4	3	5	3	7	0
Chimarata Rusitu	1	0	2	1	4	3	2	7	7	0
Murewa 1Cross	2	0	1	2	8	3	3	7	5	3
Chimutanja	1	6	6	3	1	7	3	3	3	3

Genotype	FreshWeight kgperPlant	Makertable per Ha	NonMakertable perHa	Roots Per plot	TotalYield t_Ha	Vinetip pubescence	Storage root shape	Storageroot surface defects	Storage root cortex thickness	Storage Root skin colour
Chigondo 4Chigondo irrigation	1	1	1	0	0	7	3	5	5	0
Mutengangehuku	1	0	2	0	0	3	9	5	7	0
Unknown 2Igava	2	3	2	4	4	7	5	7	5	0
Cordner	2	2	6	4	5	5	1	3	3	3
Kori Ngaoni	1	0	2	0	0	3	5	5	7	0
Chibhutata	1	0	1	2	8	5	5	3	3	0
Germany 2Chigondo Irrigation	3	0	1	2	8	3	3	5	7	0
Chigondo 3Chigondo irrigation	3	0	2	0	0	3	5	3	3	0
Unknown 1Merino	1	0	2	3	7	3	5	3	5	0
Hwedza 1	2	0	1	2	3	3	3	5	5	0
Chidhumbedhumbe	3	0	1	8	6	3	5	3	7	0
Chidhikisoni	1	0	1	2	8	7	5	3	7	0

Genotype	FreshWeight kgperPlant	Makertable per Ha	NonMakertable perHa	Roots Per plot	TotalYield t_Ha	Vinetip pubescence	Storage root shape	Storageroot surface defects	Storage root cortex thickness	Storage Root skin colour
Murehwa 2Cross	1	0	1	0	0	3	5	7	7	0
Mozambique white	1	1	1	0	0	7	5	5	7	0
Chingova Cnyamhemba Irrigation	1	0	6	2	8	5	3	5	3	0
Murewa	2	6	1	0	0	3	3	5	5	3
Unknown Chipinge	1	0	6	4	8	7	5	5	5	3
Carrot I	2	0	1	0	0	5	5	7	5	7
Nyekete	2	0	1	0	0	7	3	5	5	7
Hwedza Chigondo irrigation	3	0	2	0	0	5	1	3	7	0
Gwassharandima	2	0	1	0	0	3	3	5	7	0
Harare Chako	1	0	1	2	3	3	3	7	5	3
Hwedza 5H Nyamhemba	1	0	2	1	8	3	3	3	7	3
Unkown Rusitu	2	0	4	1	3	7	5	5	5	0

Genotype	FreshWeight kgperPlant	Makertable per Ha	NonMakertable perHa	Roots Per plot	TotalYield t_Ha	Vinetip pubescence	Storage root shape	Storageroot surface defects	Storage root cortex thickness	Storage Root skin colour
Unknown 12Tamandai	2	6	1	0	0	3	7	7	5	0
Kwasakwasa	1	0	1	2	8	3	5	7	3	3
Pamhai	2	0	1	8	2	3	3	3	3	0
Kau 7	2	4	4	4	6	7	3	7	7	0
Dambararwa	1	1	1	2	2	7	5	3	3	0
Dambaradzi	1	0	1	2	3	3	7	7	7	0
Gemany 2	2	0	1	0	0	3	3	5	5	0
KAU 8	2	0	1	2	3	3	3	7	5	0
Unknown 4Domboshawa										0
Carrot merino	2	7	6	6	9	3	5	7	7	7
Unknown 1Domboshawa	2	1	2	0	0	3	3	5	7	0
Mukadziusaende	1	0	1	0	0	5	3	3	7	0
Carrot Nyamhemba irrigation	1	0	2	1	8	5	5	7	7	0

Genotype	FreshWeight kgperPlant	Makertable per Ha	NonMakertable perHa	Roots Per plot	TotalYield t_Ha	Vinetip pubescence	Storage root shape	Storageroot surface defects	Storage root cortex thickness	Storage Root skin colour
Chibhahlengwe	2	0	1	0	0	3	3	5	7	0
Beargard	2	0	6	2	6	3	3	5	7	0
Hwedza 5	1	7	1	0	0	3	5	5	7	0
Unknown 10Rusitu	2	0	2	4	3	7	3	3	3	3
Kori Tandamai	2	0	1	0	0	3	5	5	7	0
Chibikiravaenzi	2	0	2	0	0	5	3	5	5	0
Unknown 2Domboshawa	1	0	1	2	3	3	3	5	5	7
KAU 1	2	0	1	2	6	3	7	7	7	0
Unknown 10Tandamai	3	0	6	3	3	3	5	5	7	0
Ndire-ndire	3	0	1	0	0	3	3	7	7	0
KAU 5	2	0	2	0	0	3	3	5	5	0
Chigondo 8	1	0	2	0	0	3	3	5	5	0
KAU 4	3	0	2	0	0	5	3	3	3	0
Chigondo 2Chigondo irrigation	1	0	1	2	6	3	5	5	5	0

Genotype	FreshWeight kgperPlant	Makertable per Ha	NonMakertable perHa	Roots Per plot	TotalYield t_Ha	Vinetip pubescence	Storage root shape	Storageroot surface defects	Storage root cortex thickness	Storage Root skin colour
Unknown 8Rusitu	3	0	1	8	6	3	7	7	7	0
Mukambachaza	1	1	1	2	3	7	3	5	7	0
KAU 3	1	1	1	2	3	5	5	5	5	0
Unknown 6Chako	3	0	1	2	8	3	5	5	5	0
Unknown 3Domboshava	1	1	1	0	0	3	3	5	5	0
Unknown 13Ngaoni	3	0	4	0	0	7	6	5	5	0
Boarding Rusitu Kopa	1	0	1	2	3	7	3	7	7	3
Kazambia	1	1	2	4	3	7	3	7	7	0
Hwedza 6	3	0	2	0	0	3	1	3	5	0
Mukambachaza	1	0	2	1	6	3	5	3	7	3
Unknown 11Tandamai	2	0	1	0	0	1	7	7	5	0