Breeding of sweetpotato for improvement of root dry matter and β-carotene contents in Ethiopia

By

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Thesis Abstract

Sweetpotato [*Ipomoea batatas* (L.) Lam] is the second major crop among the root and tuber crops in Ethiopia contributing to food and nutrition security. Especially, the orange fleshed sweetpotato (OFSP) is a low-priced and sustainable source of vitamin A. It is useful to combat the problem of vitamin A deficiency (VAD) prevailing in Ethiopia and most sub-Saharan African countries. However, acceptance and adoption rate of the OFSP varieties by farmers is low due to the low root dry matter content (RDMC) of the released OFSP varieties. Thus, improving the RDMC of the OFSPs through breeding is vital to increase the adoption rate and thereby to improve vitamin A intake by the rural communities. Therefore, the objectives of the studies were: (1) to assess and document the major constraints affecting production, pre- and post-harvest handling, and farmers' preferences for sweetpotato in Ethiopia; (2) to determine the combining ability, type of gene action and heritability of RDMC and β-carotene content, and yield related traits of selected sweetpotato clones, for further evaluation and breeding; (3) to estimate the magnitude of genotype-by-environment (G x E) interactions and to select stable and high yielding candidate sweetpotato clones for RDMC, β-carotene content and fresh root yield, and to identify the most discriminating and representative test environments in Ethiopia; (4) to assess associations between yield and yield related traits, and to identify the most efficient yield-predicting traits in sweetpotato for effective selection; and (5) to determine the nutritional value of newly developed OFSP clones and to establish the associations between β-carotene content and micro-nutrients for targeted large scale production to alleviate nutrient deficiencies.

Firstly, a participatory rural appraisal (PRA) study was conducted in six selected districts from three major sweetpotato growing administrative zones in southern Ethiopia involving 183 farmers. PRA techniques including semi-structured interview, focus group discussions and discussion with key informants were used to collect data. The results indicated that sweetpotato is among the major crops grown in the study areas. According the respondents, the major pre-harvest constraints were heat and drought (21.6% respondents), shortage of planting materials (20.1%), shortage of land (15.7%), diseases (10.0%), insect pests (9.4%), a lack of draft power (8.1%) and shortage of money to cover input costs (7.9%) were the major pre-harvest production constraints. The major post-harvest constraints were poor access to markets (22.6% of respondents), poor market prices (19.1%), low yields (14.2%), low root dry matter content (13.6%), a lack of knowledge on processing (11.7%), a lack of processing equipment (11.1%) and transportation problem (7.7%). The primary criteria for sweetpotato variety selection by farmers were identified as resistance to heat and drought

(19.6% of respondents), RDMC (16.4%), taste (14.3%), root yield (13.6%) and, resistance to diseases and insect pests (13.3%).

Secondly, seven genotypes selected for their high RDMC, β-carotene content or fresh root yield were crossed using a half diallel mating design. A total of 28 genotypes: 21 crosses and 7 parents, were evaluated at four locations in Ethiopia using a 7 x 4 alpha lattice design with two replications. Significant differences ($p < 0.01$) were observed among genotypes across the four test environments for the following traits: RDMC, β-carotene, SPVD, fresh root yield and harvest index (HI). The general combining ability (GCA) to the specific combining ability (SCA) variance ratios were 0.96, 0.94, 0.74, 0.96 and 0.97 for RDMC, β-carotene content, SPVD, fresh root yield and HI, respectively, indicating that the inheritance of these traits was controlled mainly by additive genes. The following parents were considered good general combiners for the three traits: Ukrewe and PIPI for RDMC; Ukrewe, Resisto and Ejumula for β-carotene content and; Resisto and NASPOT-1 for fresh root yield. Good specific combiners were the families belonging to Ukrewe x Resisto, Resisto x Ogansagan, Ejumula x PIPI and NASPOT-1 x Temesgen with high RDMCs of 36.6, 37.5, 38.2 and 37.2%; β-carotene contents of 9844.7, 10590.3, 4685.6 and 5153.4 µg 100 g^{-1}, respectively. Also, these crosses had medium to high mean fresh root yields. Clones from these families were selected for advanced selection and breeding for high RDMC, β-carotene content and root yield.

Thirdly, G x E interaction and stability analyses were conducted across six environments (Halaba, Kokate, Areka, Arbaminch, Hawassa and Dilla) in southern Ethiopia. A total of 24 experimental clones selected based on their specific combining ability effects for RDMC, β-carotene content and root yield along with one local check variety were evaluated. Superior and stable candidate clones, and suitable environments were identified using Additive Main Effects and Multiplicative Interaction (AMMI) and Genotype Main Effect and Genotype by Environment Interaction (GGE) biplot analyses. Accordingly, four candidate clones designated as G1 (Ukrewe x Ejumula-10), G6 (Resisto x Ejumula-7), G19 (Resisto x Ogansagen-23) and G20 (Ejumula x PIPI-10) with above average RDMCs of 31.82, 32.60, 33.09 and 30.06%; high β-carotene contents of 12.48, 14.27, 16.30 and 13.99 mg 100 g^{-1}; and, stable and high fresh root yields of 25.09, 26.92, 21.30 and 25.46 t ha^{-1}, in that order, were selected for finishing off and recommendation. Among the sites covered in this study, Arbaminch was identified as the best environment for sweetpotato testing or production in the southern Ethiopia with a high mean RDMC of 32.9%, mean β-carotene content of 7.2 mg 100 g^{-1} and the highest mean fresh root yield of 37.1 t ha^{-1}.

Fourthly, correlation and path-coefficient analyses were conducted involving 24 newly developed sweetpotato genotypes and one check variety using 15 quantitative traits. Root

yield showed significantly positive correlations with most traits studied, indicating that component characters should be simultaneously selected for sweetpotato improvement. β-carotene content and root flesh colour showed a highly positive correlation (r = 0.76), suggesting the importance of root flesh colour as an indirect selection criterion of high β-carotene content in sweetpotato. With path-coefficients of 0.821, 0.776, 0.276, and 0.410, individual root weight, number of roots per plant, RDMC and above ground fresh weigh had high positive direct effects on fresh root yield, respectively. These traits can be used for indirect selection to improve root yield.

Finally, eight nutritional traits: β-carotene, protein, iron, zinc, starch, fructose, glucose and sucrose of the 25 newly developed sweetpotato genotypes were examined. The genotype designated as G8 (Resisto x PIPI-2) was the most promising with the highest contents of β-carotene (20.01 mg 100 g^{-1}), protein (7.08%), iron (2.55 mg 100 g^{-1}), zinc (1.42 mg 100 g-1), fructose (4.45%), glucose (5.34%) and sucrose (16.20%) followed by the genotypes G15 (Resisto x Temesgen-23) and G19 (Resisto x Ogansagen-23). This shows the potential of developing OFSP varieties enriched with these important micro-nutrients.

The present study revealed the possibility of breeding sweetpotato varieties that combined high RDMC, moderate β-carotene content, and high fresh root yields with wide or specific adaptation for large scale production in Ethiopia. Overall, the study assessed the major sweetpotato production constraints, developed valuable sweetpotato families with high combining ability and heterosis for RDMC, β-carotene content and fresh root yield. Four traits, including individual root weight, number of roots per plant, RDMC and above ground fresh weight, were identified for indirect selection to improve root yield. The newly developed candidate OFSP clones are good sources of vitamin A, iron and zinc with high levels of protein and soluble sugars including sucrose, glucose and fructose.

Declaration

I, Fekadu Gurmu Balcha, declare that:

1. The research reported in this thesis, except where otherwise indicated, is my original research.
2. The thesis has not been submitted for any degree or examination at any other university.
3. This thesis does not contain other persons' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from other persons.
4. This thesis does not contain other persons' writing, unless specifically acknowledged as being sourced from other researchers. Where other written sources have been quoted, then:
   a) Their words have been re-written but the general information attributed to them has been referenced.
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5. This thesis does not contain text, graphics or tables copied and pasted from the internet, unless specifically acknowledged, and the source being detailed in the thesis and in the reference sections.

Signed:

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Fekadu Gurmu Balcha

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

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Prof. Shimelis Hussein (Supervisor)

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Prof. Mark Laing (Co-Supervisor)

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Dedication

This thesis is dedicated to my beloved children Nufis and Natol who were born in 2012 and 2014 within my PhD study period.

Acronyms

AMMI	Additive Main Effects and Multiplicative Interaction
ANOVA	Analysis of Variance
CIP	International Potato Center
CSA	Central Statistical Agency
EIAR	Ethiopian Institute of Agricultural Research
GCA	General Combining Ability
GGE	Genotype and Genotype by Environment Interaction
G x E	Genotype-by-Environment
HI	Harvest Index
IPCA	Interaction Principal Component Axis
NIRS	Near Infrared Reflectance Spectrometry
OFSP	Orange Fleshed Sweetpotato
PRA	Participatory Rural Appraisal
RAE	Retinol Activity Equivalents
RDA	Recommended Daily Allowance
RDMC	Root Dry Matter Content
SARI	South Agricultural Research Institute
SAS	Statistical Analysis System
SCA	Specific Combining Ability
SNNPR	Southern Nation, Nationalities and People's Region
SPSS	Statistical Package for Social Sciences
SPVD	Sweetpotato Virus Disease
SSA	Sub-Saharan Africa
VAD	Vitamin A Deficiency
WFSP	White Fleshed Sweetpotato
WHO	World Health Organization

Table of Contents

Publications related to this thesis

Chapter 1

Fekadu Gurmu, Shimelis Hussein and Mark Laing. 2015. The potential of orange-fleshed sweetpotato to prevent vitamin a deficiency in Africa. International Journal of Vitamin and Nutrition Research 84(1): 65-78.

Fekadu Gurmu, Shimelis Hussein and Mark Laing. 2013. Self- and cross-incompatibilities in sweetpotato and their implications on breeding. Australian Journal of Crop Science 7(13): 2074-2078.

Chapter 2

Fekadu Gurmu, Shimelis Hussein and Mark Laing. 2015. Diagnostic assessment of sweetpotato production in Ethiopia: constraints, post-harvest handling and farmers' preferences. Research on Crops 16(1):104-115.

Introduction to Thesis

Background

Sweetpotato [*Ipomoea batatas* (L.) Lam] is the second major crop among the root and tuber crops in Ethiopia (CSA, 2015). During the 2014/15 main season, sweetpotato, potato and taro covered about 81% of the total area cultivated with root and tuber crops in country.

Nearly 20 million Ethiopians are dependent on sweetpotato as a staple food, reflecting the importance of the crop for food security and the livelihoods of rural communities. It is mainly grown in the eastern, southern and south western parts of the country (Tadesse, 2006; Tofu et al., 2007; Gurmu et al., 2015b). Currently, sweetpotato is being distributed to drought affected areas of the country where maize and other crops regularly fail due to recurrent droughts. Therefore, the importance of the crop is increasing in terms of cultivated area, production and number of sweetpotato growing households. According to Central Statistical Agency (CSA) of Ethiopia (CSA, 2011), in 2010, sweetpotato covered 81,000 ha with production of 736,349 tons. In the 2014/15 main cropping season, sweetpotato covered 59,269 ha with a production of 2,701,599 tons (CSA, 2015). These values could have increased if the production data for the short-rainy season were included. Over the last three years (2013-2015), sweetpotato production has shown a remarkable increase, while the area coverage has only slightly increased (CSA, 2013; 2014; 2015). For instance, the area coverage and productions over the three years were: 41,634 ha (1,185,051 tons) during 2012/13, 53,369 ha (1,782,725 tons, 2013/14) and 59,269 ha (2,701,599 tons, 2014/15) main cropping seasons. The production of 2014/15 is more than three-fold of the 2010 production, while production area being smaller. This was attributed to increased productivity per unit area due to the use of improved technologies by farmers, such as clean planting materials, fertilizers and timely weeding. Currently, the government has given due attention for root crops production due to the prevailing drought condition in the country.

In Ethiopia and other sub-Saharan African (SSA) countries sweetpotato is a preferred crop due to its high yield potential, adaptability to a wide range of environmental conditions, its versatility to grow as a companion crop, flexible planting and harvesting dates and its convenience for piece-meal harvest. However, sweetpotato production is challenged by various biotic (viruses and weevils), abiotic (drought, low soil fertility) and socioeconomic (shortage of planting materials, poor market prices) constraints. Low root dry matter content (RDMC) in the orange fleshed sweetpotato (OFSP) varieties and a lack of knowledge on post-harvest storage and

processing are some of the overriding constraints of the crop (Kapinga and Carey, 2003; Tadesse, 2006; Tofu et al., 2007; Ndunguru et al., 2009; Gurmu et al., 2015a). The OFSP varieties are known for their enhanced β-carotene content useful to alleviate vitamin A deficiency (VAD).

In Ethiopia a total of 24 sweetpotato varieties have been released, among which six are orange fleshed. Out of these 24 varieties, only one variety, named 'Awassa-83', is predominantly grown in most of the sweetpotato growing areas of the country. Farmers prefer to grow this variety due to its high fresh root yield, high RDMC and total biomass when compared to other varieties. However, this variety is a white fleshed type and has no β-carotene. VAD is a major public health problem in Ethiopia. Consequently, breeding and dissemination of OFSP varieties with enhanced β-carotene content remains an important goal of sweetpotato breeders in the country. The major challenge is that the OFSPs currently available in the country have low root dry matter content (RDMC) and this hampers their acceptance and adoption by smallholder farmers (Belehu, 1987; Belehu, 2003; Kapinga and Carey, 2003; Tadesse, 2006; Tofu et al., 2007). This necessitates breeding of a new generation OFSP varieties with high RDMC, enhanced micro-nutrients such as vitamin A, iron and zinc, resistance to the biotic and abiotic constraints, and a high level of consumer acceptance.

The roles of vitamin A in human nutrition

Vitamin A is an essential compound for human health. Children require vitamin A for normal mental and physical development. It is an essential micronutrient for pregnant and lactating mothers as well as for adults for healthy eyesight (Kapinga et al., 2005). Generally, it plays a role in metabolic functions, eyesight, regular growth and development, and the immune system (Bhaskarachary et al., 1995). According to the United States Institute of Medicine, vitamin A is a family of compounds including retinol, retinoic acid, and retinyl esters. Retinyl esters are the storage forms of vitamin A, usually as retinyl palmitate (United States Institute of Medicine, 2000). Retinyl palmitate is the most common storage form of vitamin A, although there are other common forms such as retinyl stearate, retinyl linoleate, and retinyl myristate (Burri, 2011).

Vitamin A plays an important role in the early embryonic development of all mammals, and in proper functioning of the immune system, rod cells in the retina of the eye and mucous membranes throughout the body (Toenniessen, 2000). It also helps with the maintenance of cell function for growth, epithelial integrity, red blood cell production, immunity and reproduction (Toenniessen, 2000; Hechtman, 2012). As mammals cannot synthesize vitamin A, they obtain it from their food. Therefore, consumption of a diversified diet with adequate amount of vitamin A

is vital. The major sources of vitamin A are: 1) animal products such as milk, butter, cheese, egg, chicken, kidney, liver, liver pate and fish oils in the form of retinol; and 2) plant products such as dark green and yellow vegetables including kale, yellow pepper, broccoli, spinach, turnip greens, carrot, squash, yellow fruits such as pumpkin, cantaloupe, apricot, ripe mango, and papaya, and root crops such as sweetpotato in the form of β-carotene (Toenniessen, 2000; Mwanga et al., 2003; Kapinga et al., 2005; Gurmu et al., 2015a).

Vitamin A plays a role in a variety of functions throughout the body. It is required for healthy vision, skin, tooth growth, hair, tissues, new cell growth, mucous membranes, gene transcription, immune function, embryonic development and reproduction, bone metabolism, haematopoiesis, antioxidant activity and, reduction of the risk of degenerative diseases such as cancer, cardiovascular diseases, cataract, and macular degeneration (Rodriguez-Amaya, 2001; West, 2002). It also affects vision, gene transcription, immune function, embryonic development and reproduction, bone metabolism, hematopoiesis, skin and cellular health and antioxidant activity (Graham and Rosser, 2000). It has a positive synergistic effect on iron and zinc bioavailability and hence, through the improvement of vitamin A status in children, it is possible to increase the bio-availability of various micro-nutrients and reduce child mortality rates by 23 to 30% (Beaton et al., 1993; Graham and Rosser, 2000; West, 2002, 2003; WHO, 2009).

Orange fleshed sweetpotato as a source of vitamin A

OFSP is a rich, low-priced and sustainable source of vitamin A. It provides vitamin A in the form of β-carotene, which is a precursor of vitamin A, that is converted to vitamin A by the human body (Mwanga et al., 2003; Kapinga et al., 2005). Orange is among the different sweetpotato storage root flesh colours which include white, cream, yellow, or red-purple (Burri, 2011). Orange flesh, with various degrees of color intensity, reflects a high β-carotene content. Most of the orange-fleshed sweet potato varieties contain 3000-16000 µg 100 g^{-1} of β-carotene and this contributes to 250-1300 µg 100 g^{-1} retinol activity equivalents **(**RAE) (Kapinga et al., 2010). Other major dietary pro-vitamin A carotenoids are alpha-carotene and beta-cryptoxanthin (Ohnishi and Kojinra, 1997).

Some of the recommended daily allowances (RDAs) by age and sex are: 1-3 years = 400 µg RAE, 4-6 years = 500 µg RAE, 7-10 years = 700 µg RAE, non-pregnant female over 10 years = 800 µg RAE, and males over 10 years = 1000 µg RAE. Therefore, small quantities of OFSPs, which may contain from 300-3000 µg RAE 100 g^{-1} fresh weight, can easily provide such RDAs and also serve as a rich source of other vitamins and nutrients (Woolfe, 1992). For example, the addition of 100 g OFSP in a daily diet can prevent VAD in children and significantly reduce the

death of mothers (Kapinga et al., 2005). This is because 6 µg β-carotene is equivalent to 1 µg of RAE (Woolfe, 1992; Toenniessen, 2000) and the RDA of vitamin A in adults on average basis is 750 µg RAE day^{-1}.

A 100 g OFSP can provide more than 6500 µg β-carotene (Christina, 2007), which is equivalent to more than 1000 µg RAE. Therefore, 100 g of OFSP day^{-1} exceeds the RDA to prevent VAD. As a result, depending upon the colour intensity of the OFSP variety used, and taking into account losses of β-carotene during cooking, which accounts for an approximately 20% loss through boiling (van Jaarsveld et al., 2006), a quarter of a cup to one cup of boiled and mashed sweetpotato meets the RDA of vitamin A of a young child (Hagenimana et al., 2001; Fleshman et al., 2011; Gurmu et al., 2015a). OFSP is also a good source of energy, which is equivalent to 293-460 kJ 100 g^{-1} (Woolfe, 1992; Hagenimana et al., 2001).

Problem statement

Vitamin A deficiency is among main health problems of major concern. VAD leads to blindness, retarded growth and death in many of the developing countries. It is estimated that some 3 million children in SSA under the age of 5 years suffer from partial or total blindness as a result of VAD (Kapinga et al., 2005; WHO, 2009; Gurmu et al., 2015a). It affects especially pre-school children and pregnant and lactating mothers. WHO (2009) report of VAD estimates between 1995 and 2005 indicated prevalence of night blindness and biochemical VAD in 45 and 122 countries, respectively in preschool-age children.

VAD is a serious health problem in most communities in Ethiopia, particularly affecting, young children and mothers. The deficiency is reaching alarmingly high proportions in some regions of the country (Tofu et al., 2007; Demissie et al., 2009; WHO, 2009). Demissie et al. (2009) reported 23-48% VAD prevalence among children, pregnant and lactating mothers in Ethiopia. A very high prevalence rate of clinical VAD, close to 8%, was reported in some parts of the country (Demissie et al., 2009).

Different strategies have been used to control VAD. The strategies include vitamin A supplementation of large doses in the form of capsules, fortification of commonly consumed food items such as oil, sugar, breakfast cereals and grain flour; and dietary diversification, which includes eating food items naturally rich in pro-vitamin A such as yellow/orange root crops, leafy vegetables and yellow/orange fruits (Kapinga et al., 2005; WHO, 2009; Gurmu et al., 2015a). The food items that provide vitamin A in its true form (retinol) such as fish oils, liver, milk, eggs and butter are expensive and therefore most African families with a subsistence livelihoods cannot afford to purchase them (Mwanga et al., 2003). Therefore, their major

sources of vitamin A are foods that are easily available and that provide vitamin A in the form of β-carotene.

OFSPs are relatively cheap and easily accessible sources of vitamin A to combat the problem of VAD affecting the poor community of most sub-Saharan African countries, including Ethiopia. Some OFSP varieties have been released in Ethiopia and are being widely promoted (Tofu et al., 2007). However, the acceptance of these varieties by farmers is very low, mainly due to the low RDMC of the OFSP varieties (Tadesse, 2006; Gurmu et al., 2015b). Farmers prefer to grow the white fleshed sweetpotato (WFSP) varieties that have high RDMC. However, the WFSP varieties have no β-carotene and this limits the efforts that are being made to combat VAD. To date, there was no strategic breeding program in Ethiopia targeted at enhancing the RDMC of OFSPs in order to increase their acceptance and adoption by farmers.

Therefore, improving the RDMC of the OFSP in Ethiopia through a deigned breeding program is vital to enhance their adoption by farmers and thereby improve the vitamin A intake of various communities. Consequently, selection of complementary parents with high levels of RDMC, β-carotene or other useful traits followed by designed crosses is needed to develop promising cultivars incorporating end users' preferences. This has to be followed by combining ability tests of parents and crosses, gene action and heritability of chosen traits and subsequent selection, and genotype-by-environment interaction testing of candidate clones before national variety release. Participatory rural appraisal is an integral component which involves farmers and other stakeholders to appraise pre- and post-harvest constraints and farmers' preferences for sweetpotato varieties.

Therefore, the following objectives were set forth in the present study:

Research objectives

The specific objectives of the study were:

1. To assess and document the major constraints affecting production, pre- and post-harvest handling, and farmers' preferences for sweetpotato in Ethiopia.
2. To determine the combining ability, type of gene action and heritability of RDMC and β-carotene content, and yield related traits of selected sweetpotato clones, for further evaluation and breeding.
3. To estimate the magnitude of G x E interactions and to select stable and high yielding candidate sweetpotato clones for root dry matter content, β-carotene content and fresh root yield, and to identify the most discriminating and representative test environments in Ethiopia.

4. To assess associations between yield and yield related traits and to identify the most efficient yield-predicting traits in sweetpotato for effective selection.
5. To determine the nutritional value of newly developed OFSP clones and to establish the associations between β-carotene content and other micro-nutrients for targeted large scale production to alleviate nutrient deficiencies.

Research hypotheses

The following hypotheses were tested:

- Sweetpotato production and post-harvest handling are constrained by various factors and farmers select sweetpotato varieties based on various criteria;
- Some clones have high combining ability and show heterosis for root dry matter, β-carotene and fresh root yield;
- There are significant G x E interaction effects on root dry matter, β-carotene and fresh root yield of sweetpotato across different environments;
- There are reasonable associations between different traits in sweetpotato;
- Newly developed sweetpotato clones will have different levels of nutrients, vitamins and minerals.

Outline of the thesis

This thesis comprises six chapters addressing the above objectives. Chapters 2 to 6 are written in the form of discrete research chapters, each following the format of a stand-alone research paper. Each chapter of the thesis was written following the system of referencing of the Journal of Crop Science, which is the main thesis format adopted by the University of KwaZulu-Natal. There are some unavoidable overlapping of contents and references between chapters.

The chapters are outlined as follows:

1. Introduction to thesis
2. Chapter 1: A review of the literature
3. Chapter 2: Diagnostic assessment of sweetpotato production in Ethiopia: constraints, post-harvest handling, and farmers' preferences
4. Chapter 3: Genetic analysis of root dry matter and β-carotene contents, and yield related traits in sweetpotato
5. Chapter 4: Genotype-by-environment interaction and stability of sweetpotato clones for root dry matter and β-carotene contents, and fresh root yield

6. Chapter 5: Correlation and path-coefficient analyses of root yield and related traits among selected sweetpotato clones
7. Chapter 6: Evaluation of newly developed orange fleshed sweetpotato clones for nutritional traits
8. Chapter 7: Thesis Overview

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CHAPTER 1

A review of the literature

This review describes the importance of Orage fleshed sweetpotato (OFSP) as a food security crop and as a source of vitamin A to combat the problem of vitamin A deficiency in Ethiopia. The constraints related to production and post-harvest handling of sweetpotato and possible solutions are highlighted. Furthermore, environmental requirements of sweetpotato and self- and cross-incompatibility problems related to the crop are briefly discussed. Finally, combining ability, heterosis, genotype-environment interaction and association among traits in sweetpotato are highlighted. This review may serve a guide to sweetpotato breeding for improved root dry matter, β-carotene, fresh root yield and a number of nutritional qualities.

1.1. Introduction

Sweetpotato [*Ipomoea batatas* (L.) Lam] belonging to the family Convolvulaceae is believed to have originated in the northern parts of South America and Central America (Zhang et al., 2000; Gichuki et al., 2003; Lebot, 2010). It is widely grown throughout the tropics and warm temperate regions of the world (Woolfe, 1992; Ray and Edison, 2005). Sweetpotato is one of the world's most important food crops, especially in developing countries, due to its high yield potential and adaptability to a wide range of environmental conditions (Lebot, 2010; Wang et al., 2011). It ranks seventh globally after wheat, rice, maize, potato, barley and cassava (Woolfe, 1992; Settumba et al., 2003; Mwololo et al., 2008). It is the fifth most important crop in sub-Saharan Africa (SSA). Sweetpotato is usually used as staple food, animal feed and a raw material for different industrial products. Some sweetpotato varieties, especially the OFSPs, are rich in β-carotene. The OFSPs could play a crucial role in preventing vitamin A deficiency that leads to blindness and maternal and pre-school children mortality in many of the developing countries (WHO, 2009; Wang et al., 2011; Gurmu et al., 2015a).

Sweetpotato is one of the food security crops in Ethiopia grown by smallholder farmers (Tadesse, 2006; Tofu et al., 2007; Gurmu et al., 2015b). Sweetpotato covered over 59,000 ha with production of over 2.7 million tons in the 2014/15 cropping season (CSA, 2015). A two year data of area coverage and production of selected root crops in Ethiopia is summarised in Table 1.1.

Production of sweetpotato is mainly confined to two regions in Ethiopia: the Southern Nation, Nationalities, and Peoples Region (SNNPR) and Oromia. The two regions contributed for 52

and 45%, respectively, of the total area covered by sweetpotato (Figure 1.1) during the 2014/15 main cropping season (CSA, 2015). Within the two regions, three zones: Sidama, Wolayta and Gamo Gofa of SNNPR (Figure 1.2) and West Welega, West Hararge and East Hararge of Oromia (Figure 1.3) are the major production areas. Sweetpotato is an integral part of cropping system in the eastern, southern and southwestern parts of the country (Tofu et al., 2007; CSA, 2010, 2010a). However, it was not a traditional crop in the northern parts of the country but efforts are being made to introduce the crop to these areas due its drought tolerant nature and the importance of the crop for food and nutritional security. The adaptability of sweetpotato to marginal environments makes it an important food security crop in the country. Some varieties take only a short period (3-4 months) to reach maturity, and therefore can reliably provide food in areas with short rainy seasons and prolonged droughts, especially when there is scarcity of other foods. Its convenience for mixed farming systems makes it an important component supporting resource poor farmers in improving their livelihoods (Belehu, 1987).

Moreover, sweetpotato is grown with minimal external inputs. The possibility of piecemeal-harvest is another advantage for the poor and women farmers to have a year-round food production and also to earn cash incomes (Kaguongo et al., 2010). However, sweetpotato production is constrained by biotic, abiotic and socio-economic factors that tend to reduce its production and productivity.

Currently there are six OFSP varieties released in Ethiopia (Tofu et al., 2007). Two of the varieties were widely disseminated to farmers for production. However, the acceptance of these varieties by farmers is very low. This has been attributed to the low RDMC of the OFSP varieties (Tadesse, 2006; Gurmu et al., 2015b). Most African farmers prefer to grow WFSP varieties due to their high RDMC. However, the WFSP varieties have no β-carotene, which limits their value as a source of vitamin A.

Table 1.1 Area cultivated and production of selected root crops in Ethiopia in 2013/14 and 2014/15 cropping seasons

Root crops	Area in hectares		Production in tones		Proportion of area coverage (2014/15)	Proportion of production (2014/15)
	2013/14	2014/15	2013/14	2014/15		
Beetroot	1,643.15	1,949.77	14,074.94	18,207.94	0.90	0.34
Carrot	1,602.46	3,697.27	6,712.03	14,297.01	1.71	0.26
Onion	24,375.70	22,769.52	219,735.27	230,745.19	10.51	4.25
Garlic	16,411.19	9,257.81	159,093.58	93,486.87	4.27	1.72
Yam	3,075.62	3,714.07	-	-	1.71	-
Taro	42,656.73	48,658.84	1,193,538.30	1,448,834.52	22.46	26.69
Potato	66,745.61	67,356.84	784,993.40	921,832.07	31.09	16.98
Sweetpotato	53,369.19	59,269.07	1,782,724.99	2,701,598.99	27.35	49.76
Total	209,879.56	216,672.29	4,160,872.51	5,429,004.41	100.00	100.00

Source: adapted from CSA (2015).

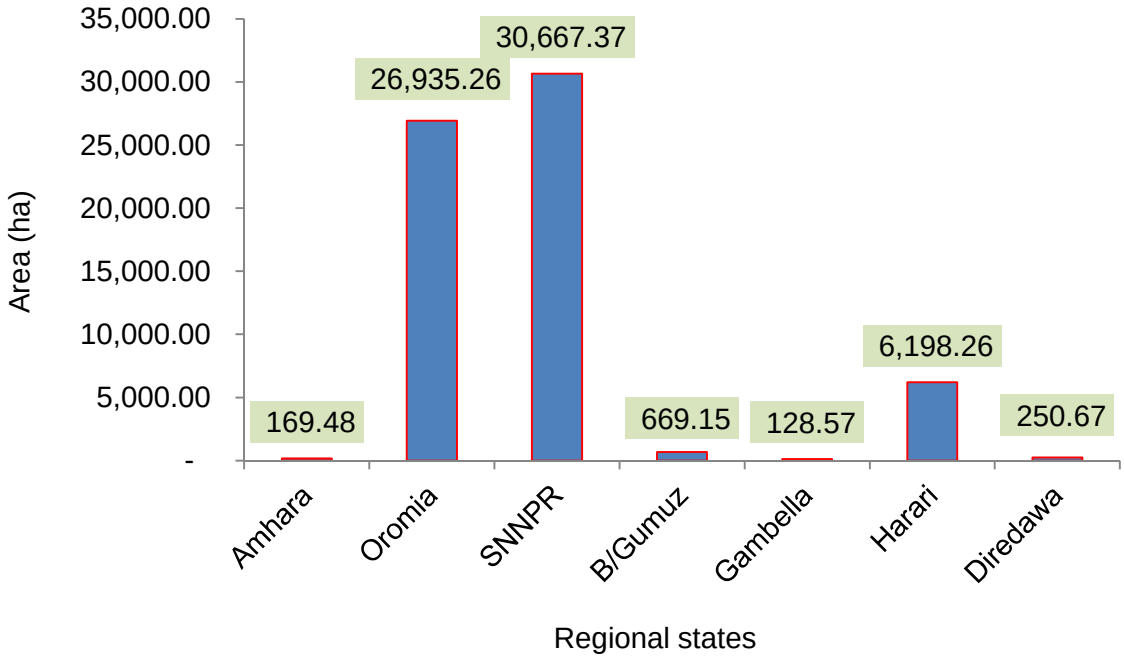

Figure 1.1 Major sweetpotato producing regions in Ethiopia in 2014/15 cropping season

Source: adapted from CSA (2015).

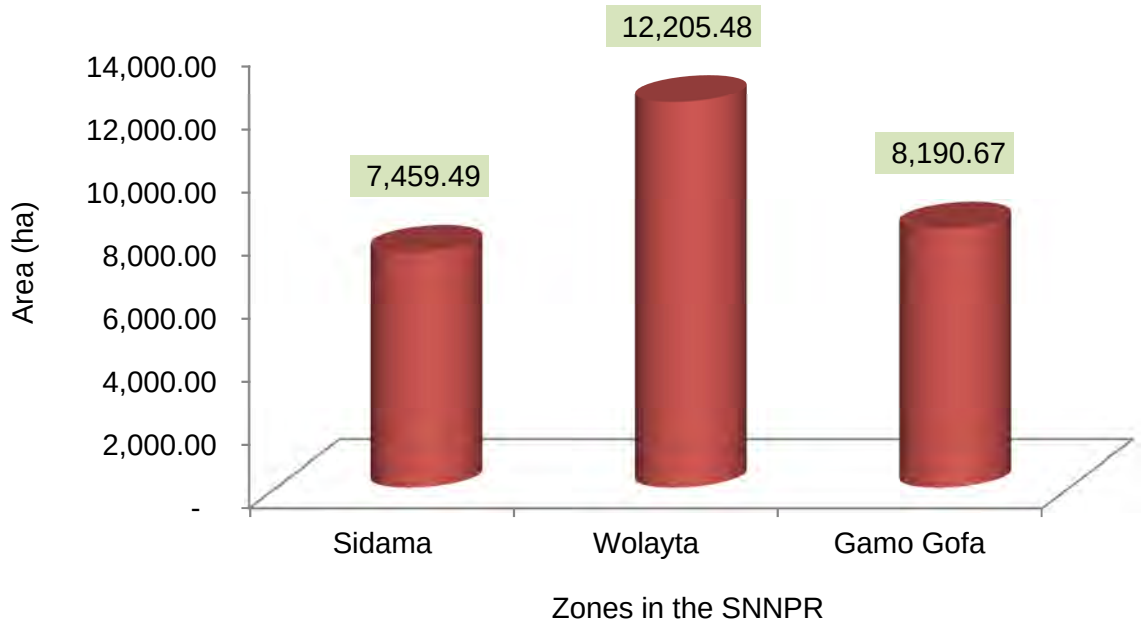

Figure 1.2 Major sweetpotato producing zones in the SNNPR of Ethiopia in 2014/15

Source: adapted from CSA (2015).

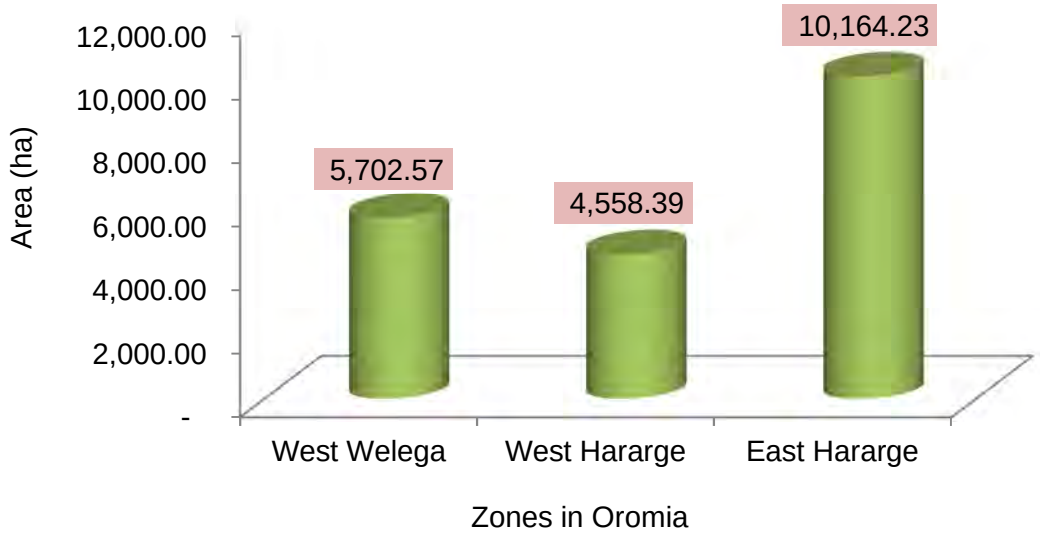

Figure 1.3 Major sweetpotato producing zones in Oromia region of Ethiopia in 2014/15

Source: adapted from CSA (2015).

1.2. Botanical description of sweetpotato

Sweetpotato is a perennial plant that has long trailing vines and leaves but it is treated as an annual crop when cultivated (Huaman, 1999; Lebot, 2010). The development of the crop from establishment to harvesting can take 90-150 days, depending on the variety and the environmental conditions under which the crop is grown (O'Sullivan et al., 1997). Sweetpotato storage roots are eaten while vines are used for propagation of the crop and as feed.

The root system of sweetpotatoes starts with adventitious roots that develop into primary fibrous root and then branch into lateral roots. If cuttings are used to grow sweetpotato, the adventitious roots arise from the cuttings within a day or two (Belehu, 2003). These roots grow fast to form the root system of the plant. When the plant matures, thick pencil roots are produced and become lignified. Those roots without lignin are fleshy and bulky, forming the major edible part of the sweetpotato plant (Huaman, 1999). Storage root formation can be either enhanced or inhibited by various factors. Belehu (2003), citing different authors, noted that exposure of sweetpotato plants to long photoperiods, water logged soil conditions, high levels of nitrogen supply and gibberellic acid applications inhibit root formation by encouraging lignification of the roots. On the other hand, a high potassium supply, aerated soil condition, low temperatures and short days encourage storage root formation. Sweetpotato plants start to form storage roots 30 to 35 days after planting and there is a continuous increase in root dry weight until harvesting time (Agata, 1982). The number of the storage root per plant varies depending on the variety and growing conditions.

Storage roots of sweetpotato vary in shape and size due to various factors such as the variety and soil type where the crop is grown. According to Huaman (1999), the outline of the root shape can be round, round-elliptic, elliptic, ovate, obovate, oblong, long oblong, long elliptic, and long irregular or curved. The roots also have different skin and flesh colour. The skin colour can be whitish, cream, yellow, orange, brown-orange, pink, red-purple, and very dark purple. The intensity of the root colour depends on the environmental conditions where the plant is grown (Huaman, 1999). The flesh colour can be white, cream, yellow, or orange. Some varieties show red-purple pigmentation in the flesh in a few scattered spots, pigmented rings or throughout the entire flesh of the root. The orange flesh colour with various degree of intensity reflects β-carotene content, while red and purple flesh colour show a high anthocyanin content (Huaman, 1999; Yoshinaga et al., 1999; Vimala and Hariprakash, 2011).

The sweetpotato vines are used as planting materials. The vine length depends on the growth habit of the variety and the availability of water in the soil (Huaman, 1999). Varieties with an erect growth habit are approximately 1 m long, whereas the spreading varieties can grow up to

5 m long. Typically vines are used as planting materials because they are relatively free of disease and insects, especially if the apical portion of the vine is used (Wilson, 1988; Belehu, 2003). Moreover, the roots are saved for consumption and marketing (Belehu, 2003). It is worth considering the number of nodes on a vine while taking cuttings for planting. There may be long cuttings with a few nodes. Therefore, vine internodes length determines the length of the vine to be used as planting material. According to Wilson (1988), if the internodes length is short or medium, cuttings of 30 cm length can be used. However, if the internodes are long, the cuttings should have a length of about 40 cm. The age of the crop also determines the quality of the planting material and hence the final storage root yield. Therefore, cuttings should be taken from plants that are two to three months old (CIP, 2009). These sweetpotato vines will produce a vigorous plant with better yield than cuttings from four to six months old plants. Vine cuttings can be planted immediately after cutting, while stored cuttings for one to three days under shade in humid conditions promotes root growth from nodal regions. Storage of the cutting for one to three days does not significantly affect the final yield (CIP, 2009).

Sweetpotato flowers are bisexual with five free sepals, five fused petals and five stamens fused at the base of the petals tube (Lebot, 2010). The colour of the petals is white to purple with many colour variations (Bassett, 1986). The petal is the most conspicuous part of the flower. At the base of the ovary, there are basal yellow glands that contain insect-attracting nectar (Huaman, 1999). Therefore, insects are the major means of pollination in sweetpotato. The five stamens that are attached to the corolla tube may be white, light or dark purple in colour. Since filaments vary in length (5 to 21 mm), the anthers height may be below, equal to or above the stigma height. The stigma is mostly white but may also be light or dark lavender (Bassett, 1986). Sweetpotato flowers usually open in groups soon after daybreak and fade by noon. They stay open only for a few hours. The stigma is receptive early in the morning and therefore crossing of sweetpotato is performed during the early morning hours. There are two ovaries in the pistil that develop to fruit (Onwueme, 1978; Bassett, 1986).

The fruits, also called capsules, can be glabrous (without hair) or pubescent (hairy). The mature fruit has four chambers, each of which may contain a seed, resulting in a maximum of four seeds per fruit (Bassett, 1986; Huaman, 1999). The mature seeds are flat on two sides and round on the other. They are usually dark brown or black in colour and weigh about 2 g per 100 seeds, which may vary based on parental type from 1.3 to 3 g (Bassett, 1986). The embryo and endosperm of sweetpotato seeds are protected by a thick, hard and impermeable testa. Therefore, seed germination is difficult and requires scarification either by mechanical abrasion or chemical treatment (Bassett, 1986; Huaman, 1991; Lebot, 2010). Sulphuric acid is often recommended for chemical scarification of sweetpotato seeds. Soaking the seeds in

concentrated sulphuric acid (98%) for 20-60 minutes, followed by washing in water for 5-10 minutes or neutralizing with a solution containing carbonate of soda, and rinsing in clean water is the recommended technique (Lebot, 2010). This technique gives about 95% germination success. It is also possible to soak the seeds overnight in water to improve germination, although germination will be irregular, occurring over several weeks (Lebot, 2010). Hand scarification using a sharp needle or a mechanical scarifier is also another option. Sweetpotato seeds do not have a dormancy period and therefore if the scarified seeds are provided with good environmental requirements, they can germinate within one to two days (Belehu, 2003; Gasura et al., 2008). Fruit and seed setting in sweetpotato depend on environmental factors, especially photoperiod and temperature, as well as genetic compatibility of parental clones.

1.3. Pre- and post-harvest production constraints to sweetpotato and methods used to identify the constraints

Sweetpotato production is limited by multiple factors including biotic, abiotic and socioeconomic constraints (Gurmu et al., 2015b). The biotic stresses include diseases, insect pests and weeds, whereas the abiotic factors are drought, very high/low temperatures and low soil fertility (Ndunguru et al., 2009; Gurmu et al., 2015b). Constraints related to socioeconomic and quality attributes are lack of improved varieties, lack of planting materials, low root yield, low β-carotene content in the WFSPs and RDMC in OFSPs (Belehu, 2003; Tadesse, 2006; Tofu et al., 2007; Gurmu et al., 2015b). Lack of proper post-harvest handling techniques is among the key factors that reduce the yield and quality of the crop.

Mudiope et al. (2000) reported that the lack of planting materials, pests (especially weevils), prolonged droughts, poor soils, labour shortages, land shortages, lack of tools, low prices for the crop and a lack of organized markets were among the production and marketing constraints of sweetpotato in Uganda. The lack of processing equipment is another constraint that affects the post-harvest shelf-life of the crop (Mudiope et al., 2000).

New sweetpotato varieties should meet farmers' criteria in terms of quality, disease resistance, taste, flavour, early maturity, and texture (RDMC) (Ssebuliba et al., 2006). RDMC of sweetpotato is a key trait. Sweetpotato varieties with high RDMC are preferred by farmers, consumers and industries (Tumwegamire et al., 2004; Kwach et al., 2010; Gurmu et al., 2015a). RDMC has an influence on eating quality, shelf-life and processing quality and therefore influences the acceptability of OFSPs, since OFSP varieties, in general, tend to have lower RDMCs.

A study conducted by Tumwegamire et al. (2007) on the acceptability of OFSP varieties in Uganda reflected that most of the farmers preferred the OFSP varieties to their local varieties. Their criteria were foliage cover, disease resistance, pest resistance, drought tolerance, early maturity, root yields, root shape, root size, skin colour, flesh colour, taste, flavour, starchiness, fibrousness and general acceptance. Kaguongo et al. (2010) suggested there was an association between education and adoption of OFSPs from their study on factors that influence the adoption of OFSP in western Kenya.

In Ethiopia, sweetpotato production and its post-harvest handling is hindered by many factors. However, there is limited information on the constraints of sweetpotato production and farmers' preferences for sweetpotato varieties. Tadesse (2006) studied farmers' perception for sweetpotato clones in some sweetpotato growing zones of the country and found that female farmers preferred their local cultivar that is white-fleshed. This was mainly due to its high RDMC. The male farmers were interested in agronomic traits such as establishment, ground cover, vine length, vine thickness, disease resistance, earliness, storage root length, storage root thickness and total storage root yield than the root flesh colour. Gurmu et al. (2015b) conducted a survey on the pre- and post-harvest constraints of sweetpotato and reported heat and drought, shortage of planting materials, shortage of land, diseases, insect-pests, a lack of draft power, shortage of money, a lack of labour and weeds as the major pre-harvest constraints in Ethiopia. The authors identified poor access to markets, poor market prices, low yields, low RDMC, a lack of knowledge on processing, a lack of processing equipment and a problem of transporting bulky products as the major post-harvest constraints in Ethiopia (Gurmu et al., 2015b). Resistance to heat and drought, high RDMC, good taste, high root yields, resistance to disease and insects, earliness and cookability were identified as the predominant selection criteria for sweetpotato varieties by farmers in Ethiopia (Gurmu et al., 2015b).

Participatory rural appraisal (PRA) is one of the tools that are used to identify production constraints and farmers-preferred varieties and traits through farmers' participation. It is defined as a family of approaches and methods that are used to enable the rural people to share, enhance, and analyse their own knowledge of life and conditions, to make plans and take actions (Chambers, 1994a). PRA methods are useful for gaining a preliminary understanding of the research area in a relatively short period of time. It is based on interdisciplinary, exploratory studies relying on a high use of community interaction and indigenous knowledge (Mark et al., 1992). PRA is a means of learning about rural life and the environment from the rural people. Researchers or other field workers act as facilitators so that the local people can conduct their own analysis, plan and take action. This is based on the principle that local people are creative and capable, and can do their own research, analysis, and planning to overcome their problems.

There are different tools that are used to undertake a PRA study. These are semi-structured interviews; ranking and scoring such as preference ranking, pair-wise ranking, matrix scoring and ranking, well-being analysis and wealth ranking, proportional piling and pie charts; diagramming, mapping and modelling such as transect walks, maps (resource, social, farm), Venn diagrams, seasonal calendars, historical analysis (time lines, trend lines, activity profiles); problem analysis such as identification and specification, and causal chaining, triangulation and use of secondary resources (Mark et al., 1992; Chambers, 1994a, 1994b; Bhandari, 2003). The use of these PRA tools is very important to better approach the farmers, understand their situations, preferences and problems, and to plan for possible interventions with them. It helps to address the problems of the community by conducting focused breeding programmes that are based on the needs and preferences of the community. The resource-poor farmers in marginal environments who have not benefited from modern plant breeding can also make direct and indirect contributions to the planning of the breeding programme that benefits them.

1.4. Environmental requirements of sweetpotato

Sweetpotato can be grown in different climatic conditions of the tropics and warm temperate regions of the world. It is cultivated between 40^0 latitudes of northern and southern hemispheres and altitudinal ranges between sea level and 2500 meter above sea level. (Ramirez, 1992; Huaman, 1999). Negeve et al. (1992) stated that yield, number of roots and proportion of marketable roots decline with increasing altitude. It has an optimum temperature of 25^0C where the minimum and maximum temperatures are 15 and 33^0C, respectively (Negeve et al., 1992; Ramirez, 1992). When the temperature drops below 10^0C, the growth of the crop is severely retarded. The crop is sensitive to frost (Negeve et al., 1992) and therefore its cultivation is confined to the tropics and warm temperate regions. Sweetpotato is a short day plant (Ramirez, 1992; Belehu, 2003; Andrade et al., 2009). It needs light for maximum vegetative development, while short days promote flowering and root growth.

Moisture is a critical factor for sweetpotato growth and production. Rainfall between 750-1000 mm per annum is ideal for sweetpotato production. The crop should receive about 500 mm rainfall during its growing season (Belehu, 2003). The soil should be moist during planting and a growth period for at least two months (Ramirez, 1992). This helps to achieve good germination, establishment and yield. Although sweetpotato is a drought tolerant crop, it should get sufficient moisture during tuber initiation, 50-60 days after planting. Sweetpotato is intolerant to water logging and hence good drainage is essential during excessive rain. Sweetpotato can be grown in a wide range of soils but it performs best on sandy loam soils. It performs poorly in soils with poor aeration such as clay soils (Ramirez, 1992; Belehu, 2003). Light-textured soils generally

encourage the production of roots with smoother skins whereas heavy clay loams often result in rough and irregular shaped roots. Sweetpotato prefers slightly acidic or neutral soils with pH of 5.5-6.5. Both excessively alkaline and acidic soils reduce yields (Ramirez, 1992).

1.5. Self- and cross-incompatibility problems in sweetpotato

The success of pollination and fertilization in sweetpotato depends on various factors. These are photoperiod, the duration for which the flower remains open, self- and cross-incompatibility problems, and variation in the length of stamen as compared to the style (Onwueme, 1978). Moreover, flowering ability in sweetpotato is variety dependent and some varieties may not flower at all, whereas others produce very few flowers. However, self- and cross-incompatibility are the major challenges in sweetpotato improvement, hindering crossing and sexual seed production (Vimala and Hariprakash, 2011; Gurmu et al., 2013).

According to Acquaah (2011), there are two types of self-incompatibilities: heteromorphic and homomorphic. Heteromorphic self-incompatibility is due to the difference between the length of stamens and style (heterostyly). Homomorphic self-incompatibility on the other hand is of two types: gametophytic and sporophytic. In the case of gametophytic self-incompatibility, it is the pollen's genotype that controls its normal function and not the plant that produces it. But in the case of sporophytic self-incompatibility, the incompatibility of the pollen is determined by the plant (sporophyte) that produces the pollen. In both cases, the incompatibility reaction is controlled by an *S*-locus with multiple alleles (Acquaah, 2011).

Martin (1965) noted that the incompatibility problem in sweetpotato is not associated with the length of the style and stigma, and the relationship between heterostyly and incompatibility in this crop has no experimental basis**.** Latter Kowyama et al. (2000) reported that the type of self-incompatibility in the genus *Ipomoea* is a homomorphic sporophytic self-incompatibility system, in which male and female organs have the same morphology within the interbreeding flowers, in contrast to the heteromorphic sporophytic systems where floral morphology differs between mating types. Self-incompatibility system in sweetpotato results in a total collapse of pollen germination on the stigma after self-pollination. Therefore, if self-pollination takes place, there is no pollen germination and hence there is no seed set. On the other hand, if cross-pollination has taken place and mating is compatible, pollen germination occurs quickly on the stigma, in about 10-20 minutes after pollination (Kowyama et al., 2000).

The presence of self- and cross-incompatibility in sweetpotato slows down breeding of sweetpotato (Gurmu et al., 2013). It effects seed set, which in turn holds back utilization of some gene combinations during breeding and hence it is an impediment to genetic advances.

For effective improvement of the crop, it is wise to use a method that provides good crossing results and detailed genetic information. Therefore, the knowledge on the types, advantages and limitations of different mating designs available in plant breeding is desirable to choose the one that best fits sweetpotato improvement.

1.6. Mating designs in sweetpotato breeding

A careful choice of mating design is crucial before starting any plant breeding program. Stuber (1980) suggested that any of the known mating designs can be used to generate genetic data from a population representing a crop species, depending on various factors. The factors are: the predominant type of pollination (self- or cross-pollination), type of crossing used (artificial or natural), means of pollen dissemination (wind or insect), unique features (cytoplasmic or genetic sterility), purpose of project (breeding or genetic), and size of population required. Therefore, it is the breeder's task to choose which design to use.

The most commonly used mating designs in crop improvement are Bi-parental, top cross, line x tester, North Carolina Designs (NCD-I, NCD-II and NCD-III), diallel and polycross mating designs. However, in sweetpotato, polycross, NCD-II and diallel mating designs are commonly used. Therefore, some of the features and limitations of these mating designs are highlighted with respect to the sweetpotato crop.

1.6.1. Polycross mating design

Polycross refers to natural inter-crossing of a group of plants in an isolated crossing block (Stuber, 1980; Bassett, 1986; Saladaga, 1989; Acquaah, 2011). The polycross mating design is most suited to species that are self-incompatible such as forage grasses and legumes, sugar cane and sweetpotato (Stuber, 1980; Acquaah, 2011). The polycross design is a widely used mating design for sweetpotato improvement. Due to the pollination incompatibilities, only a small percentage of controlled crosses in sweetpotato lead to fruit setting and each fruit usually contains only one or two seeds (Gurmu et al., 2013). Polycross rely on natural hybridization. However, it has some basic limitations. One of the limitations is that it generates insufficient statistics to estimate all the genetic parameters. The components of variance are only estimated from the maternal half sibs, thus information about the males is lost. There is no control over the pollen source and hence expected genetic gains are reduced by half. Non-randomness of mating due to lack of synchronisation of flowering, unequal pollen production and positional effects in the crossing block are also major limitations (Sharma, 2006; Acquaah, 2011). The other limitation is that if the size of parents increases, it would become difficult to accommodate them all into the polycross nursery (Sharma, 2006) since large numbers of replications are

required for randomness of pollination. Therefore, due to the above limitations, most breeders prefer NC-II and diallel mating designs for genetic studies in sweetpotato.

1.6.2. North Carolina design

North Carolina Design I (NCD-I) is one of the most frequently used mating designs for maize improvement. In this design, from a reference population, some plants are selected and labelled as males and females. Each male is crossed to a different set of females to produce progenies for evaluation. North Carolina Design II (NCD-II) is a modified form of NCD-I to make it suitable for multi-flowered/tillering plant species so that each plant can be used repeatedly as both male and female in a population (Hallauer et al., 1988; Sharma, 2006; Acquaah, 2011). However, in crops like sweetpotato where a genotype can be reproduced vegetatively, this assumption of multi-flowering is not a problem. The number of flowers can be increased by using cuttings of the same genotype and by planting as many plants as required. Therefore, this design is commonly used for vegetatively propagated crops such as sweetpotato. In this design, all the random *m* pollen parents are crossed to each of the random *n* females producing *mn* possible crosses (Hallauer et al., 1988). The third design, NCD-III, is considered the most powerful of the three designs. It has been used in maize breeding in the F2 population to determine the effects of linkages on the estimates of additive and dominance genetic variances and average level of dominance (Hallauer et al., 1988). Backcrossing the individual S_o plants (males) selected from the F_2 population to both homozygous parents (females) generate the progenies that are evaluated. However, this design has little or no practical importance to sweetpotato improvement since it is difficult to generate F2 progenies in sweetpotato due its self-incompatibility problem.

1.6.3. Diallel mating design

A diallel cross can be defined as the mating of a set of genotypes in all possible combinations. It has been used in various analyses such as to study the genetic control of quantitative traits (Hayman, 1954; Hayman, 1958), to assess general combining ability (GCA) and specific combining ability (SCA) (Griffing, 1956a, 1956b), and to determine heterosis. It allows for selection of superior parents for crosses and, in cross-pollinating species, to screen populations for use in intra- and inter-population breeding programmes. It is also used to estimate the genetic variance components among crosses (Hayman, 1954; Griffing, 1956a; Kempthorne, 1957).

There are four types of diallel mating methods described by Griffing (1956a). These are: Method 1 where parents, one set of F1's and reciprocal F1's are included (all p^2 combinations); Method 2 where only parents and one set of F1's are included resulting in p(p+1)/2

combinations; Method 3 where one set of F1's and reciprocal F1's are included but not the parents, giving p(p-1) combinations; and Method 4 one set of F1's but neither parents nor reciprocal F1's included, providing p(p-1)/2 combinations. Each method necessitates a different form of analysis. Each of these four methods of the Griffing's diallel is further sub-divided, based on the distinction between fixed or random effect models. Each of the four methods can be attached with Model-I (fixed model) and Model-II (random model). Therefore, when each of the four methods is aligned with the two models (fixed and random effect model), the total number of diallel analyses is eight.

The fixed effect model (Model-I), assumes that the experimental material itself is the population about which inferences are to be drawn, and hence the estimate obtained from the analysis apply to those genotypes alone. No assumptions are made about the reference population and genotypic effects are considered constant, i.e., the parents are deliberately chosen and cannot be regarded as a random sample from any population. Therefore, the experimental material constitutes the entire population about which valid inferences can be made (Griffing, 1956a). In a random effects model (Model-II), the parents are assumed to be a selected sample from some reference population, i.e., the experimental material as a whole is assumed to be a random sample from some population about which inferences are to be made. Therefore, random samples drawn as parents from some populations are dealt with and inferences do not apply to the sample but to the parental population from which samples were drawn (Sharma, 2006). This distinction between a fixed and a random effect model applies to all statistical analyses in a diallel approach. The two different assumptions give rise to different estimation problems and different tests of hypotheses regarding combining ability effects.

The diallel mating design has some limitations. One of the limitations is its restriction to a limited number of parents. As the number of parents included in the diallel cross increases, the number of treatments (F1 and parents) increase geometrically and the trial become unmanageable and costly (Fikret, 2009). Acquaah (2011) also reported that diallel mating design takes a large amount of space, seed, labour and time because a large numbers of crosses have to be made by hand pollination.

1.7. Genetic analysis in sweetpotato

Sweetpotato is self-incompatible and out-crossing crop. Consequently, there exists wide variability within the species, presenting a great opportunity for breeders (Bassett, 1986). Each clone of the crop is genetically different from the others within the species. However, the exiting variability alone is not adequate to improve the crop for traits of interest and there is a need to

conduct crosses involving different complementary traits. However, the nature of the sweetpotato crop is an impediment to its genetic improvement. Polyploidy, high heterozygosity, self- and cross-incompatibility and large chromosome numbers (Cervantes-Flores, 2006; Chang et al., 2009; Gurmu et al., 2013) are some of the challenges in sweetpotato breeding. Mcharo and LaBonte (2007) observed that the hexaploid, self-incompatibility and heterozygous nature of the sweetpotato make inheritance studies very complicated. Breeding and selection of sweetpotato for quantitative traits is greatly affected by these genetic conditions of the crop, which slow down progress in genetic advances that can be attained within sweetpotato breeding programmes (Mcharo and LaBonte, 2007). Moreover, Cervantes-Flores et al. (2010) indicated that most traits of economic importance in sweetpotatoes follow a quantitative inheritance due to the polyploid nature of the crop, and this makes their improvement difficult. Gasura et al. (2008) also commented that self- and cross-incompatibilities in sweetpotato have remained major challenges in its breeding, and that these incompatibilities hinder production of segregating populations from specific crosses. However, efforts have been made to improve the crop for different traits through estimation of combining abilities and thereby the type of gene action controlling the traits of interest, and the inheritance and heritability of different traits.

1.7.1. Combining ability effects and gene action

Combining ability refers to the measure of the mean performance of a parent in all its crosses when it is crossed to several other parents (Falconer and Mackay, 1996). Combining ability analysis is one of the most important methods in plant breeding in identifying the parents for hybridization. The GCA is the comparative ability of a parent or a genetic stock to combine with a tester or a group of testers. It is the value being expressed as a deviation from overall mean crosses which is the mean of all F_1's having this parent in common (Falconer and Mackay, 1996). The SCA is the deviation in the performance expected on the basis of GCA. GCAs are main effects while SCA is an interaction effect. According to Falconer and Mackay (1996) GCA is due to the additive variance and additive x additive interaction variance in the base population, whereas SCA variance is due to non-additive genetic variance, i.e., dominance and epistatic effects (additive x dominance, dominance x dominance interaction variance). The ratio of the GCA variance to SCA variance indicates the predominance of the additive or non-additive variance. Additive genetic variance is equal to twice the variance due to GCA. Baker (1978) mentioned that the relative importance of GCA and SCA for yield and other traits in diallel crosses indicates the type of gene action that is predominating.

1.7.2. Heritability

Heritability is the proportion of phenotypic variation that is caused by variation in genetic values. It is a measure of the amount of genetic variation, and decreases as environmental component of variance increases (Cruz and Chujoy, 1994). Heritability is defined either as the ratio of the additive genetic variance (σ^2A) to the phenotypic variance (σ^2P), known as narrow sense heritability (h^2), or as the ratio of the total genetic variance (σ^2G) to the σ^2P, referred to as broad sense heritability (H) (Hallauer, 2007). Heritability estimates represent an efficient means of determining the feasibility of improving a trait through a designed selection procedure (Jones, 1986).

Heritability of traits in sweetpotato can be estimated either by using the parent-offspring regression analysis where heritability (h^2) is calculated from the regression coefficient (*b*) or from variance components that are obtained from analysis of variance (ANOVA) where mean of squares are used to derive the expected variance components. In mating designs that provide both GCA and SCA variances, such as the North Carolina and diallel mating designs, heritability can be estimated from GCA and SCA components of genetic variances. The source of variation due to GCA is the covariance of half-sibs, or (¼)σ^2A, and the variance due to SCA is the covariance of full-sibs minus two times the covariance of half-sibs, or (¼)σ^2D, with the assumption of no inbreeding of the parents and no epistasis (Hallauer et al., 1988; Hallauer, 2007).

1.8. Genotype x environment interaction and stability analysis

Genotype x environment interaction arises when the varieties of a crop perform differently when grown in a number of growing environments. The true difference between genotypes for any trait is relevant only if there is no G x E interaction effects (Annicchiarico, 2002). The presence of significant G x E interaction creates problems in comparing varieties and recommending specific varieties for wider adaptation (Moussa et al., 2011). Annicchiarico (2002) suggested that G x E interaction effects should not be ignored, but it should be analysed using appropriate techniques. This helps to explore the possible opportunities and challenges related to it. Furthermore, G x E analysis helps to understand the type and magnitude of the G x E interactions expected in a given environment, the reasons for their occurrence, and to define a strategy, such as stability analysis, to cope up with the effects of the interactions. Therefore, knowledge about the existence, pattern and magnitude of G x E interaction in sweetpotato is important.

1.8.1. Evidence of G x E interaction in sweetpotato

Sweetpotato is grown in diverse agro-ecologies and has been reported to be sensitive to G x E interactions (Janssens, 1983; Collins et al., 1987; Nasayao and Saladaga, 1988; Manrique and Hermann, 2001; Wolfgang et al., 2005; Tsegaye et al., 2007; Osiru et al., 2009; Moussa et al., 2011). Manrique and Hermann (2001) reported that many of the important traits in sweetpotato are sensitive to G x E interaction effects. The authors reported large interaction effects on yield related traits across environments and less interaction effects for nutritional traits. Nasayao and Saladaga (1988) found significant G x E interaction effects from their study on yield stability of sweetpotato. Grüneberg et al. (2005) reported the presence of significant G x E interactions, strong enough to cause changes in the ranking of genotypes across locations and years.

The existence of significant G x E interaction effect hinders cultivar recommendation. G x E interactions reduce wider adaptability and stability of sweetpotato varieties to different growing conditions across locations. Furthermore, it can slow down the selection progress in a sweetpotato improvement programme (Mbwaga et al., 2008). According to Tsegaye et al. (2009), most of the OFSP clones in Ethiopia evaluated in yield trials were sensitive to environmental variations. Therefore, the authors suggested that it is equally important to consider both wider and narrow adaptation of cultivars to exploit their genetic potential. In the past years, there has been little breeding work on sweetpotato in Ethiopia to enhance quality attributes and productivity. Also limited information is available on G x E interactions and stability of released varieties. Therefore, development of promising sweetpotato clones, understanding the nature of G x E interactions and quantifying their magnitude is essential for Ethiopian sweetpotato.

1.8.2. Quantifying G x E interactions

The presence of significant G x E interaction effects complicate the recommendation of varieties for wider adaptation. Therefore, there should be some means of selecting varieties that have consistent performance across the test environments. Therefore, effective analysis of multi-location data is important because this becomes an integral part of crop improvement (Yan and Rajcan, 2003). Stability analysis should be conducted to identify superior varieties that show consistent performance across environments or to recommend a few for a given environment based on the traits of interest. There are a number of techniques that are designed to analyze G x E interactions, to quantify their magnitude and to explain the nature of the interaction effects. Some of these techniques have been reviewed by other authors (Lin et al., 1986; Flores et al., 1998; Hussein et al., 2000). The techniques that are used to quantify G x E interactions are also used to analyse a variety's stability across multiple environments for different traits.

1.8.3. Stability analysis

Additive main effects and multiplicative interaction (AMMI) (Gauch, 1988; Gauch and Zobel, 1988) and, genotype plus genotype by environment interaction (GGE) bi-plot analysis (Yan et al., 2000; Yan, 2001; Yan and Rajcan, 2002) are the most commonly used statistical methods for analyzing multi-environment data. Yan et al. (2002), Yan and Rajcan (2003) and Yan et al. (2007) noted that among genotype (G), environment (E), and G x E, only G and G x E are important and must be simultaneously considered. The authors suggested that a GGE biplot best identifies G x E interaction patterns of data and clearly shows which variety performs best in which environments, and thus facilitates mega-environment identification. On the other hand, Gauch (2006) and Gauch et al. (2009) suggested that AMMI is more powerful for attaining the best estimate of G x E interaction effects and stability of varieties tested across environments because it integrates ANOVA and PCA in a unified approach, partitions the overall variation into G main effects, E main effects and G x E interaction effects (Gauch, 1988; Gauch and Zobel, 1988; Zobel et al., 1988). However, both GGE and AMMI models are equivalent as far as their accuracy is concerned. Therefore, a researcher can consider both of them or either of the two for quantifying G x E interaction and for stability analysis.

1.9. Correlation and path-coefficient analyses in sweetpotato

Correlation and path-coefficient are among the important analyses in crop improvement programs. The purpose of correlation and path-coefficient analyses are to describe the pattern of interrelationship among the various traits. It is useful to identify the degree of interrelationship of traits for direct and indirect selection.

1.9.1. Correlation analysis

Correlation analysis is useful for selecting for more complex and less heritable traits, such as yield, through selecting for traits that are highly correlated with yield, given that their heritability is high (De Araujo et al., 2002). Larger genotypic correlation coefficients indicate greater contribution of genetic factors and reduced effects of the environment (Iqbal et al., 2003). According to Martin and Rhodes (1983) significant correlations have direct implication on the progress of a selection program. Knowledge of the frequency of desired traits, and correlations among these, is helpful for direct/indirect selection and to develop selection index (in mass or recurrent selection) to emphasize and develop the traits most desired.

Tsegaye et al. (2006) reported that in sweetpotato clones, the genotypic correlation coefficients were lower than the phenotypic correlation coefficients among different sweetpotato traits,

indicating the significant effects of the environment. The authors indicated the presence of high positive correlations between storage root yield, and root girth, harvest index (HI) and individual root weight per plant. On the other hand, storage root number had a significant negative correlation with storage root girth and individual root weight implying that an increase in the number of roots per plant will result in competition between storage roots within a plant. This will result in many small sized roots (Tsegaye et al., 2006).

In a study by Lin et al. (2007), significant positive correlations were found between above ground biomass, fresh root weight, and storage root number; between storage root shape and above ground biomass and storage root weight; between skin colour and flesh colour of storage root, and between starch content and amylase content. This suggests that above ground biomass can be used as an indicator for storage root yield (fresh weight and number). Gasura et al. (2008) also found a positive correlation between yield and tuber number, while sugar content was negatively correlated with starch content. Protein content was positively correlated with dry matter content (Gasura et al., 2008). There exists a slight negative correlation between root dry matter and β-carotene contents of sweetpotato (Simonne et al., 1993; Chiona, 2009; Cervantes-Flores et al., 2010), implying that the simultaneous improvement of the two traits is a challenge in sweetpotato breeding for quality traits.

Several studies indicated the existence of strong positive correlation between flesh colour and β-carotene content in sweetpotato (Mcharo and LaBonte, 2007; Burgos et al., 2009; Cervantes-Flores et al., 2010; Vimala and Hariprakash, 2011). Therefore, root flesh colour ranging from pale orange to dark orange may be used as an indicator of β-carotene content especially at the beginning of screening work where many progeny have to be evaluated. A colour chart developed by Burgos et al. (2009) can serve as a useful indicator to facilitate selection for high β-carotene content.

1.9.2. Path-coefficient analysis

Path-coefficient analysis was developed by Wright (1921a), cited by Lynch and Walsh (1998), with the aim of interpreting the correlation between two variables in terms of hypothetical path of causality between the variables. The purpose of path-coefficient analysis is the quantification of the relative contributions of casual sources of variance and covariance once it is known that there is a certain degree of interrelatedness between the variables (Lynch and Walsh, 1998). It is a standard partial regression coefficient that measures the direct influence of one variable up on others, and permits the separation of the correlation coefficient into components of direct and indirect effects (Diz. et al., 1994; Shimelis and Hugo, 2011).

Each correlation coefficient between a causal or independent variable and the response or dependent variable is partitioned. This provides components with a direct effect or path-coefficient for the predictor variable and indirect effects, which involve the product of a correlation coefficient between two predictor variables with the appropriate path-coefficient in the path diagram (Diz. et al., 1994; Shimelis, 2006). Therefore, knowledge about both the direct and indirect effects of selecting for specific components can be attained by determining the inter-relationships among yield components and breeders can get a comprehensive understanding of the relationship among a set of traits and how each trait affects or contribute to yield (Diz. et al., 1994; Akheter and Sneller, 1996; Board et al., 1997).

Tsegaye et al. (2006) conducted correlation and path analysis of various traits in sweetpotato and reported that individual storage root weight had a maximum positive direct effect of 0.7576 and 0.8497, using phenotypic and genotypic correlations, respectively. Storage root number also had a high positive direct effect of 0.5325 and 0.6487 on storage root yield per plant based on phenotypic and genotypic correlations, in that order. However, the negative indirect effect through individual storage root weight, i.e., -0.3856 and -0.4512 at phenotypic and genotypic levels, respectively, resulted in a low correlation coefficient among the two traits at both phenotypic and genotypic levels (Tsegaye et al., 2006). From this study it could be deduced that that although a character seems to have a positive direct contribution to yield, it may have an indirect negative influence on yield via another character that has a direct contribution to yield. Path-coefficient analysis therefore helps to understand those relationships and to identify the trait that best correlate with and influence root yield.

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CHAPTER 2

Diagnostic assessment of sweetpotato production in Ethiopia: constraints, post-harvest handling, and farmers' preferences

Abstract

Production and post-harvest handling of sweetpotato is constrained by many factors. The objective of this study was to assess and document the major constraints affecting production, pre- and post-harvest handling, and farmers' preferences for sweetpotato in southern Ethiopia. Diagnostic assessments were conducted in three selected major sweetpotato growing zones in southern Ethiopia using PRA. The main pre-harvest production constraints identified by respondents were heat and drought (21.6% of respondents), shortage of planting materials (20.1%), shortage of land (15.7%), diseases (10.0%), insect pests (9.4%), a lack of draft power (8.1%), shortage of money (7.9%), a lack of labour (5.1%) and weeds (2.0%). Among the post-harvest constraints identified by respondents were poor access to markets (22.6% of respondents), poor market prices (19.1%), low yields (14.2%), low root dry matter content (13.6%), a lack of knowledge on processing (11.7%), a lack of processing equipment (11.1%) and transportation problem (7.7%) were identified as the major post-harvest constraints. The major farmers' selection criteria for sweetpotato varieties were resistance to heat and drought (19.6% of respondents), dry matter content (16.4%), taste (14.3%), root yield (13.6%), resistance to disease and insects (13.3%), earliness (11.6%) and cooking ability of roots (8.9%). 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 farmers.

Key words: *Ipomoea batatas*, participatory rural appraisal, post-harvest handling, production constraints, selection criteria.

2.1 Introduction

Sweetpotato [*Ipomoea batatas* (L.) Lam] plays a significant role in the livelihood of the people living in sub-Saharan Africa and Asia. Compared to other storage root crops, sweetpotato has the advantages of a high yield potential and adaptability to a wide range of agro-ecologies including drought affected environments (Lebot, 2010; Wang et al., 2011). Also, the crop is a source of vitamin A that serves in prevention of vitamin A deficiency related health problems.

In Ethiopia, it is the second most important root crop after enset [*Ensete ventricosum* (Welw.) Cheesman] (CSA, 2010, 2011). It is widely grown in two regions, the SNNPRS and Oromia. In SNNPRS sweetpotato production is concentrated mainly in three zones: Sidama, Wolayta and Gamo Gofa. The Wolayta and Gamo Gofa zones are well known for their production of sweetpotato and they are heavily dependent upon this crop for food security (Belehu, 2003; Tadesse, 2006; Tofu et al., 2007; Tesfaye, 2010).

Production of sweetpotato is constrained by biotic, abiotic and socioeconomic factors. The biotic stresses include diseases, insect pests and weeds, whereas the abiotic factors are drought, heat and low soil fertility (Kapinga and Carey, 2003; Ndunguru et al., 2009). These factors have a direct effect on storage root yield. Constraints related to socioeconomic and quality attributes are the lack of improved varieties, lack of planting materials, low storage root yield, low β-carotene content in the white fleshed sweetpotato and low RDMC in the OFSP varieties currently available.

Varieties with high RDMC are preferred by most African households since this trait is correlated with a good taste of the varieties (Belehu, 1987, 2003; Kapinga and Carey, 2003; Tadesse, 2006; Tofu et al., 2007). The white fleshed sweetpotato varieties are more accepted by farmers than the OFSP varieties due to their high RDMC. OFSP varieties have low RDMC and are not accepted by farmers in many of the African countries producing sweetpotato. However, the OFSP varieties are recommended for household consumption since they have high pro-vitamin A, which is essential for human health, specifically for regular growth and development, improved eyesight, metabolic functions, and an effective immune system (Bhaskarachary et al., 1995; Kapinga et al., 2005; Burri, 2011). Lack of proper post-harvest handling is also among the key factors that reduce the yield and quality of the crop. One of the approaches used to identify the constraints with farmers is PRA.

PRA is an approach and method that is used to enable rural people to share, enhance, and analyse their own knowledge of life and conditions, in order to make plans and take actions (Chambers, 1994a, b). PRA methods are useful for gaining a preliminary understanding of the

research area in a relatively short period of time. It is based on interdisciplinary, exploratory studies relying on a high use of community interaction and indigenous knowledge (Mark et al., 1992). Different PRA tools were used for discussion with farmers and for data collection (Chambers, 1994a, b; Mark et al., 1992). The objective of the study was to assess and document the major constraints affecting production, pre- and post-harvest handling, and farmers' preferences for sweetpotato in Ethiopia. The information may help researchers to devise a better breeding strategy that considers farmers' preferences.

2.2. Materials and methods

2.2.1. Description of study areas and sampling

The PRA study was conducted in three major sweetpotato growing administrative zones in the SNNPRS of Ethiopia during 2013. The zones are Sidama, Wolayta and Gamo Gofa (Figure 2.1). The multi-stage random sampling techniques were used to create a representative sample of the population. First-stage sampling included a simple random sample to select two districts from each zone. The second stage of sampling selected two villages from each district. The third stage of sampling selected 15 farmers from each of the villages and questionnaires were administered to these farmers, except in Gamo Gofa zone where 16 farmers participated. This provided a total of 183 participants in the study (Table 2.1).

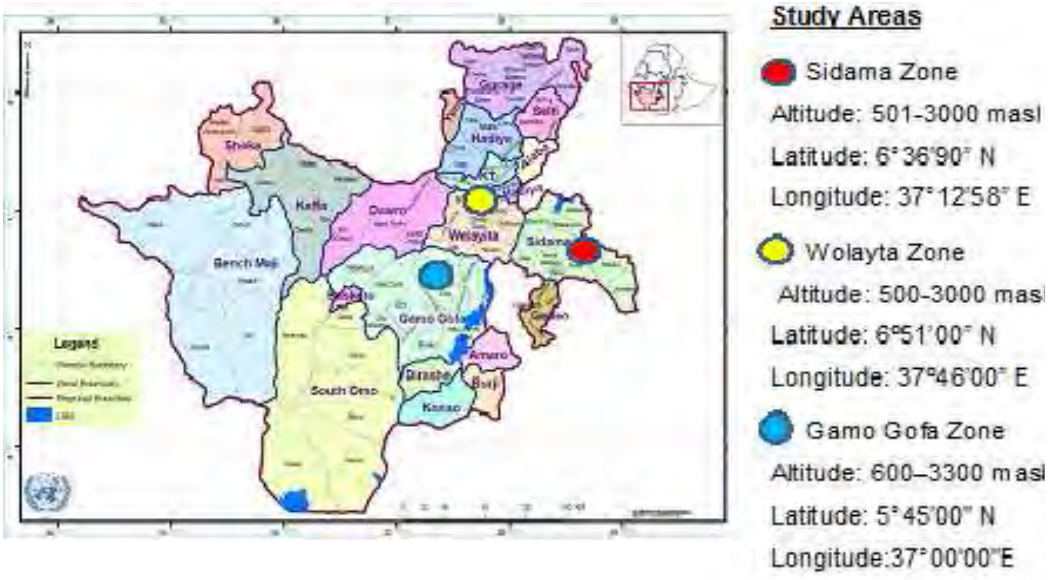

Figure 2.1 Map showing the SNNPR of Ethiopia where the PRA study was conducted

2.2.2. Data collection

Different PRA methods and techniques such as semi-structured interviews and group discussion, discussion with key informants, focus group discussions, ranking and scoring (preference ranking, pair wise ranking and matrix scoring and ranking), proportional piling, transect walk, and triangulation (using more than one source of information to cross check answers) were used for the study. Secondary data were also included. In the process of data collection, different actors participated. These were farmers (the central point and sources of information), researchers (breeder and socio-economist), technical assistant, extension officers (agricultural experts at district level and development agents at village level) and NGOs working in the area of food security and health. All members of the team participated during group discussions and a transect walk. In the case of focus group discussions and discussions with key informants, only some of the team were included in the study. However, in all cases, the team consisted of researchers and farmers.

For the primary data, semi-structured interviews were administered and discussions were made with farmers from each selected village on the farmers' preference for new sweetpotato varieties, especially the OFSPs.

2.2.3. Data analysis

The data was coded, entered and analyzed using Statistical Package for Social Scientists (SPSS) Windows Version 19.0 (SPSS Inc, 2009). Data were analyzed and summarized using cross tabulations, means, frequencies, percentages, graphical representations and chi-square tests. The percentage values were calculated out of the total of 183 respondents to which the semi-structured interview was administered.

2.3 Results

2.3.1 General description of the study areas

The three study zones, Sidama, Wolayta and Gamo Gofa, are selected among 14 administrative zones and four special districts in the SNNPRS of Ethiopia. Sidama is well known for its coffee production. In this zone, among root and tuber crops, enset is the leading crop followed by potato and sweetpotato. Khat (*Catha edulis*), a stimulant crop, is also widely grown as a cash crop. Wolayta is a densely populated zone where land shortage is a major problem. Many crops are grown on small plots of land. Enset, sweetpotato and potato are the leading root and tuber crops. Gamo Gofa neighbours the Wolayta Zone. Sweetpotato, enset and

cassava are the major root crops produced in this zone. The zones, districts, villages, and number of farmers participated in the PRA study is presented in Table 2.1.

Table 2.1 Description of zones, districts and villages selected for the PRA study in the Southern Nations, Nationalities, and Peoples' Region of Ethiopia

Zone	District	Village	Respondents (N)		
			Male	Female	Total
Sidama	Hawassa Zuria	Kajima	11	4	15
		Lab Koromo	13	2	15
	Boricha	Medo Mukanka	7	8	15
		Shelo Elancho	9	6	15
Wolayta	SodoZuria	Warazasho	10	5	15
		Wojakeru	12	3	15
	Damot Gale	Ade Aro	13	2	15
		Buge	11	4	15
Gamo Gofa	Demba Gofa	Borda	12	4	16
		Uzete	13	3	16
	Kucha	Baso	11	4	15
		Zanga	14	2	16
Total	6	12	136	47	183
% M and F			74.3	25.7	100

N = number of respondents, M and F = male and female, respectively.

2.3.2. Sources of income

The major sources of income of households in the study area are crop production (82.3% of respondents) followed by livestock (9.4%) and poultry (6.5%) farming. Other sources of income include off farm employment and tuck-shops that have insignificant contributions (Figure 2.2). More respondents indicated livestock as a major source of income in Sidama and Gamo Gofa zones than Wolayta.

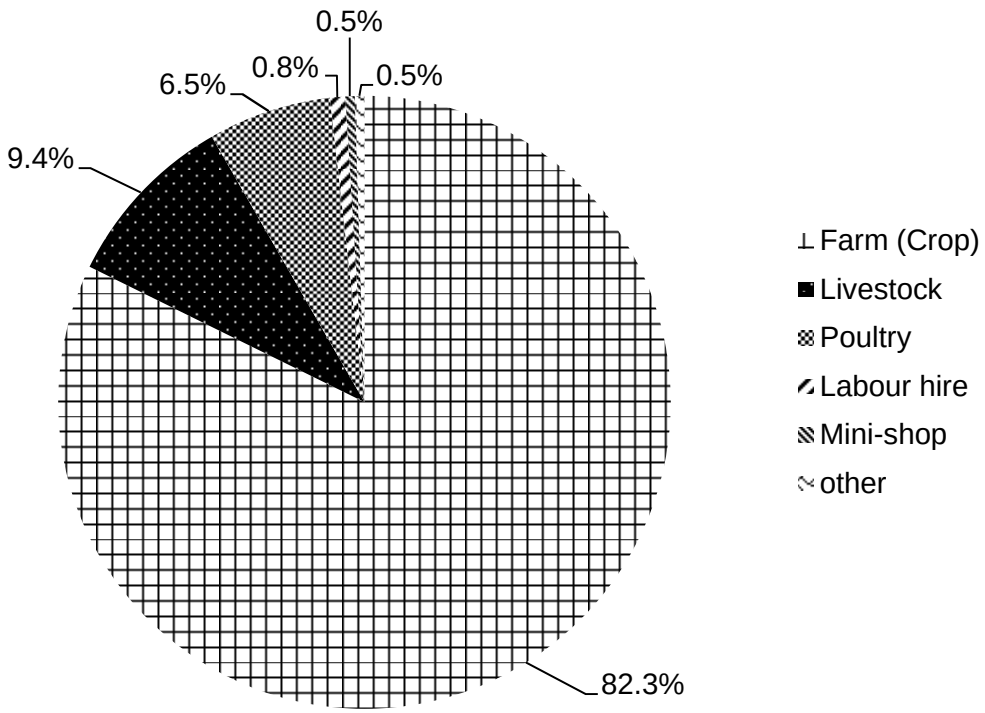

Figure 2.2 Proportion of income sources of the respondents in the Sidama, Wolayta and Gamo Gofa zones of the Southern Nations, Nationalities, and Peoples' Region of Ethiopia

2.3.3. Types of crops grown

More than 13 different crops are grown in the study sites. However, the dominant crops grown are maize, enset, common bean, sweetpotato and potato (Figure 2.3). Maize is the number one crop mentioned by all farmers at all places as an indispensable crop for their livelihood. The second is enset followed by common bean and sweetpotato, depending on the locality. This was also confirmed via pairwise ranking of these crops (Table 2.2) and from group discussions. Apart from these dominant crops, other crops were also mentioned by farmers as valuable ones in their farming systems. For instance, in Sidama coffee and khat, in Wolayta taro and Gamo Gofa ground nut are some of the important crops in their farming system.

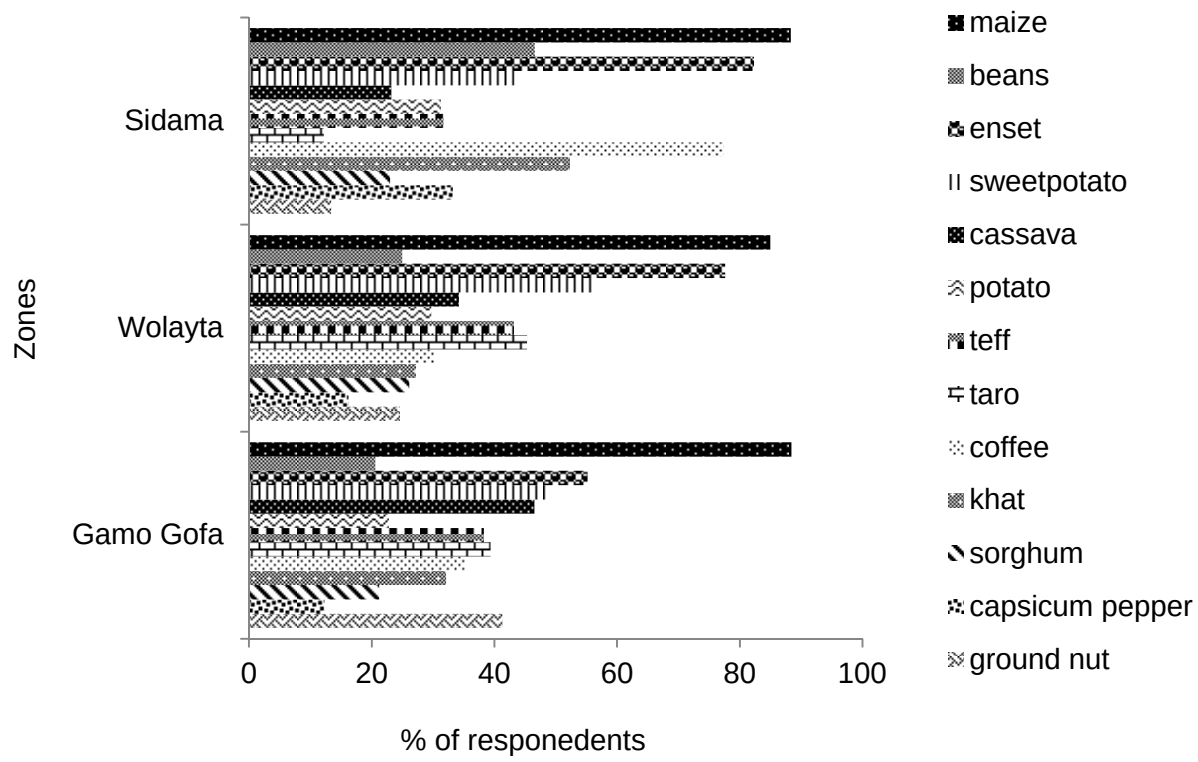

Figure 2.3 Major crops grown in the Sidama, Wolayta and Gamo Gofa zones of the Southern Nations, Nationalities, and Peoples' Region of Ethiopia

Table 2.2 Pairwise ranking of crops grown in the Sidama, Wolayta and Gamo Gofa zones of the Southern Nations, Nationalities, and Peoples' Region of Ethiopia

Crop	A	B	C	D	E	F	G	Score	Rank
A		A	A	A	A	A	A	6	1
B			C	D	E	B	G	1	6
C				C	C	C	C	5	2
D					E	D	D	3	4
E						E	E	4	3
F							G	0	7
G								2	5

A = maize, B = potato, C = enset, D = sweetpotato, E = common bean, F = sorghum, G = teff

2.3.4. Status of sweetpotato production

Sweetpotato is one of the priority food security crops in the region. In Gamo Gofa farmers placed sweetpotato second after maize. In Wolayta it was ranked after maize and enset. In Sidama, it is the sixth crop after maize, enset, common bean, coffee and khat. Overall, sweetpotato stands the fourth important food crop in the study zones. Among root and tuber crops, it is the second after enset. The majority of the respondents, 58.3, 94.8 and 91.9% in Sidama, Wolayta and Gamo Gofa zones, respectively, indicated that sweetpotato is among their priority crops (Table 2.3). The remaining respondents, i.e., 41.7, 5.2, 8.1% in that order either did not grow sweetpotato or grew it as a complementary crop in their backyards.

According to the Central Statistical Agency reports of 2011-2013, the SNNPRS is the major sweetpotato growing region in Ethiopia followed by Oromia except in the first half of 2013 where Oromia was the leading zone (CSA, 2011, 2012, 2013). The trend of sweetpotato production over the last three years (2011-2013) is displayed in Figure 2.4. Sidama, Wolayta and Gamo Gofa are the leading sweetpotato producing zones in SNNPRS. These zones contributed for 88.0, 86 9 and 91.7% of the total sweetpotato production in SNNPRS in 2011, 2012 and 2013, respectively.

Table 2.3 Farmers' response towards sweetpotato production in the Sidama, Wolayta and Gamo Gofa zones of the Southern Nations, Nationalities, and Peoples' Region of Ethiopia

Sweetpotato production	Zone			Average
	Sidama (%)	Wolayta (%)	Gamo Gofa (%)	
Yes	58.3	94.8	91.9	81.7
No	41.7	5.2	8.1	18.3
Total	100.0	100.0	100.0	100.0

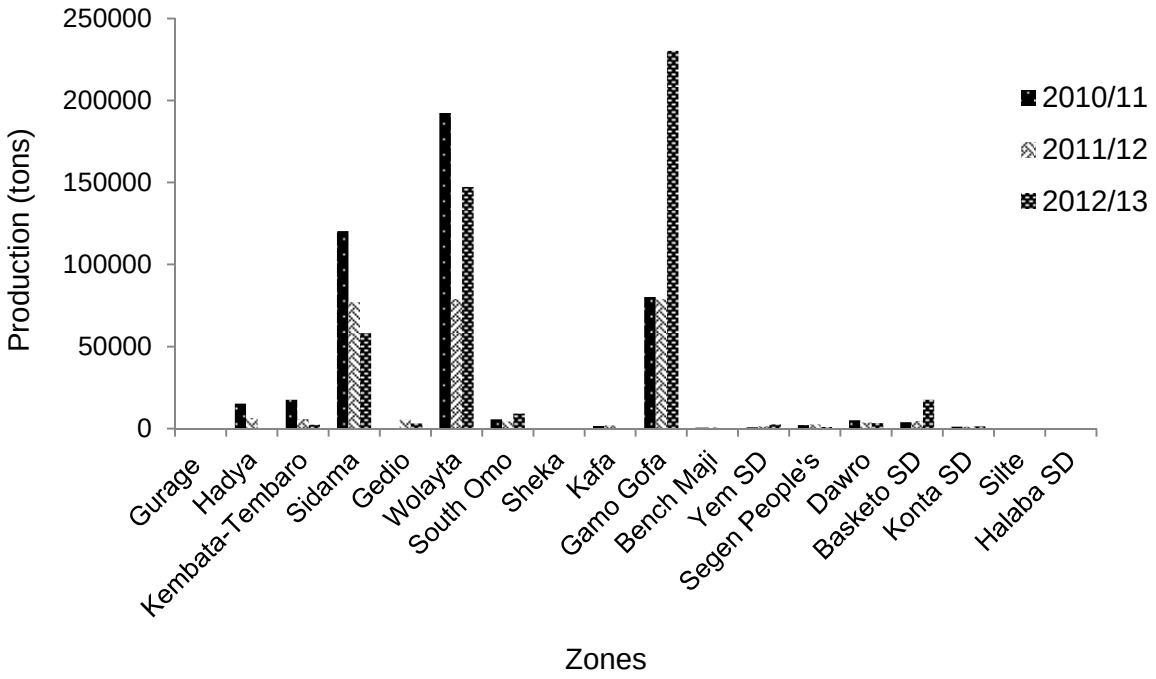

Figure 2.4 Trends of sweetpotato production in the Southern Nations, Nationalities, and Peoples' Region of Ethiopia from 2011-2013

2.3.5. Constraints affecting sweetpotato production

Different sweetpotato production constraints were identified. The major sweetpotato production constraints in Ethiopia as described by respondent farmers included heat and drought at 21.6%, shortage of planting materials (20.1%), shortage of land (15.7%), diseases (10.0%), insect pests (9.4%), a lack of draft power (oxen, donkeys, horses, mules) (8.1%), shortage of money to cover input costs (7.9%), a lack of labour (5.1%) and weeds (2.0%). The major constraints affecting sweetpotato production in the study areas are given in Table 2.4. Pair-wise ranking of major production constraints in the three zones is summarized in Table 2.5.

Of the respondent farmers, 86.3% grew sweetpotato when there was a drought or when their major cereal crops such as maize, sorghum and wheat failed. Many of the farmers (87.6%) indicated that a shortage of planting material was one of the serious impediments affecting sweetpotato production.

Table 2.4 Sweetpotato production constraints in the Sidama, Wolayta and Gamo Gofa zones of the SNNPR of Ethiopia

Production constraints	Farmers	
	Number	Percent
Heat and drought	40	21.6
Shortage of planting materials	37	20.1
Shortage of land	29	15.7
Diseases	18	10.0
Insect pests	17	9.4
Lack of draft power (oxen, donkeys etc.)	15	8.1
Shortage of money to purchase inputs	14	7.9
Shortage of labour	9	5.1
Weeds	4	2.0
Total	183	100
Chi-square	60.00	
Significance level	0.000	

Table 2.5 Pair-wise ranking of sweetpotato production constraints in the Sidama, Wolayta and Gamo Gofa zones of the SNNPR of Ethiopia

Constraints	A	B	C	D	E	F	G	H	I	Score	Rank
A		A	A	A	A	A	A	A	A	8	1
B			B	B	E	F	G	H	B	3	6
C				C	E	F	G	H	C	2	7
D					E	F	G	H	D	1	8
E						E	E	E	E	7	2
F							F	F	F	6	3
G								G	G	5	4
H									H	4	5
I										0	9

A = heat and drought, B = a lack of draft power, C = shortage of money, D = labour shortage, E = shortage of planting materials, F = shortage of land, G = diseases, H = insects, I = weeds

2.3.6 Post-harvest constraints

The major post-harvest constraints of sweetpotato were identified by the farmers as: poor access to markets at 22.6%, poor market prices (19.1%), low yield (14.2%), low dry matter content of storage roots of existing varieties (13.6%), a lack of knowledge about sweetpotato processing and preservation (11.7%), access to processing equipment (11.1%) and the logistics of transporting a heavy, bulky crop (7.7%) to market (Figure 2.5).

In Ethiopia sweetpotato is traditionally processed into numerous products, including: bread, enjera, flour, cookies, wot (stew), local beer and juice. Given proper training, and access to appropriate equipment, farmers could make a range of food items from sweetpotato. This would reduce the post-harvest losses of the crop and would help to optimize its utilization.

Post-harvest problems affecting sweetpotato are mostly related to its short shelf-life, which is affected by the quality of the storage roots. Of all the farmers, 1.6% in Gamo Gofa were using solar energy to dry sweetpotato storage root slices after harvest. The rest of the respondents (98.4%) stored the storage roots in-situ in the soil, harvesting them as and when they were needed for food. The major constraints that affect sweetpotato storage roots while leaving them in the soil were described by the respondents as heat at 31.6%, insect pests (mainly weevil) (25.6%), diseases (21.8%) and rodents (20.9%) (Figure 2.6). The respondent farmers believed that some rain is favourable for prolonging the lives of the storage roots in the soil, which was an unexpected observation.

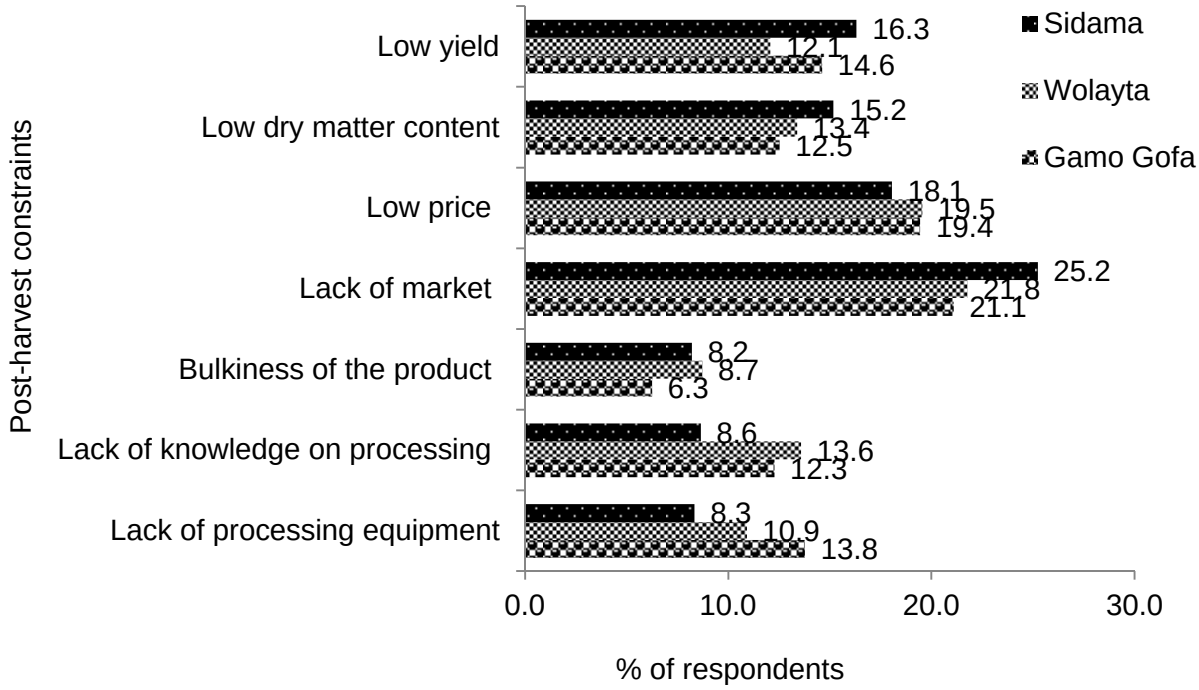

Figure 2.5 Post-harvest constraints affecting sweetpotato in the Sidama, Wolayta and Gamo Gofa zones of the Southern Nations, Nationalities, and Peoples' Region of Ethiopia

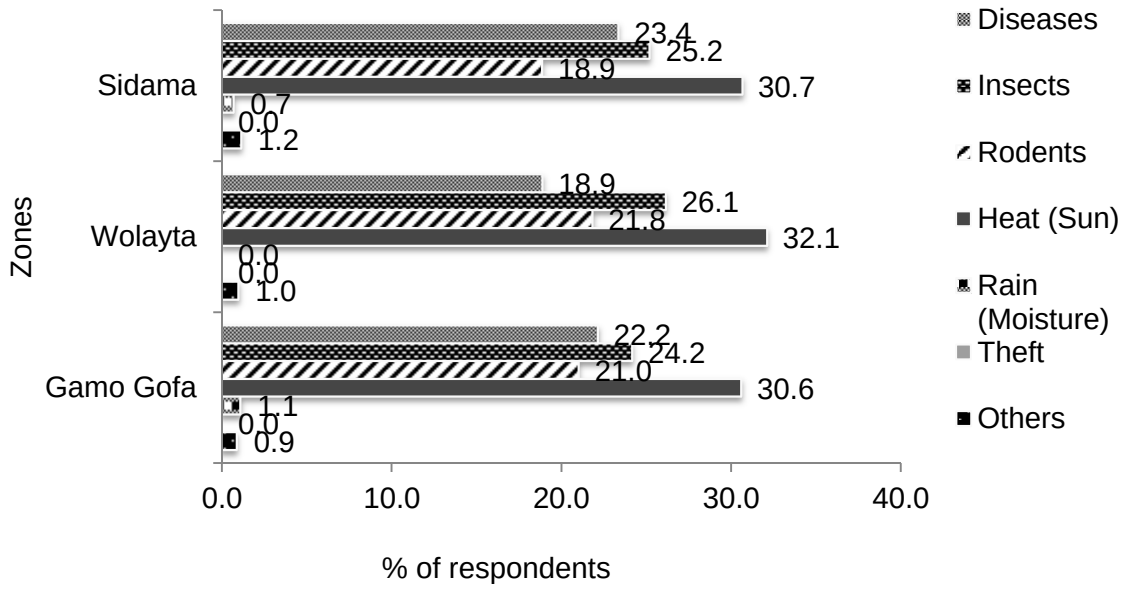

Figure 2.6 Post-harvest root storage problems in Sidama, Wolayta and Gamo Gofa zones of the Southern Nations, Nationalities, and Peoples' Region of Ethiopia

2.3.7 Farmers' preferences for sweetpotato varieties

The major sweetpotato variety selection criteria as described by respondent farmers in the three study zones are resistance to heat and drought at 19.6%, dryness of storage root after boiling i.e RDMC (16.4%), taste (14.3%), storage root yield (13.6%), resistance to disease and insects (13.3%), earliness (11.6%) and cookability (8.9%) (Table 2.6). There were significant ($P < 0.05$) differences among the respondents with respect to their selection criteria for sweetpotato varieties in Wolayta and Gamo Gofa, but not in the Sidama zone. When the total number of respondents in the three zones was considered, the selection criteria significantly differed (Table 2.6). Skin and flesh colour, and flavour were ranked relatively low.

Table 2.6 Different selection criteria of sweetpotato varieties in the Sidama, Wolayta and Gamo Gofa zones of the Southern Nations, Nationalities, and Peoples' Region of Ethiopia

Selection criteria	Zone						Total	
	Sidama		Wolayta		Gamo Gofa			
	No	%	No	%	No	%	No	%
Resistance to heat and drought	12	20.0	13	21.7	11	17.5	36	19.7
Root dry matter content	10	16.7	10	16.7	10	15.9	30	16.4
Taste	9	15.0	8	13.3	9	14.3	26	14.2
Root yield	8	13.3	9	15.0	8	12.7	25	13.7
Resistance to disease and insects	7	11.7	7	11.7	9	14.3	23	12.6
Earliness	7	11.7	7	11.7	7	11.1	21	11.5
Cookability	7	11.7	4	6.7	6	9.5	17	9.3
Root skin colour	0	0.0	1	1.7	1	1.6	2	1.1
Root flesh colour	0	0.0	1	1.7	1	1.6	2	1.1
Flavour	0	0.0	0	0.0	1	1.6	1	0.5
Total	60	100	60	100	63	100	183	100
Chi-square		2.53		19.50		21.92		77.38
Significance level		0.865		0.012		0.009		0.000

RDMC = root dry matter content, No = number of respondents, % = percent of respondents

2.3.8 Farmers' awareness on orange fleshed sweetpotato (OFSP)

OFSP is a β-carotene-rich crop that is a good, low-priced and sustainable source of vitamin A (van Jaarsveld et al., 2005). In Sidama 78.3%, Wolayta 83.1% and Gamo Gofa 67.7% of the respondents are familiar about OFSPs. Given a chance to choose and grow among the WFSP and OFSP, 54.7% responded to grow both WFSP and OFSP, while 27.6% indicated WFSP and 17.8% preferred OFSP only (Table 2.7). Of the respondents who are aware about OFSPs, 77.7% dislike the varieties due to the inherent wateriness on cooking (low RDMC) and hence the associated poor taste.

Table 2.7 Preference of farmers to grow white and/or orange fleshed sweetpotato in the Sidama, Wolayta and Gamo Gofa zones of the Southern Nations, Nationalities, and Peoples' Region of Ethiopia

Preference	Zone			Average
	Sidama (%)	Wolayta (%)	Gamo Gofa (%)	
OFSP	1.9	31.4	20.0	17.8
WFSP	22.2	29.4	31.1	27.6
Both	75.9	39.2	48.9	54.7
Total	100.0	100.0	100.0	100.0

OFSP = orange fleshed sweetpotato, WFSP = white fleshed sweetpotato

2.4 Discussion

In the present study crop production remains the key source of income of the households. Maize is the number one crop followed by root and tuber crops such as enset, sweetpotato and potato. These crops play a crucial role in sustaining food security in the SNNPRS of Ethiopia. Although sweetpotato is a very valuable crop in the region, its production shows an overall declining trend, primarily due to heat and drought, and lack of planting materials, which in turn related to the former.

The major sweetpotato production constraints mentioned by farmers were similar to previous reports from Tanzania and included drought, shortage of planting materials, land and labour shortages and, pests and diseases (Kapinga et al., 1995). Tesfaye (2010) reported that fungal, viral and bacterial pathogens are the major causes of economic losses for sweetpotato worldwide. Sweetpotato viruses such as sweetpotato feathery mottle virus (SPFMV), sweetpotato chlorotic stunt virus (SPCSV) and sweetpotato virus G (SPVG) were reported as affecting sweetpotato production in some parts of Ethiopia. Among sweetpotato insect pests, stem and root feeders such as weevils, sweet potato butterfly, sweetpotato hornworm, tortoise beetles and virus transmitter aphids were reported as yield limiting factors of sweetpotato production in Ethiopia. Among these pests, sweetpotato weevil and sweetpotato butterfly were the major ones in the country (Getu and Adahanom, 1989; Azerefegn, 1999; Shonga et al., 2013).

Sweetpotato is known as a relatively drought tolerant crop. However, due to the global climate change, even this crop is now affected by heat and drought, and its yield potential is being diminished. This also holds true for other regional crops that have been considered to be highly drought tolerant, such as cassava and enset (Belehu, 2003; Tesfaye, 2010).

Shortage of planting materials, affecting sweetpotato production, is partly caused by severe heat and drought that was described by many of the respondents. A shortage of suitable land was considered to be another challenge. This is because the land holdings of most of the households are small, averaging less than one hectare (CSA, 2003). Although disease and pests are among major constraints of sweetpotato, the farmers in the study area were less concerned about these constraints because the lack of planting materials and shortage of suitable land were the dominant constraints, stopping production of the crop entirely.

The post-harvest constraints mentioned by the respondents are comparable to those reported by Fawole (2007) in Nigeria. The report indicated that limited access to credit, lack of storage facilities, lack of processing technologies, poor market channels, limited support from the

government, high labour cost and high incidence of pests and disease were the major constraints affecting sweetpotato production, processing and marketing. The problem of low yield and low dry matter content can be solved through breeding and agronomic interventions, whereas the problems related to the marketing and processing of the products are more complex socio-economic issues.

Most of the farmers store their storage roots *in-situ* in the soil and harvest them gradually when they need them. A similar trend was reported from Uganda where farmers practice harvesting of sweetpotato in a piece meal manner by storing them in pits (CIP, 2005).

The farmers' selection criteria for sweetpotato varieties were similar to those reported from Rwanda where plant establishment, early maturity, drought tolerance, tolerance to pests and diseases, high RDMC, high storage root yield and cooking qualities were the major selection criteria for sweetpotato varieties (Ndirigwe et al., 2005). Farmers value resistance to heat and drought as the number one criterion for selecting sweetpotato varieties. RDMC, which is expressed by farmers as dryness of storage root after boiling, was considered to be the second important selection criterion. Heat and drought has a direct effect on the yield of storage roots. Hence breeding for heat and drought tolerance can significantly improve storage root yields in areas where these problems are prevailing. Early maturity was not expressed by the respondents as immediate solution to the problem of heat and drought. Farmers realize that early maturing varieties generate lower yields than medium and late maturing types.

Some of the respondents chose both WFSP and OFSP varieties because they need to ensure food security and to test the new OFSP varieties. Some respondents indicated their preference to grow either of the two as far as they are available. The preference towards the WFSP was mainly due to its high RDMC. Farmers who preferred OFSP have tested it before and found out to be good, except for its wateriness on boiling due to its low RDMC.

African farmers producing sweetpotato prefer varieties with high RDMC (Kapinga and Carey, 2003; Tumwegamire et al., 2004; Ssebuliba et al., 2006; Kwach et al., 2010). This is also true in Ethiopia as reported by Tadesse (2006) and Tofu et al. (2007). RDMC has direct relation with the taste of sweetpotato varieties. Varieties with low RDMC are watery and have poor taste in the opinion of farmers. This indicates that farmers are not only concerned about yield per se but also culinary taste. Hence varieties with high RDMC are preferred and this trait has direct relevance in sweetpotato breeding.

In general, OFSP is a staple food source of vitamin A, which is cheap and most accessible than other food items which are unavailable or unaffordable to poor farmers (Hagenimana et al., 1997; Low et al., 2001; Mwanga et al., 2003; Kapinga et al., 2005; van Jaarsveld et al., 2005;

Low et al., 2009; Kaguongo et al., 2010). Therefore, enhancing farmers' awareness on the importance of OFSPs as a source of vitamin A is very essential with concomitant increase of its dry matter content through targeted breeding.

2.5. Conclusions

Sweetpotato is widely grown in the SNNPR and Oromia regional states of Ethiopia. In SNNPRS, Sidama, Wolayta and Gamo Gofa are the major sweetpotato producing zones. Sweetpotato is not only a food security crop but can play a significant role in prevention of vitamin A deficiency related health problems. OFSP, which is rich in β-carotene, is a good source of vitamin A. However, sweetpotato production and its post-harvest handling is constrained by many factors that need to be alleviated. The major constraints such as heat and drought, disease and insect pests and shortage of planting materials, can be solved through integrated research approaches with different disciplines and institutions. Other constraints such as shortage of land, shortage of draft power and shortage of money may need further interventions such as access to credit and entrepreneurship.

The OFSP varieties currently in use have achieved a low level of consumer acceptance due to their low RDMC. Therefore, there should be a systematic breeding program that aims at improving the RDMC of the OFSP varieties in order to increase their rate of adoption by farmers. On the other hand, there should also be other strategies such as awareness creation to consumers through training on the importance of OFSP in terms of its health benefits. This will help to increase the adoption of OFSP by the communities and to successfully fight the health consequences of vitamin A deficiency.

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CHAPTER 3

Genetic analysis of root dry matter and β-carotene contents, and yield related traits in sweetpotato

Abstract

Most of the OFSP varieties that have been released so far have low RDMC, which influences their acceptance by small-scale farmers. Hence, improving the RDMC of the OFSP through breeding is vital to increase their adoption rate by farmers and thereby improve vitamin A intake of rural communities. The objective of the study was to determine the combining ability, type of gene action and heritability of RDMC and β-carotene content, and yield related traits of selected sweetpotato clones, for further evaluation and breeding. Crosses were conducted using a 7 x 7 half-diallel mating design and a total of 28 genotypes (7 parents and 21 crosses) were evaluated at four locations in Ethiopia using a 7 x 4 alpha lattice design with two replications. The performance of the genotypes were significantly different ($p < 0.01$) across the four locations for RDMC, β-carotene content, sweetpotato virus disease (SPVD) reaction, root yield and harvest Index (HI). The GCA and SCA mean squares were significant ($p < 0.01$) for all traits except the SCA effect of RDMC. The GCA to SCA variance ratios were 0.96, 0.94, 0.74, 0.96 and 0.97 for RDMC, β-carotene content, SPVD, fresh root yield and HI, respectively, indicating that the inheritance of these traits was controlled mainly by additive genes. The GCA effects of the parents Ukrewe and PIPI were positive and significant, while all the SCA effects were not significant for RDMC. Both the GCA and the SCA effects were important in controlling the expression of β-carotene content. Two sweetpotato parents, Resisto and NASPOT-1 had significant positive GCA effects for fresh root yield. Progenies of crosses involving Ukrewe x Ejumula, Ukrewe x PIPI, Resisto x PIPI and Ejumula x PIPI exhibited high level of positive heterosis for RDMC. Similarly, progenies of crosses including Resisto x PIPI and Resisto x Ogansagan had higher positive heterosis for fresh root yield, reflecting the breeding value of these parents. Relatively high narrow sense heritability (h^2) was obtained for β-carotene content (79.8%) and HI (48.6%). However, the h^2 estimates of RDMC, SPVD and fresh root yield were low at 19.0, 14.9 and 20.4%, respectively. Crosses with high β-carotene content such as Ukrewe x Resisto, Resisto x Ogansagan, Eumula x PIPI and NASPOT-1 x Temesgen exhibited higher RDMC. These families also had medium to high mean fresh root yield. Therefore, progenies derived from these families were the best candidates to develop improved OFSP varieties with high RDMC.

Keywords: Combining ability, gene action, orange fleshed sweetpotato, vitamin A deficiency.

3.1 Introduction

Vitamin A deficiency is a major health problem globally. An estimated 140 to 190 million children aged under 5 years have low serum retinol concentrations (< 0.7 µmol l^{-1}). Out of this, nearly 100 million live in south Asia and sub-Saharan Africa (SSA) (Low et al., 2001; van Jaarsveld et al., 2005; WHO, 2009). According to a World Health Organization (WHO) report, most countries in SSA are categorized as having a public health problem concerning clinical and sub-clinical VAD (WHO, 2009). VAD leads to blindness, retarded growth and death in many of the developing countries. It is estimated that some 3 million children in SSA under the age of 5 suffer from partial or total blindness as a result of VAD. It especially affects pre-school children, and pregnant and lactating mothers, of the rural poor. For instance, the predicted prevalence of vitamin A deficiency for 36 sub-Saharan African countries is 19.1% (WHO, 2009). The recommended daily intakes of vitamin A ranges from 1000-3000 IU for children under 5 years of age, and from 3000-10,000 IU for adults (www.consumerlab.com/rdas/).

Different strategies have been used to control VAD. These include vitamin A supplementation of large doses in the form of capsules, fortification of commonly consumed food items such as oil, sugar, breakfast cereals and grain flour, and dietary diversification that includes eating food items naturally rich in pro-vitamin A such as yellow/orange root crops, leafy vegetables and yellow/orange fruits. Among these strategies, dietary diversification is the most technically feasible and cost-effective option for the poorer communities of the developing world. The advantage of this approach over vitamin A supplementation and food fortification is that it is sustainable since root crops, fruits and vegetables can be harvested and shared at a local level without the intervention of national programs (Burri, 2011; Gurmu et al., 2015).

OFSP is an effective, low-priced and sustainable source of vitamin A that can be used for human dietary diversification since it is rich in β-carotene (pro-vitamin A) (van Jaarsveld et al., 2005). The orange flesh, with various degree of colour intensity, reflects a high β-carotene content. Most of the orange fleshed sweetpotato varieties contain 3000-16000 µg 100 g^{-1} of β-carotene and this contributes to 250-1300 µg 100 g^{-1} of retinol activity equivalent (RAE) (Kapinga et al., 2010). The other pro-vitamin A carotenoids that are found in sweetpotato are alpha-carotene and beta-cryptoxanthin (Ohnishi and Kojinra, 1997). In addition to the orange flesh colour, some sweetpotato varieties have red and purple flesh colour which reflect their high anthocyanin content (Huaman, 1999; Yoshinaga et al., 1999; Vimala and Hariprakash, 2011).

Some OFSP varieties have been released in Ethiopia and are being heavily promoted (Tofu et al., 2007). However, the acceptance of these varieties by farmers is low mainly due to their low RDMC (Gurmu et al., 2015b). Farmers prefer to grow the WFSP varieties that have high RDMC. However, the WFSP varieties have little or no β-carotene. To date, there has been no strategic breeding programme in Ethiopia targeted at enhancing the RDMC of OFSP varieties in order to increase the acceptability and adoption of the OFSP varieties. Therefore, improving the RDMC of the OFSP varieties in Ethiopia through a deigned breeding is vital to enhance their adoption by farmers and thereby improve vitamin A intake of various communities.

The diallel design is a genetic design that has been widely used in genetic analyses to determine the genetic control of quantitative traits (Jinks and Hayman, 1953; Hayman, 1954; Hayman, 1958), to assess GCA and SCA effects (Griffing, 1956a, 1956b) and to determine heterosis (Gardner and Eberhart, 1966; Gardner, 1967). It allows for the selection of superior parents for crosses and, in cross-pollinating species, to screen populations for use in intra- and inter-population breeding programmes. It is also used to estimate the genetic variance components between crosses (Jinks and Hayman, 1953; Hayman, 1954; Kempthorne, 1956; Griffing, 1956a; Kempthorne, 1957), where the relative magnitude of GCA and SCA variances indicate the type of gene action and the best selection method leading to optimal genetic gain. The GCA variances and their effects indicate predominance of additive gene action, while the SCA effects indicate non-additive gene action (dominance, over-dominance or epistasis) in controlling the expression of traits. Therefore, the objective of this study was to determine the combining ability, type of gene action and heritability of RDMC and β-carotene content, and yield related traits of selected sweetpotato clones, for further evaluation and breeding.

3.2. Materials and methods

3.2.1 Study sites

A crossing block was established at the South Agricultural Research Institute (SARI) in Hawassa, Ethiopia. Hawassa (7^{o} 03’ 54” N and 38^{o} 28’ 59” E) is located 275 km south of the Ethiopian capital, Addis Ababa. The progeny tests were conducted at four locations (Hawassa, Wondogenet, Arbaminch and Dilla) in the SNNPRS of Ethiopia. The details of test sites are summarized in Table 3.1.

3.2.2 Plant materials and crosses

Hand crosses were performed in 2013 using a 7 x 7 half-diallel mating design in a net-house. The crossing block is indicated in Figure 3.1. Three parents were orange fleshed, two were

yellow fleshed, and two were white fleshed with high dry matter content. Five of the varieties were accessions from the International Potato Centre (CIP) while two were released varieties in Ethiopia (Table 3.2). The criteria for parental selection were high RDMC of the WFSPs, high β-carotene content of the OFSPs, flowering ability or compatibility of the clones.

Table 3.1 Description of the study sites

Location	Altitude (masl)*	Coordinates	Annual rainfall (mm)	Mean annual temperature (^{o}C)	
				Minimum	Maximum
Hawassa	1700	07^{o}03'54"N, 38^{o}28'59"E	1046.3	13.3	27.6
Wondogenet	1742	07^{o}19'55"N, 38^{o}38'56"E	1372.0	11.5	26.2
Arbaminch	1400	06^{o}03'56''N, 37^{o}33'40''E	940.9	17.4	30.6
Dilla	1519	06^{0}22'49"N, 38^{0}18'25"E	1354.6	12.9	28.1

masl = meter above sea level.

Table 3.2 List of the seven sweetpotato parents used in a diallel crosses

No.	Genotypes	Root flesh colour	RDMC (%)	Source	Resistance to SPVD
1	Ukrewe	Pale orange	28.5	CIP	Unknown
2	Resisto	Deep orange	25.0	CIP	Susceptible
3	Ejumula	Deep orange	29.0	CIP	Susceptible
4	PIPI	Pale yellow	31.5	CIP	Resistant
5	NASPOT-1	Pale yellow	26.5	CIP	Resistant
6	Temesgen	White	33.0	Ethiopia (Released variety)	Susceptible
7	Ogansagan	White	34.5	Ethiopia (Released variety)	Unknown

CIP = International Potato Center; RDMC = root dry matter content, SPVD = sweetpotato virus disease.

3.2.3. Preparation of seeds, growing seedlings and progeny evaluation

The F1 seeds developed from the crosses (Figure 3.2) were scarified by soaking in concentrated sulphuric acid (98%) for 40 minutes. Then the seeds were rinsed with tap water for 5 minutes to remove the acid (Lebot, 2010). A floating technique was used to separate viable and nonviable seeds by immersing the seeds in a 200 ml beaker containing water. Germination evaluation and subsequent planting of the scarified seeds was conducted by sowing the seeds in petridishes (Figure 3.3).

The germinated seeds were planted on polystyrene seedling trays (Figure 3.4) and later transplanted to plastic pots of 10 L capacity (Figure 3.5) containing a mixture of topsoil, sand and manure in the ratio of 3:1:1, in that order. From the F1 seedling plants, 20-30 cm long vine cuttings were prepared from each pot. Cuttings from the F1 seedlings and the parents were field planted at four sites for progeny evaluation (Figure 3.6).

Figure 3.1 Sweetpotato crossing block established at Hawassa

Figure 3.2 Sweetpotato botanical seeds derived from crosses of Resisto x PIPI

Figure 3.3 Germinating F1 seeds of sweetpotato after scarified with sulphuric acid

Figure 3.4 The F1 seedlings grown in plastic seedling trays

At each test site the 28 sweetpotato families and parents (21 crosses and 7 parents) were established using a 7x4 alpha lattice design with two replications. Per replication, a two row plot of three meters long was used for each family to accommodate 20 plants per family. The inter-row spacing was 1m and intra-row spacing was 0.30m. The spacing between blocks and replications was 1m and 2m, respectively.

Figure 3.5 Seedling plants of sweetpotato crosses and parents established at Hawassa for multiplication of cuttings for field planting

Figure 3.6 Partial view of the F1 families and parents established at Arbaminch site

3.2.4. Data collection

The following five traits were considered for the genetic analysis. These included RDMC - expressed as percentage of root dry weight (g) to fresh roots weight (g). Fresh root samples of 100-200 g were taken from each plant in the family and later dried in an oven at 80^{o}C for 48 hours to determine RDMC. β-carotene content was analysed at the Melkassa Agricultural Research Center in Ethiopia using spectrophotometry according to the protocol developed by Rodriguez-Amaya (2001) and the results were expressed as µg 100 g^{-1}. β-carotene content analysis was done on samples of two locations due to the limited capacity of the laboratory. Fresh root yield - expressed in gram per plant averaged over the 20 plants in the family. Harvest index (HI) was calculated as a ratio of fresh root yield to total fresh biomass (above ground fresh weight + root fresh weight) on family basis. The SPVD was recorded on a single plant basis using a scale of 1 to 9; where: 1 = no visible virus symptoms; 3 = faint mosaic; 5 = mosaic clear; 7 = heavy mosaic and stunted; 9 = necrosis (dead patches) (Hahn, 1979; Mwanga et al., 2002a; Ndunguru et al., 2009).

3.2.5. Data analyses

Analysis of variance

ANOVA of data across environments was conducted using GenStat 14th edition (Payne et al., 2011) and SAS version 9.3 (SAS Institute Inc., 2003) statistical packages.

Estimation of GCA and SCA effects, heritability and heterosis

The statistical model for the combined analysis of variance across environments is given as follows (Hallauer et al., 2010).

$$Y_{ijkl} = \mu + E_e + k(re)_k + g_i + g_j + s_{ij} + gE_{ie} + sE_{eij} + \varepsilon_{ijkl}$$

where Y_{ijkl} is the observed measurement for the ijth cross grown in the lth environment; μ is the grand mean; E_e is environment effect; $k(re)_k$ is the estimate of the kth incomplete block within replications nested in the environment; g_i + gj are the GCA effects of ith and jth parents, respectively; s_{ij} is the SCA effect; gE_{ie} is the interaction effect between GCA and the environment; sE_{eij} is the interaction effect between SCA and the environment; ε_{ijkl} is the error term associated with the ijth cross evaluated in the kth replication and E_e environment.

The GCA and SCA variance components were computed according to Griffing's (1956b) fixed-effects Model I, Method 2 (parents and F1s excluding reciprocals) using the DIALLEL-SAS05 program developed by Zhang et al (2005). Sources of variations were partitioned as presented in the partial analysis of variance of Table 3.3.

Table 3.3 ANOVA of a half diallel including parents and their crosses repeated over environments using Griffing's (1956) Model I, Method 2

Source of variation	df	E(MS)
Environments (E)	e-1	
Replications/E	e(r-1)	
Treatments	[n(n+1)/2]-1	$\sigma^2_E + r\sigma^2_{en} + erK^2_n$
GCA	n-1	
SCA	n(n-3)/2	
E x GCA	(e-1) (n-1)	
E x SCA	(e-1) (n(n-3)/2)	
Pooled error	e(r-1) [(n(n+1)/2) -1]	σ^2_E
Total	[ern(n+1)/2]-1	

df = degrees of freedom, e = environment, r = replication, n =number of parents; GCA= general combining ability; SCA= specific combining ability.

The type of gene action was calculated according to Baker (1978) expressed as the ratio of variances: $2\sigma^2_{GCA} / \left(2\sigma^2_{GCA} + \sigma^2_{SCA}\right)$. If the ratio is closer to unity, it indicates predominance of additive gene action and greater predictability of progeny performance based on GCA effects.

Narrow sense heritability were estimated from the outputs of DIALLEL-SAS05 program as follows:

$$h^2 = \sigma^2_{GCA}/(\sigma^2_{GCA} + \sigma^2_{SCA} + \sigma^2_{E})$$

where: h^2 = narrow sense heritability estimates

σ^2GCA = genetic variance for general combining ability

σ^2SCA = genetic variance for specific combining ability

σ^2_E = error variance

Mid-parent heterosis (MPH) and better-parent heterosis (BPH) were estimated for RDMC, SPVD and fresh root yield using the formula of Falconer and Mackay (1996):

MPH (%) = ((F1 - MP)/MP)*100 and BPH (%) = ((F1 - BP)/BP)*100

Where: F1 = mean of the F1 hybrid, MP = mean of the two parents involved in the cross, BP = mean of better parent in the cross.

3.3. Results

3.3.1. Analysis of variance and mean performance of genotypes

The combined ANOVA of RDMC, β-carotene content, SPVD, fresh root yield and HI, is presented in Table 3.4. There was a highly significant ($p < 0.001$) difference between genotypes across the four test environments for all the five traits. Genotype x environment interaction variances were also significant except for RDMC.

Table 3.4 ANOVA showing the degrees of freedom and mean square values of five traits of seven sweetpotato parents and their 21 crosses evaluated across four locations.

Source of variation	df	Mean square β-carotene content (µg 100 g^{-1})	df	Mean square RDMC (%)	SPVD (1-9 score)	Fresh root yield (g plant^{-1})	Harvest Index
Environment (E)	1	9959719.0***	3	339.40***	12.22***	3971492.62***	0.316***
Replication (R)	1	4048715.0*	4	20.19^{ns}	6.38***	9101.23^{ns}	0.024***
Genotypes (G)	27	49364618.0***	27	27.18***	2.56***	371175.29***	0.088***
G x E	27	2818286.0***	81	15.86^{ns}	0.89*	182205.26***	0.008***
Error	54	906010.0	108	11.56	0.70	16906.80	0.003
Total	111		223				

df = degrees of freedom; *,**, *** significant at $p < 0.05$, $p < 0.01$, $p < 0.001$ probability levels, respectively; ns = not significant, SPVD = sweetpotato virus disease, RDMC = root dry matter content.

The sweetpotato genotypes Temesgen and Ogansagan yielded the highest RDMC of 35.5 and 36.0%, respectively, while the lowest (25.2%) was recorded for Resisto (Table 3.5). Crosses of Ukrewe x PIPI and PIPI x Ogansagan provided the highest mean RDMC of 40.5 and 40.8%, respectively, across the four locations. Resisto had the highest mean β-carotene content of 11,103.4 µg 100 g^{-1} followed by Ukrewe, which provided a mean β-carotene content of 8,934.2 µg 100 g^{-1} across locations. Temesgen and Ogansagan had the lowest mean β-carotene content of 34.7 and 26.0 µg 100 g^{-1}, respectively. The highest β-carotene content was recorded for the crosses Ukrewe x Resisto and Resisto x Ogansagan with means of 9844.7 and 10,590.3 µg 100 g^{-1}, respectively (Table 3.5).

All parents except Temesgen had SPVD score less than 3.0. Temesgen, with a mean score of 3.75, was found to be relatively susceptible (Table 3.5). All the crosses showed SPVD scores of 1.0 to 2.3. Resisto and NASPOT-1 had higher mean fresh root yields of 982.7 and 969.8 g plant^{-1}, respectively. The cross Resisto x NASPOT-1 had the highest mean fresh root yield of 1020.6 g plant^{-1}, followed by the crosses Resisto x PIPI, Ukrewe x Resisto and Resisto x Temesgen, which had mean fresh root yields of 978.6, 958.1 and 952.5 g plant^{-1}, respectively. Across the four environments, Resisto had the highest HI with a mean of 0.56 across locations. The family of Resisto x NASPOT-1 recorded high HI of 0.52, followed by the cross Resisto x PIPI, which had a mean HI of 0.50 (Table 3.5).

Table 3.5 Means of five traits of seven sweetpotato parents and 21 crosses when evaluated across four test locations in southern Ethiopia

		Traits				
No.	**Parents/crosses**	**RDMC (%)**	**β-carotene content (µg 100 g^{-1})**	**SPVD (1-9 score)**	**Fresh root yield (g plant^{-1})**	**Harvest Index**
Parents						
1	Ukrewe	30.0	8934.2	1.25	626.9	0.32
2	Resisto	25.2	11,103.4	1.75	982.7	0.56
3	Ejumula	29.0	7403.6	1.75	669.8	0.25
4	PIPI	30.6	137.9	1.25	337.5	0.18
5	NASPOT-1	25.4	461.0	1.25	969.8	0.27
6	Temesgen	36.0	26.1	3.75	571.9	0.30
7	Ogansagan	35.5	34.9	1.88	854.4	0.28
Mean		**30.3**	**4014.4**	**1.80**	**716.4**	**0.31**
Crosses						
1	Ukrewe x Resisto	36.6	9844.7	1.75	958.1	0.43
2	Ukrewe x Ejumula	39.9	4585.3	1.25	673.3	0.25
3	Ukrewe x PIPI	40.5	3968.0	1.50	522.3	0.19
4	Ukrewe x NASPOT-1	37.5	2019.7	1.75	711.9	0.25
5	Ukrewe x Temesgen	39.3	1150.7	1.25	719.8	0.27
6	Ukrewe x Ogansagan	38.9	1651.7	1.25	542.1	0.30
7	Resisto x Ejumula	36.0	4977.8	1.50	848.9	0.39
8	Resisto x PIPI	38.7	4170.0	2.00	978.6	0.50
9	Resisto x NASPOT-1	35.6	7264.7	1.75	1020.6	0.52
10	Resisto x Temesgen	35.0	6282.8	2.25	952.5	0.48
11	Resisto x Ogansagan	37.5	10590.3	2.25	812.9	0.43
12	Ejumula x PIPI	38.2	4685.6	1.75	549.4	0.28
13	Ejumula x NASPOT-1	35.9	5584.0	1.25	833.9	0.27
14	Ejumula x Temesgen	38.1	6323.5	1.25	457.1	0.26
15	Ejumula x Ogansagan	37.9	1905.0	1.00	716.9	0.29
16	PIPI x NASPOT-1	37.8	1052.3	1.25	740.0	0.27
17	PIPI x Temesgen	38.9	82.9	1.00	478.8	0.20
18	PIPI x Ogansagan	40.8	78.1	1.00	485.4	0.19
19	NASPOT-1 x Temesgen	37.2	5153.4	1.00	538.1	0.24
20	NASPOT-1x Ogansagan	34.6	421.5	1.75	786.0	0.24
21	Temesgen x Ogansagan	34.5	62.7	1.50	445.2	0.31
Mean		**37.4**	**3897.8**	**1.49**	**703.4**	**0.31**
CV (%)		**9.0**	**25.7**	**49.50**	**18.2**	**16.36**
R2		**0.71**	**0.97**	**0.76**	**0.95**	**0.94**

RDMC = Root dry matter content, SPVD = Sweetpotato virus disease.

3.3.2. Combining ability effects

The GCA and SCA mean squares for RDMC, β-carotene content, SPVD, fresh root yield and harvest index, from a combined analysis of the four locations were highly significant except for the SCA of RDMC (Table 3.6).

GCA x environment and SCA x environment interaction effects were highly significant ($p < 0.001$) for all traits except RDMC (Table 3.9). The GCA to SCA variance ratios were 0.74 for SPVD, 0.96 for fresh root yield, 0.97 for harvest index, 0.96 for RDMC and 0.94 for β-carotene content.

Percent contributions of GCA and SCA were also calculated from the sum of squares of GCA and SCA values of all the five traits and the result is shown in Table 3.6. The percent contribution of GCA was higher in four traits, namely RDMC, β-carotene content, fresh root yield and HI. Accordingly, GCA contributed 3.7 times more than SCA for RDMC, 2.4 times more for β-carotene content, 3.5 times more for fresh root yield and 6.4 times for HI. For SPVD, SCA provided a higher contribution and was 2.5 times GCA.

Table 3.6 ANOVA showing the significance effects of combining ability for five traits of seven sweetpotato parents and their 21 F1 crosses evaluated across four locations

		Mean square		Mean square			
Source of variation	**df**	**β-carotene content (µg 100 g^{-1})**	**df**	**RDMC (%)**	**SPVD (1-9 score)**	**Fresh root yield (g plant^{-1})**	**HI**
Replication (R)	1	4048715.00*	4	20.19^{ns}	6.38***	9101.23^{ns}	0.02***
GCA	6	140772980.37***	6	91.73***	2.95***	1192683.30***	0.34***
SCA	21	16973039.16***	21	7.13^{ns}	2.09***	96579.60***	0.02***
GCA x E	6	5207077.88***	18	17.90^{ns}	0.92***	458660.10***	0.01***
SCA x E	21	2574264.94***	63	15.23^{ns}	0.89***	96306.00***	0.01***
Pooled Error	54	906010.00	108	11.56	0.70	16906.80	0.003
%GCA		70.32		78.61	28.74	77.92	86.49
%SCA		29.68		21.39	71.26	22.01	13.51

df = degrees of freedom, *,**, *** significant at $p < 0.05$, $p < 0.01$, $p < 0.001$ probability levels, respectively; ns = not significant, RDMC = root dry matter content, SPVD = sweetpotato virus disease, HI = harvest index.

General combining ability effects

The GCA effects of the parents, Ukrewe, PIPI, Resisto and NASPOT-1, were positive and significant for RDMC, (Table 3.7). The other three parents showed non-significant GCA effects for this trait. Ukrewe and Resisto showed positive and highly significant ($p < 0.001$) GCA effects for β-carotene content. Similarly, Ejumula showed a positive GCA effect at $p < 0.05$. The other

four parents, PIPI, NASPOT-1, Temesgen and Ogansagan, had highly significant ($p < 0.001$) GCA effects that were negative (Table 3.7).

Desirable GCA effects for SPVD should be negative. Resisto exhibited positive and highly significant ($p < 0.001$) GCA effects for SPVD in an undesirable direction. Temesgen also had positive and significant ($p < 0.5$) GCA effects, confirming their historic susceptibilities to SPVD. The GCA effects of other parents were not significant for this trait (Table 3.7).

The desirable GCA effects for fresh root yield should be positive. The GCA effect of Resisto and NASPOT-1 were positive and significant ($p < 0.05$). The parents PIPI and Ogansagan had significant and negative GCA effects for fresh root yield (Table 3.7). The parent Resisto had positive and highly significant ($p < 0.001$) GCA effect for HI (Table 3.7). Ukrewe, Ejumula and PIPI had significant negative GCA effects. The GCA effect was not significant for NASPOT-1, Temesgen and Ogansagan for fresh root yield.

Table 3.7 Estimates of the general combining ability (GCA) effects of seven sweetpotato parents for five traits evaluated across four locations

No.	Parents	RDMC (%)	β-carotene content (µg 100 g^{-1})	SPVD (1-9 score)	Fresh root yield (g $plant^{-1}$)	Harvest Index
1	Ukrewe	1.28*	944.28***	-0.14ns	-31.65ns	-0.02*
2	Resisto	-1.75***	4098.49***	0.36***	264.78***	0.16***
3	Ejumula	0.20ns	467.20*	-0.14ns	-32.37ns	-0.03*
4	PIPI	1.28*	-1581.35***	-0.14ns	-126.30**	-0.05***
5	NASPOT-1	-1.38**	-898.27***	-0.11ns	89.21*	-0.02ns
6	Temesgen	0.41ns	-1672.70***	0.25*	-87.93*	-0.02ns
7	Ogansagan	-0.05ns	-1357.65***	-0.09ns	-75.73ns	-0.02ns

*,**, *** significant at $p < 0.05$, $p < 0.01$, $p < 0.001$ probability levels, respectively; ns = not significant; RDMC = root dry matter content, content, SPVD = sweetpotato virus disease.

Specific combining ability effects

None of the SCA effects were significant for RDMC (Table 3.8). For β-carotene content the families from the following crosses: Ukrewe x Resisto, Resisto x Ogansagan, Ejumula x PIPI and NASPOT-1 x Temesgen, had positive and significant SCA effects. The crosses Ukrewe x NASPOT-1, Ukrewe x Temesgen, Ukrewe x Ogansgen, Resisto x Ejumual, Resisto x PIPI and

Ejumula x Ogansagan had negative and highly significant SCA effects. The rest of the crosses exhibited non-significant SCA effects (Table 3.8).

The SCA effects of all the crosses were not significant for SPVD (Table 3.8). For fresh root yield, the SCA effects were not significant for most crosses except for Ukrewe x Temesgen, Resisto x PIPI, Ejumula x Ogansagan and PIPI x Ogansagan, which had positive and significant SCA effects. Crosses with significant but negative SCA effects were Ejumula x Temesgen, NASPOT-1 x Temesgen, Temesgen x Ogansagan. Only two crosses, Resisto x PIPI and Resisto x NASPOT-1, had positive and significant SCA effects for HI (Table 3.8). The rest of the parents had non-significant SCA effects.

Table 3.8 Estimates of the SCA effects involving five traits of 21 sweetpotato crosses derived from a 7 x 7 half diallel evaluated across four locations

No.	Crosses	RDMC (%)	β-carotene content (µg 100 g^{-1})	SPVD (1-9 score)	Fresh root yield (g $plant^{-1}$)	Harvest Index
1	Ukrewe x Resisto	-0.596ns	1152.762*	-0.003ns	14.152ns	-0.018ns
2	Ukrewe Ejumula	0.737ns	-475.394ns	-0.003ns	26.498ns	-0.009ns
3	Ukrewe x PIPI	0.330ns	955.864ns	0.247ns	-30.602ns	-0.045ns
4	Ukrewe x NASPOT-1	-0.071ns	-1675.515**	0.462ns	-56.532ns	-0.017ns
5	Ukrewe x Temesgen	0.355ns	-2085.156***	-0.056ns	116.332*	0.007ns
6	Ukrewe x Ogansagan	-0.215ns	-4665.522***	-0.143ns	-28.507ns	-0.023ns
7	Resisto x Ejumula	-0.128ns	-3237.051***	-0.253ns	-94.306ns	-0.056ns
8	Resisto x PIPI	-1.509ns	-1996.281***	0.247ns	129.219*	0.079**
9	Resisto x NASPOT-1	1.032ns	415.258ns	-0.038ns	-44.211ns	0.069*
10	Resisto x Temesgen	-0.860ns	-107.226ns	0.444ns	52.603ns	0.025ns
11	Resisto x Ogansagan	0.367ns	5258.073***	0.607ns	-102.079*	0.048ns
12	Ejumula x PIPI	-0.961ns	2150.543***	0.497ns	-2.809ns	0.054ns
13	Ejumula x NASPOT-1	-0.612ns	-334.231ns	-0.038ns	66.273ns	-0.001ns
14	Ejumula x Temesgen	0.303ns	514.811ns	-0.056ns	-145.663*	-0.005ns
15	Ejumula x Ogansagan	-1.273ns	-4258.638***	-1.143ns	102.650*	0.028ns
16	PIPI x NASPOT-1	0.272ns	-117.288ns	-0.038ns	66.235ns	0.029ns
17	PIPI x Temesgen	0.059ns	-627.234ns	-0.306ns	-30.075ns	-0.036ns
18	PIPI x Ogansagan	1.030ns	-268.409ns	-0.643ns	109.550*	-0.023ns
19	NASPOT-1 x Temesgen	0.973ns	3760.099***	-0.342ns	-186.206*	-0.029ns
20	NASPOT-1x Ogansagan	-2.598ns	734.880ns	0.143ns	-6.620ns	-0.022ns
21	Temesgen x Ogansagan	-0.230ns	343.019ns	-0.714ns	-396.959***	0.032ns

*,**, *** significant at $p < 0.05$, $p < 0.01$, $p < 0.001$ probability levels, respectively; ns = not significant; RDMC = root dry matter content, SPVD = sweetpotato virus disease.

3.3.3 Heterosis

Heterosis was estimated for the 24 clones selected from 420 clonal stage-I of the original 21 F1 families. The mid-parent heterosis were mostly positive for RDMC. Among the better-parent heterosis estimates, only progenies derived from the cross Resisto x Temesgen had negative estimates for RDMC. The highest positive mid-parent heterosis of 48.0% was observed for a clone Ukrewe x NASPOT-1-1, which was originally derived from a cross of Ukrewe x NASPOT-1. The highest better-parent heterosis of 41.3% was obtained in a clone Ukrewe x Ejumula-13, which was originally derived from the cross between Ukrewe x Ejumula (Table 3.9). For SPVD, a negative heterosis is desirable. A higher negative mid-parent heterosis of -54.2% was observed in a resistant cross of Ukrewe x Ogansagan. Other higher negative mid-parent heterosis of -45.5, -56.4 and -63.6% were observed in the crosses of Resisto x Ogansagan. High negative better-parent heterosis of -25.7% for SPVD was observed in a cross of Resisto x Ejumula and -42.9 in a cross of Resisto x Ogansagan. These crosses had higher resistance to SPVD than the rest of the crosses (Table 3.9). Conversely, clones such as Resisto x Temesgen-10 and Resisto x Temesgen-12 had high positive mid-parent heterosis of 32.7 and 33.3%, respectively, and better-parent heterosis of 20.0 and 60.0%, in that order. These clones were susceptible to SPVD. Both of these clones were derived from the cross of Resisto x Temesgen.

For fresh root yield, high positive mid-parent of 83-170% and 45-62% were observed in the progenies derived from the crosses of Resisto x PIPI and Resisto x Ogansagan, respectively (Table 3.9). Similarly high positive better-parent heterosis of 47-117% and 43-60% were observed in progenies derived from the crosses of Resisto x PIPI and Resisto x Ogansagan, respectively.

Table 3.9 Estimates of percent mid-parent and better-parent heterosis for RDMC, SPVD and fresh root yield of 24 clones selected from the F1 families

No.	Crosses	Heterosis (percentage)					
		RDMC		SPVD		FRY	
		%MPH	%BPH	%MPH	%BPH	%MPH	%BPH
1	Ukrewe x Ejumula - 10	41.7	39.3	-21.4	-12.0	25.5	21.5
2	Ukrewe x Ejumula- 13	43.7	41.3	-7.1	4.0	11.3	7.7
3	Ukrewe x PIPI-1	35.0	33.7	10.6	0.0	28.3	-1.3
4	Ukrewe x NASPOT-1-1	48.0	36.7	-25.7	-25.7	1.7	-16.2
5	Ukrewe x Ogansagan-5	15.8	6.1	-54.2	-12.0	6.1	1.4
6	Resisto x Ejumula-7	25.8	17.6	9.9	14.3	65.4	51.6
7	Resisto x PIPI-1	37.3	25.2	1.6	5.7	126.2	81.5
8	Resisto x PIPI-2	33.0	21.2	0.0	12.0	120.4	76.9
9	Resisto x PIPI-4	19.7	9.2	0.0	12.0	83.7	47.4
10	Resisto x PIPI-14	42.7	30.1	-20.0	-4.0	170.4	117.0
11	Resisto x Temesgen -10	6.1	-10.6	32.7	20.0	73.0	43.0
12	Resisto x Temesgen -12	3.5	-12.8	33.3	60.0	51.0	24.8
13	Resisto x Temesgen -14	4.4	-11.9	1.6	5.7	29.4	7.0
14	Resisto x Temesgen -17	18.6	0.0	3.3	7.4	13.6	-6.1
15	Resisto x Temesgen-23	24.9	6.8	-1.4	2.6	16.9	-3.4
16	Resisto x Ogansagan-5	20.3	3.7	-63.6	-42.9	62.3	60.2
17	Resisto x Ogansagan-16	33.0	14.6	-27.3	14.3	45.5	43.7
18	Resisto x Ogansagan-20	25.5	8.2	-45.5	-14.3	49.8	47.9
19	Resisto x Ogansagan-23	32.4	14.1	-56.4	-31.4	62.4	60.4
20	Ejumula x PIPI-10	38.6	35.0	0.0	20.0	21.7	-8.5
21	Ejumula x PIPI-18	34.9	31.4	0.0	20.0	8.4	-18.5
22	Ejumula x PIPI-19	28.2	24.8	-20.0	-4.0	42.2	7.0
23	Ejumula x Temesgen-15	13.2	1.4	-28.6	-25.7	-31.5	-38.9
24	Ejumula x Ogansagan-17	24.7	11.7	-34.1	-31.4	-18.8	-27.6

RDMC = root dry matter content, SPVD = sweetpotato virus disease, FRY = fresh root yield, HI = Harvest Index, MPH = mid-parent heterosis, MBH = better-parent heterosis.

3.3.4 Heritability estimates

The narrow sense heritability estimates were relatively low for RDMC (19.0%), SPVD (14.9%) and fresh root yield (20.4%), whereas it was relatively high for β-carotene content (79.8%) and HI (48.6%). The calculated broad sense heritability were close to the narrow sense heritability. With broad sense heritability of 89.4 and 51.5%, β-carotene content and HI had higher estimates than RDMC (20.5%), SPVD (25.5%) and fresh root yield (22.1%).

3.4 Discussion

The presence of a highly significant difference between the four test locations for all the five traits indicated that the genotypes performed differently across the test environments. The significant G x E interaction emphasizes the need for evaluating sweetpotato genotypes across environments. More than 75% of the crosses had a mean RDMC that exceeded the mean of the best parent. This shows the presence of heterosis for this trait. Similar results were reported by Chiona et al (2009) who estimated the presence of heterosis for RDMC in sweetpotato genotypes evaluated in Zambia. Crosses with high RDMC can be considered for continuous selection, although this depends on their β-carotene content. Resisto was the best parent that provided progenies with high β-carotene content. Most crosses had lower mean scores for SPVD across locations, which clearly showed that all the crosses were resistant or tolerant to SPVD. Across the four test locations, some of the crosses which involved Resisto, such as Ukrewe x Resisto, Resisto x PIPI, Resisto x NASPOT-1 and Resisto x Temesgen had higher mean fresh root yields that were comparable to the yield of the best parent in the cross. Crosses involving the high yielding parent, Resisto, such as Ukrewe x Resisto, Resisto x PIPI, Resisto x NASPOT-1 and Resisto x Temesgen resulted in higher mean harvest indices that were comparable to the HI of Resisto.

The significance of GCA and SCA mean squares for the four traits (SPVD, fresh root yield, HI and β-carotene content) indicated the importance of both additive and non-additive gene action in controlling the expression of these traits. Similar result was reported by Chiona (2009) who found significant GCA and SCA mean squares for β-carotene, RDMC, HI and fresh root yield in sweetpotato crosses. The GCA mean square was significant only for RDMC. This suggests that additive gene action is more important than non-additive genes in controlling the expression of this trait. The GCA x environment and SCA x environment interaction effects were highly significant ($p < 0.001$) for all traits except RDMC. The significance of the interaction effects shows the implication of environment for selection with regards to the four traits.

All the ratios of GCA to SCA variances were closed to unity for all the five traits. This implies that additive gene action was the predominant type of gene action controlling the traits. Therefore, progeny performance can be predicted based on GCA for the four traits. Mwanga et al. (2002b) reported similar results for SPVD where the ratio of GCA to SCA variances were 0.87, 0.59 and 0.51 in the screen-house, in the field, and in the recovery experiments, respectively. From this result, Mwanga et al. (2002b) suggested that GCA effects were more

important than SCA effects in predicting progeny performance for SPVD resistance. Chiona (2009) reported higher ratios of GCA to SCA variances, where the ratios were 0.76, 0.92, 0.76 and 0.68 for β-carotene content, RDM, HI, fresh root yield, respectively.

Percent contributions of GCA and SCA were calculated from sum of squares of GCA and SCA of all the five traits and GCA contributed higher percentage in four of the traits (RDMC, β-carotene content, fresh root yield and HI). Generally, GCA contributed 2.4-6.4 times more than SCA for the four traits. For SPVD, SCA contributed 2.5 times more than GCA, although the effects were not significant, as discussed below.

The GCA effects of Ukrewe and PIPI for RDMC were positive and significant at $p < 0.05$, suggesting the presence of additive gene action controlling the expression of this trait. All the SCA effects were not significant for this trait. This result is in agreement with the reports of other authors who indicated that GCA was more important than SCA in progeny performance for high RDMC (Sakai, 1964; Grüneberg et al., 2005; Chiona, 2009; Shumbusha et al., 2014).

Both the GCA and SCA effects were important in controlling the expression of β-carotene content. Ukrewe, Resisto and Ejumula had positive and significant GCA effects, which indicated the presence of additive gene action. Chiona (2009) reported that two high β-carotene parents exhibited positive high GCA effects, which reflected the predominance of additive gene effects in the inheritance of β-carotene. The following crosses: Ukrewe x Resisto, Resisto x Ogansagan, Ejumula x PIPI and NASPOT-1 x Temesgen had positive and significant SCA effects. This shows the presence of non-additive gene action in addition to the additive gene action. Some crosses, such as Ukrewe x NASPOT-1, Ukrewe x Temesgen, Ukrewe x Ogansagan, Resisto x Ejumula, Resisto x PIPI and Ejumula x Temesgen had highly significant but negative SCA effects, implying undesirable combinations for improvement of this trait. It was difficult to pick one or two parents and predict the crosses that would result from these parents with good SCA effects. Parents that were included in the crosses that resulted in a significant positive SCA effect were also found in crosses that resulted in a significant negative SCA. Therefore, it would be important to make as many crosses as possible to get desirable combinations with high and positive SCA effects.

Resisto and Temesgen exhibited positive and significant GCA effects, which indicates that these parents were not good combiners for a breeding program targeting SPVD resistance. This result is supported by the reports of Sseruwu (2012) and Sibiya (2009) who reported that a positive GCA effect for disease indicates an undesirable contribution to increased susceptibility

in the progeny. This is because the desirable GCA effects for SPVD resistance should be negative. For the rest of the parents, their GCA effects were not significant. The SCA effects of all the crosses were also not significant for this trait. This is attributed to the fact that the parents were not selected based on their resistance or susceptibility to SPVD but they were selected based on other traits such as RDMC and β-carotene content.

Resisto and NASPOT-1 had positive and significant GCA effects, indicating the presence of additive gene action. The SCA effects were not significant for most of the crosses, except for the crosses Ukrewe x Temesgen, Resisto x PIPI, Ejumula x Ogansagan and PIPI x Ogansagan, which had positive and significant SCA effects. The presence of significant and positive SCA effects suggests the contribution of non-additive gene action for the expression of fresh root yield. However, it is not yet clear whether fresh root yield is controlled by additive or non-additive gene action. In some studies (Saad, 1993; Chiona, 2009), it was reported that fresh root yield was predominantly controlled by additive gene action, while Vimala and Hariprakash (2011) found non-additive gene action to controlling fresh root yield of sweetpotato, in agreement to the current findings.

Resisto was the only parent that had positive and highly significant ($p < 0.001$) GCA effect for HI, implying that additive gene action controls the inheritance of this trait. Only two crosses, Resisto x PIPI and Resisto x NASPOT-1, had positive and significant SCA effects for HI, showing the existence of non-additive gene action for the expression of this trait. Therefore, both additive and non-additive gene actions are important for the expression of HI.

Heterosis was observed in most of the crosses for RDMC. All mid-parent heterosis estimates and most estimates of better-parent heterosis were positive, indicating the possibility of selecting outperforming progenies than their corresponding parents. This was also reported by Chiona (2009). For SPVD, negative heterosis is desirable. Accordingly, Ukrewe x Ogansagan-5 and Resisto x Ogansagan-5, Resisto x Ogansagan-20 and Resisto x Ogansagan-23, which resulted from the crosses of parents involving Ukrewe, Resisto and Ogansagan, were resistant to SPVD. Sseruwu (2012) reported a negative %BPH for SPVD score, which indicated a progeny that was more resistant than the best parent. Most of the F1 progenies from Temesgen, a susceptible parent, had positive mid- and better-parent heterosis, implying susceptibility of the cross to SPVD.

For fresh root yield, progenies of the cross Resisto x PIPI and Resisto x Ogansagan had higher positive mid- and better-parent heterosis, indicating the possibility of selecting progenies that

outperform both of their parents. These crosses had Resisto in their parentage, which had high and significant positive GCA. On the other hand, PIPI had significant negative GCA and Ogansagan did not show significant GCA effects, suggesting that heterosis does not necessarily arise from a cross involving parents with high positive GCA but also from crosses with negative GCA effects. Similar observations were reported by different authors for various traits of sweetpotato including Chiona (2009) for β-carotene content, Kivuva (2013) for fresh root yield under drought, and Shumbusha et al. (2014) for RDMC.

The narrow sense heritability (h^2) estimates for RDMC, SPVD and fresh root yield were low at 19.0, 14.9 and 20.4%, respectively. The low h^2 for RDMC was an unexpected since the trait is less influenced by environmental effects. The present results contrast with previous studies that reported high values of h^2 (Jones, 1986; Martin, 1988). Courtney et al. (2008) reported a high broad-sense heritability of 93% for RDMC, among full-sib families, suggesting that traditional breeding strategies such as clonal selection could improve the micro-nutritional value of sweetpotato. Citing different authors, Cervantes-Flores (2006) also mentioned that the high narrow sense heritability and additive gene action in RDMC can result in rapid improvement of this trait. Bradshaw (2010) indicated that heritability of RDMC is estimated to be between 75-88% and hence selection for high dry matter content is very effective. In addition Cruz and Chujoy (1994) reported a narrow sense heritability of 26-49% for RDMC which is moderate to high. Two traits, namely HI and β-carotene content, had high narrow sense heritability estimates of 48.6 and 79.8%, respectively. The high h^2 obtained in this study for β-carotene content deviates from the results reported by Chiona (2009) who reported low h^2. However, the current result is in agreement with the reports of Jones (1986) and Martin (1988) who reported that flesh colour, skin colour, percent dry weight, percent crude starch, resistance to root-knot nematode and vine length had high heritabilities.

Fresh root yield and SPVD had lower h^2, which was expected since these traits are highly influenced by environmental effects. Vimala and Hariprakash (2011) reported that fresh root yield had low heritability, indicating the presence of non-additive gene action. The estimates of broad sense heritability were also close to the narrow sense heritability. β-carotene content and HI, which had higher narrow sense heritability of 79.8 and 48.6%, respectively, also had higher estimates of broad sense heritability of 89.4 and 51.5%, respectively. SPVD, fresh root yield and RDMC had lower estimates of broad sense heritability of 25.5%, 22.1% and 20.5, respectively. When broad sense heritability estimates are close to narrow sense heritability then non-additive

gene action is lower than the additive gene action. In general, heritability estimates represent an efficient means of determining the response to selection (Jones, 1986).

3.5. Conclusions

From the results of this study it is concluded that additive gene action is more important for the improvement of RDMC while both additive and non-additive gene actions were important in controlling the expression of β-carotene content. For all the traits studied, additive gene action was the predominant type of gene action controlling the traits and therefore progeny performance can be predicted based on GCA. Based on GCA effects, PIPI and Temesgen were better parents for RDMC while Ukrewe and Resisto for β-carotene content. For fresh root yield, Resisto and NASPOT-1 were better parents. However, Temesgen was not a good combiner for resistance breeding to control SPVD. Resisto was the best parent for improved HI.

Based on SCA effects, Ukrewe x Resisto, Resisto x Ogansagan and Ejumula x PIPI were promising families for improvement of β-carotene content. For fresh root yield, Ukrewe x Temesgen, Resisto x PIPI, Ejumula x Ogansagan and PIPI x Ogansagan, were superior families. Crosses derived from Resisto, such as Ukrewe x Resisto, Resisto x PIPI, Resisto x NASPOT-1 and Resisto x Temesgen were promising families to improve HI.

Positive heterosis was observed in some of the crosses and since clonal reproductions are used in sweetpotato, the heterozygous F1 progenies can be screened, selected, evaluated and released as a variety. Therefore, sweetpotato breeding can take advantage of both GCA effect, where poly-crosses can be applied to improve the traits of interest, and SCA, where progeny selection showing heterosis for the traits of interest would be possible. HI and β-carotene content had high heritability, while RDMC, SPVD and fresh root yield had relatively low heritability.

Crosses with high β-carotene content were Ukrewe x Resisto, Resisto x Ogansagan, Ejumula x PIPI and NASPOT-1 x Temesgen. These crosses had high RDMC that exceeded the mean of the best parent. These families also had medium to high mean fresh root yield. Therefore, it is worth undertaking continuous progeny selection among these families to develop OFSP varieties with high RDMC for further evaluation and release.

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CHAPTER 4

Genotype-by-environment interaction and stability of sweetpotato clones for root dry matter and β-carotene contents, and fresh root yield

Abstract

Sweetpotato [*Ipomoea batatas* (L.) Lam] grows in diverse agro-ecologies but its dry matter and β-carotene contents, and root yields are sensitive to genotype x environment (G x E) interaction effects. Therefore, selection of high yielding and stable genotypes using multi-environment trials may enhance genetic gains. The objectives of the study were to estimate the magnitude of G x E interactions and to select stable and high yielding candidate sweetpotato clones for RDMC, β-carotene content and fresh root yield, and to identify the most discriminating and representative test environments in Ethiopia. The study was conducted across six sweetpotato growing and diverse environments (Halaba, Kokate, Areka, Arbaminch, Hawassa and Dilla) in southern Ethiopia. Twenty four candidate clones and one check variety were evaluated using a 5 x 5 simple lattice design. Stability analysis was conducted using AMMI and GGE bi-plot methods. Environment, genotype and G x E interaction variances were significant ($p < 0.01$) for the three traits. The magnitude of environment and G x E interaction effect was higher for fresh root yield at 66.8% than RDMC (44.0%) and β-carotene content (7.6%). Using AMMI and GGE bi-plot analyses, two candidate clones, designated as G3 and G11, were identified as stable genotypes with high RDMC values of 37.15 and 40.19%, respectively, while genotypes G8 and G15 were stable with high β-carotene contents of 20.01 and 16.59 mg 100 g^{-1}, respectively. AMMI analysis identified one clone (G19) as the most stable genotype with above average fresh root yield of 21.3 t ha^{-1}, while GGE analysis identified three clones, G1, G6 and G20, as stable genotypes with relatively high mean fresh root yields of 25.09, 26.92 and 25.46 t ha^{-1}, respectively. Therefore, the four candidate clones designated as G1, G6, G19 and G20 with above average RDMCs values of 31.82, 32.60, 33.09 and 30.06%, high β-carotene contents of 12.48, 14.27, 16.30 and 13.99 mg 100 g^{-1} and, stable and high fresh root yields of 25.09, 26.92, 21.30 and 25.46 t ha^{-1}, respectively were selected for final evaluation and recommendations. Among the test sites included in this study, Arbaminch was identified as the best environment for sweetpotato testing or production in southern Ethiopia giving high a RDMC of 32.9%, an average β-carotene content of 7.2 mg 100 g^{-1} and the highest fresh root yield of 37.1 t ha^{-1}. The current study demonstrated the possibility of breeding sweetpotato varieties with a balance of high RDMC, medium β-carotene content and a high fresh root yield, with wide or specific adaptation for large scale production.

Keywords: AMMI, candidate clones, GGE, multi-environment, stability analysis.

4.1 Introduction

Genotype by environment (G x E) interaction is a differential response of crop varieties when grown across target environments. The occurrence of G x E interaction implies the need for systematic selection and ranking of candidate varieties across representative growing environments to determine their level of adaptation and yield expression prior to recommendation to growers. Annicchiarico (2002) suggested that G x E interaction effects should be analysed using appropriate statistical methods to determine if the new varieties have narrow and/or broad adaptation for a range of key traits. Furthermore, understanding the type and magnitude of the G x E interaction defines breeding strategy and the need for further stability analyses. Therefore, knowledge of G x E interactions and their magnitude is important in sweetpotato breeding poised to release cultivars with improved genetic constitutions with regards to high dry matter and β-carotene contents, and fresh root yields.

Sweetpotato [Ipomoea batatas (L.) Lam] is a versatile crop widely cultivated in diverse agro-ecologies globally. However, its dry matter and β-carotene content, and root yields are sensitive to genotype x environment (G x E) interaction (Wolfgang et al., 2005; Chiona, 2009; Osiru et al., 2009; Moussa et al., 2011). Gruneberg et al. (2005) reported the presence of a significant G x E interaction of a cross-over type that implied differential ranking of sweetpotato genotypes across locations and years. Tsegaye et al. (2009) reported that most OFSP clones evaluated in Ethiopia were sensitive to environmental variations. The authors suggested the need to consider both wider and specific adaptation in OFSP varietal evaluation for yield and yield components. However, there is limited data available in Ethiopia that has reported on G x E interactions and the stability of promising sweetpotato clones. Therefore, understanding the nature of G x E interactions and quantifying its magnitude is essential for breeding, cultivar release and to identify the most discriminating and representative test environments in Ethiopia.

A number of statistical parameters are available to analyze G x E interaction and to quantify its magnitude. AMMI (Gauch, 1988; Gauch and Zobel, 1988) and GGE bi-plot (Yan et al., 2000; Yan et al., 2001; Yan, 2002) are the most commonly used statistical methods for analyzing multi-environment data. The AMMI model combines analysis of variance for the genotype and environment main effects with principal components analysis of the G x E interactions (Gauch and Zobel, 1996). The GGE integrates the genotypic main effect with the G x E interaction effect (Yan et al., 2000).

Twenty four candidate clones were selected from a diallel cross during 2013 in Ethiopia. Among these, best performing and stable clones should be ranked and selected across representative test environments in Ethiopia for release or breeding purposes. Therefore, the objectives of the study were to estimate the magnitude of G x E interactions and to select stable and high yielding candidate sweetpotato clones for RDMC, β-carotene content and fresh root yield, and to identify the most discriminating and representative test environments in Ethiopia.

4.2. Materials and methods

4.2.1. Study sites

The study was conducted at six environments, namely Halaba, Kokate, Areka, Arbaminch, Hawassa and Dilla in the SNNPRS of Ethiopia (Table 4.1). The test sites represent a low to mid altitude with diverse agro-ecologies in Ethiopia where sweetpotato is widely produced.

4.2.2 Plant materials

Twenty four F1 sweetpotato clones were selected from families constituted from diallel crosses. These were evaluated along with one released OFSP check variety. The list of the clones is presented in Table 4.2. The clones were selected based on their high RDMC, flesh colour (as indicator of the level of β-carotene content) or fresh root yield.

4.2.3 Experiential design and field establishment

A 5 x 5 simple lattice design with two replications was used to layout the test materials. Experimental plots consisted of a four row plot of three meter long for each genotype. The spacing between each row was 0.60 meter and between plants was 0.30 meter which resulted in a total of 10 plants per row and 40 plants per plot. The two central rows were used for data recording and harvesting. All required agronomic practices were followed as recommended for sweetpotato production in the study sites.

Table 4.1 Description of the experimental sites

Location	Code	Altitude (masl)*	Coordinates	Annual rainfall (mm)	Mean annual temperature (°C)		RH (%)
					Min	Max	
Halaba	HAL	1772	07°18’38’’N, 38°05’38’E	928.8	14.6	28.6	58.3
Kokate	KOK	1854	06°49’18’’N, 37°44’56”E	1352.9	12.7	25.5	63.1
Areka	ARE	1752	07°03’45’’N, 37°42’28’’E	1499.8	13.2	27.9	60.8
Arbaminch	AM	1400	06°03’56’’N, 37°33’40’’E	940.9	17.4	30.6	55.9
Hawassa	HAW	1700	07°03’54’’N, 38°28’59’’E	1046.3	13.3	27.6	62.1
Dilla	DIL	1519	06°22’49’’N, 38°18’25’’E	1354.6	12.9	28.1	65.0

*masl = meter above sea level, RH = relative humidity.

Source: National Meteorological Agency, Hawassa Main Branch.

Table 4.2 Description of sweetpotato genotypes used for the study

No	Genotypes	Genotypes ID	Predominant flesh color		RDMC	Flowering habit
			Code*	Color		
1	Ukrewe x Ejumula-10	G1	7	IO	31.8	None
2	Ukrewe x Ejumula-13	G2	7	IO	32.4	None
3	Ukrewe x PIPI-1	G3	2	CM	40.9	None
4	Ukrewe x Naspot-1	G4	2	CM	41.0	Moderate
5	Ukrewe x Ogansagan-5	G5	7	IO	32.2	None
6	Resisto x Ejumula-7	G6	7	IO	34.1	None
7	Resisto x PIPI-1	G7	7	IO	31.3	None
8	Resisto x PIPI-2	G8	8	DO	29.1	Profuse
9	Resisto x PIPI-4	G9	2	CM	38.4	Sparse
10	Resisto x PIPI-14	G10	2	CM	39.8	None
11	Resisto x Temesgen-10	G11	2	CM	40.2	Sparse
12	Resisto x Temesgen-12	G12	7	IO	31.4	None
13	Resisto x Temesgen-14	G13	7	IO	31.7	None
14	Resisto x Temesgen-17	G14	7	IO	36.0	None
15	Resisto x Temesgen-23	G15	8	DO	28.9	Moderate
16	Resisto x Ogansagen-5	G16	4	PY	36.8	Profuse
17	Resisto x Ogansagen-16	G17	8	DO	29.7	None
18	Resisto x Ogansagen-20	G18	2	CM	38.4	Moderate
19	Resisto x Ogansagen-23	G19	7	IO	30.5	Profuse
20	Ejumula x PIPI-10	G20	7	IO	31.3	Sparse
21	Ejumula x PIPI-18	G21	8	DO	26.2	Moderate
22	Ejumula x PIPI-19	G22	8	DO	28.2	Profuse
23	Ejumula x Temesgen-15	G23	2	CM	32.5	None
24	Ejumula x Ogansagen-17	G24	7	IO	30.2	None
25	Tula	G25	6	PO	28.5	None

ID = identification, IO = intermediate orange, CM = cream, DO = dark orange, PY = pale yellow, PO = pale orange, RDMC = root dry matter content.

*The flesh colour was coded using a scale of 1-9 as described by Huaman (1991) and (1999), where 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 anthocyanin.

4.2.4 Data collection

Three major traits were used for the G x E analysis including RDMC - expressed as percentage of root dry weight (g) to fresh root weight (g). Hundred to 200 g samples were taken from roots of sampled plants in the plot and the samples were dried in an oven at 80^{o}C for 48 hours. β-carotene content (mg 100 g^{-1}) was analysed using Near Infrared Reflectance Spectrometry

(NIRS). Fresh root samples were freeze dried at the Ethiopia Institute of Agricultural Research (EIAR), Agricultural Research Quality Laboratory and the dried samples were sent to International Potato Center (CIP) in Uganda for analysis of β-carotene and other micro-nutrients. The results are expressed as mg 100 g^{-1}. Some of the freeze dried samples that were sent to Uganda for analysis are displayed in Figure 4.1. Fresh root yield (t ha^{-1}) was measured from two central rows and expressed as harvested fresh root weight in kg per plot and later converted to tonnes per hectare.

Figure 4.1 Some of the freeze dried sweetpotato samples sent to Uganda for nutrient analysis

Note: A11 = cream type (Resisto x Temesgen-10), A6 = pale orange (Resisto x Ejumula-7), A17 = dark orange (Resisto x Ogansagen-16), A24 = intermediate orange (Ejumula x Ogansagen-17).

4.2.5 Statistical analyses

Analysis of variance

A combined analysis of data across environments were analysed using GenStat 14th edition (Payne et al., 2011) and SAS version 9.3 (SAS Institute Inc., 2003) statistical packages.

The following statistical model was used for combined analysis of variance over environments:

$$Y_{ijkl} = \mu + G_i + E_j + GE_{ij} + R_{k(j)} + B_{l(k)} + \varepsilon_{ijkl}$$

Where: Y_{ijkl} is observed value of genotype *i* in block *l* and replication *k* of environment *j*, μ is grand mean, G_i is effect of genotype *i*, E_j is environment or location effect, GE_{ij} is the interaction effect of genotype *i* with environment *j*, $R_{k(j)}$ is the effect of replication *k* in environment *j*, $B_{l(k)}$ is the effect of block *l* in replication *k*, ϵ_{ijkl} is error (residual) effect of genotype *i* in block *l* and replication *k* of environment *j*.

G x E and stability analysis

G x E and stability analyses were conducted using two methods, AMMI (Gauch, 1988; Gauch and Zobel, 1988) and GGE bi-plot (Yan, 2001).

The AMMI statistical model is given below:

$$\bar{Y}_{ijk} = \mu + G_i + E_j + \sum_{k=1}^{m} \lambda_k \alpha_{ik} \gamma_{jk} + \rho_{ij}$$

Where: $\bar{Y}_{ijk}$ = the yield of the i[th] genotype in the j[th] environment, G_i = the mean of the i[th] genotype minus the grand mean, E_j = the mean of the j[th] environment minus the grand mean, λ_k = the square root of the eigen value of the k[th] IPCA axis, α_{ik} and γ_{jk} = the principal component scores for IPCA axis k of the i[th] genotypes and the j[th] environment, ρ_{ij} = the deviation from the model.

The model for a GGE bi-plot (Yan, 2002; Yan et al., 2007) based on singular value decomposition (SVD) of *t* principal components is:

$$\bar{Y}_{ij} - \mu_i - \beta_j = \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

Where: $\bar{Y}_{ij}$ is the performance of genotype *i* in environment *j*, μ is the grand mean, β_j is the main effect of environment *j*, *k* is the number of principal components (PC); λ_k is singular value of the *k*[th] PC; and α_{ik} and γ_{jk} are the scores of *i*[th] genotype and *j*[th] environment, respectively for PC_k; ε_{ij} is the residual associated with genotype *i* in environment *j*.

4.3 Results

4.3.1 Combined analysis of RDMC, β-carotene content and fresh root yield

A combined analysis of variance was conducted for RDMC, β-carotene content and fresh root yield and there was a highly significant ($p < 0.001$) difference among the six test environments and the genotypes. Genotypes x environment interaction variances were significant ($p < 0.01$) for the three traits (Table 4.3).

Table 4.3 Analysis of variance of three traits of sweetpotato genotypes evaluated across six environments

Source of variation	df	Mean squares		
		RDMC (%)	β-carotene content (mg 100 g^{-1})	Fresh root yield (t ha^{-1})
Environment (E)	5	170.50***	23.07***	5136.80***
Block (B)	9	4.50ns	0.46ns	299.80ns
Replication (R)	5	2.10ns	0.09ns	390.90***
Genotype (G)	24	142.60***	489.45***	250.80***
G x E	120	26.20***	8.61***	75.30***
Error	136	3.00	0.81	48.50
Total	**299**			

df =degrees of freedom, *** significant at p < 0.001 probability level, Rep = replication, ns = not significant, RDMC = root dry matter content, G x E = genotype by environment interaction.

4.3.2 G x E and stability analysis using AMMI

4.3.2.1 Root dry matter content

AMMI analysis of variance revealed a highly significant (p < 0.001) effects of genotype, environment and G x E interaction (Table 4.4). The largest proportion of the total variation (50.76%) was contributed by genotypic effect followed by G x E interaction effect. Environment effect contributed for less than 10% of the total variation.

All the four IPCAs were highly significant (Table 4.4). IPCA1 accounted for 36.55% of the total G x E interaction followed by IPCA2, IPCA3 and IPCA4, which accounted for 21.47, 20.26 and 12.85%, respectively. The G x E residual effect contributed for 8.87% of the total variation.

The AMMI adjusted mean RDMC of the genotypes is shown in Table 4.5. Halaba was the best environment with an RDMC of 33.12%. The highest mean RDMC was recorded for G16 at Halaba and Kokate, which was 41.63 and 42.22% respectively, and for G9 and G12 at Areka which was 43.12 and 41.54%, respectively. At Arbaminch, G11 was the best performer with an RDMC of 43.10%. The lowest mean RDMC close to 20% was recorded for G15 at Hawassa and Dilla, and for G10 and G21 at Hawassa, and G25 at Dilla. More than two-third of the genotypes studied had mean RDMC values that were above 30% across the test environments. The highest mean RDMC value of 40.19% was recorded for G11, followed by G16, G3 and G18

with means of 38.23, 37.15 and 36.23%, respectively. The lowest mean RDMC of 24.30% was recorded for G25 (Tula, a released OFSP variety used as a check) (Table 4.5).

Based on IPCA1, G1, G17 and G18 showed highly positive interactions with the environment while G2, G9, G12 and G24 showed highly negative interactions with the environment. Genotypes G19 and G23 had the lowest positive IPCA1 scores while G11 and G14 had the lowest negative IPCA1 scores (Table 4.5).

Table 4.4 AMMI analysis of variance of RDMC of sweetpotato genotypes evaluated across six environments

Source of variation	**df**	**SS**	**MS**	**Total variation explained (%)**	**G x E explained (%)**
Environments	5	853	170.51***	9.38	-
Genotypes	24	4614	192.26***	50.76	-
Block	6	23	3.80ns	0.25	-
Interactions (G x E)	120	3146	26.21***	34.61	-
IPCA 1	28	1149	41.05***	-	36.55
IPCA 2	26	675	25.98***	-	21.47
IPCA 3	24	637	26.56***	-	20.26
IPCA 4	22	404	18.37***	-	12.85
Residuals (G x E)	20	279	13.96***	-	8.87
Pooled error	144	453	3.15	4.98	-
Total	**299**	**9088**	**30.40**	**-**	**-**

df = degrees of freedom, *** significant at $p < 0.001$ probability level, ns = not significant, SS = sum of squares, MS = mean squares, G x E = genotype by environment interaction, IPCA = interaction principal component axis.

Table 4.5 AMMI adjusted mean RDMC (%) and IPCA scores of sweetpotato genotypes evaluated across six environments

Genotypes ID	Environments							IPCA1	IPCA2
	Halaba	Kokate	Areka	Arbaminch	Hawassa	Dilla	Mean		
G1	37.98	32.30	29.92	31.63	27.64	31.48	31.82	1.02	0.44
G2	25.04	35.32	37.93	37.47	30.17	28.87	32.47	-1.85	-0.24
G3	40.79	32.48	39.19	42.80	36.56	31.10	37.15	-0.26	-1.69
G4	35.67	34.83	32.63	39.67	35.32	30.95	34.84	0.33	-1.18
G5	37.22	34.37	30.75	33.03	30.13	32.72	33.03	0.91	0.31
G6	37.49	31.54	31.44	33.46	30.87	30.81	32.60	0.71	-0.32
G7	28.81	30.98	30.03	35.14	28.01	26.05	29.84	-0.31	-0.69
G8	26.27	33.31	25.39	28.43	20.85	27.66	26.99	0.26	1.29
G9	31.93	29.30	43.12	31.78	29.33	30.05	32.59	-1.87	0.10
G10	32.06	33.95	28.53	29.99	21.49	30.12	29.36	0.47	1.48
G11	41.26	40.60	40.56	43.10	38.06	37.57	40.19	-0.03	-0.35
G12	27.77	29.84	41.54	29.17	27.22	29.50	30.84	-2.07	0.60
G13	35.87	26.62	37.74	29.81	24.81	28.46	30.55	-0.72	0.34
G14	34.48	33.57	33.46	33.03	24.22	30.77	31.59	-0.06	0.97
G15	32.09	22.49	25.22	28.59	21.32	21.69	25.23	0.54	-0.57
G16	41.63	41.13	37.74	42.22	30.04	36.59	38.23	0.28	0.78
G17	35.20	31.27	22.12	25.95	30.93	31.22	29.45	2.18	0.12
G18	39.34	39.22	32.80	34.49	34.15	37.40	36.23	1.12	0.65
G19	35.90	33.93	33.95	35.01	28.33	31.45	33.09	0.09	0.29
G20	31.21	31.64	28.26	34.64	27.46	27.11	30.06	0.29	-0.42
G21	26.06	27.27	29.66	20.66	21.11	27.33	25.35	-0.37	1.46
G22	28.36	25.18	26.18	24.82	30.33	25.65	26.75	0.46	-0.80
G23	36.20	30.34	34.29	24.47	32.28	29.86	32.91	0.06	-0.77
G24	23.89	33.83	34.71	35.44	27.76	27.24	30.48	-1.54	-0.12
G25	25.50	22.27	22.58	27.71	27.52	20.20	24.30	0.34	-1.67
Mean	**33.12**	**31.90**	**32.39**	**32.90**	**28.64**	**29.67**	**31.44**		

ID = identification, IPCA = interaction principal component axis.

4.3.2.2 β-carotene content

AMMI analysis of variance showed highly significant ($p < 0.001$) effects of genotype, environment and G x E interaction (Table 4.6). The largest proportion of the total variation (91.57%) was due to the genotypic effect followed by the G x E interaction effect, which accounted for only 6.74% of the variation. The environment effect contributed for less than 1% of the total variation.

All the four IPCAs were highly significant (Table 4.6), accounting for 33.62, 23.05, 19.74 and 15.05% of the total G x E interaction, respectively. The G x E residual effect contributed for 8.54% of the total variation.

The adjusted AMMI mean of genotypes for β-carotene content is presented in Table 4.7. Areka was the best environment for β-carotene. The highest mean β-carotene content that was greater than 20 mg 100 g^{-1} was recorded at Areka and Dilla, both for G8. Across the test environments, G8, G15 and G19 had the highest β-carotene of 20.01, 16.59 and 16.30 mg 100 g^{-1}, respectively. Eight genotypes, namely G3, G4, G9, G10, G11, G16, G18 and G23, had no β-carotene content across all the test environments (Table 4.7).

Regarding G x E for β-carotene, based on IPCA1 scores, genotypes G2, G6 and G25 showed high positive interactions with their environment while G19 and G24 showed high negative interactions. Genotypes G8 and G13, and all the eight genotypes with no β-carotene, had the lowest positive IPCA1 scores. On the other hand, genotypes G1, G12, G15, G20 and G21 had low negative IPCA1 scores (Table 4.7).

Table 4.6 AMMI analysis of variance of β-carotene content of sweetpotato genotypes evaluated across six environments

Source of variation	**df**	**SS**	**MS**	**Total variation explained (%)**	**G x E explained (%)**
Environments	5	121	24.15***	0.87	-
Genotypes	24	12739	530.78***	91.57	-
Block	6	1	0.13ns	0.01	-
Interactions (G x E)	120	937	7.81***	6.74	-
IPCA 1	28	315	11.25***	-	33.62
IPCA 2	26	216	8.32***	-	23.05
IPCA 3	24	185	7.71***	-	19.74
IPCA 4	22	141	6.39***	-	15.05
Residuals (G x E)	20	80	4.01***	-	8.54
Pooled error	144	114	0.79	0.82	-
Total	**299**	**13912**	**46.53**	**-**	**-**

df = degrees of freedom, *** significant p < 0.001 probability level, respectively, ns = not significant, SS = sum of squares, MS = mean squares, G x E = genotype by environment interaction, IPCA = interaction principal component axis.

Table 4.7 AMMI adjusted mean β-carotene content (mg 100 g-1) and IPCA scores of sweetpotato genotypes evaluated across six environments

Genotypes ID	Environments							IPCA1	IPCA2
	Halaba	Kokate	Areka	Arbaminch	Hawassa	Dilla	Mean		
G1	13.29	15.31	12.92	9.27	12.84	11.26	12.48	-0.31	-0.01
G2	12.99	6.54	5.07	2.81	6.79	7.25	6.91	1.56	-0.48
G3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.36
G4	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.36
G5	15.27	10.75	15.56	12.22	11.35	13.81	13.16	0.62	-0.62
G6	16.44	12.79	12.14	13.41	15.08	15.74	14.27	1.02	0.21
G7	15.36	12.33	14.35	11.56	12.71	14.85	13.53	0.56	-0.54
G8	18.54	17.32	22.73	17.38	18.09	26.00	20.01	0.02	-1.73
G9	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.36
G10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.36
G11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.36
G12	10.01	11.28	11.87	10.04	10.95	11.17	10.89	-0.28	0.07
G13	11.35	9.42	9.67	7.02	9.18	10.10	9.46	0.44	-0.34
G14	9.78	12.25	13.6	6.17	8.95	11.15	10.32	-0.72	-1.08
G15	18.89	19.70	19.19	11.37	15.35	15.06	16.59	-0.32	-0.87
G16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.36
G17	3.61	8.88	5.36	3.75	6.62	3.33	5.26	-0.90	0.71
G18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.36
G19	13.15	17.69	18.87	14.57	15.92	17.60	16.30	-1.06	-0.40
G20	11.88	16.56	11.63	11.39	16.21	16.25	13.99	-0.45	0.24
G21	12.19	16.00	12.56	14.09	16.36	14.38	14.26	-0.42	0.92
G22	13.45	16.04	16.31	11.04	13.70	15.01	14.26	-0.61	-0.63
G23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.36
G24	8.34	13.50	15.55	12.44	10.85	7.56	11.37	-1.44	0.74
G25	14.00	6.74	7.73	10.97	9.93	7.71	9.51	1.60	0.95
Mean	**8.74**	**8.92**	**9.05**	**7.18**	**8.44**	**8.73**	**8.50**		

ID = identification, IPCA = interaction principal component axis.

4.3.2.3 Fresh root yield

AMMI analysis of variance for fresh root yield is presented in Table 4.8. The genotype, environment and G x E interaction effects were highly significant ($p < 0.001$). For this trait, the largest proportion of the total variation (49.4%) was contributed by the environmental effect

followed by the G x E interaction effect, which accounted for 17.38%. The genotypic effect contributed 15.04% of the total variation (Table 4.8).

Among the four IPCAs, only two were significant (Table 4.8). The two IPCAs accounted for 83.8% of the total G x E interaction, where IPCA1 accounted for 60.98% and IPCA2 accounted for 22.85%. The G x E residual effect contributed only 1.44% of the total variation.

Table 4.8 AMMI analysis of variance of fresh root yield of sweetpotato genotypes evaluated across six environments

Source of variation	df	SS	MS	Total variation explained (%)	G x E explained (%)
Environments	5	25684	5136.8***	49.40	-
Genotypes	24	7821	325.9***	15.04	-
Block	6	2602	433.6***	5.01	-
Interactions (G x E)	120	9037	75.3**	17.38	-
IPCA 1	28	5511	196.8***	-	60.98
IPCA 2	26	2065	79.4*	-	22.85
IPCA 3	24	911	38.0ns	-	10.08
IPCA 4	22	420	19.1ns	-	4.65
Residuals (G x E)	20	130	6.5	-	1.44
Pooled error	144	6843	47.5	13.16	-
Total	**299**	**51988**	**173.9**	**-**	**-**

df = degrees of freedom, *, *** significant at $p < 0.05$ and $p < 0.001$ probability level, respectively, ns = not significant, SS = sum of squares, MS = mean squares, G x E = genotype by environment interaction, IPCA = interaction principal component axis.

AMMI adjusted mean of fresh root yield is presented in Table 4.9. Arbaminch was the best environment for fresh root yield with a mean yield of 37.05 t ha^{-1}, followed by Halaba with 23.94 t ha^{-1}. Kokate was the poorest environment, providing a mean yield of 8.62 t ha^{-1}, followed by Areka with 11.78 t ha^{-1}. The genotypes showed stunted growth at Kokate, which is a relatively cool environment, but grew better at Arbaminch, which is a warmer environment (Figure 4.2).

At Hawassa about half of the genotypes studied provided a mean fresh root yield greater than 25 t ha^{-1}. At Arbaminch, some of the genotypes had mean yields that exceeded 50 t ha^{-1}. Almost all genotypes performed poorly at Kokate and Areka. G6 was the highest yielder across environments with a mean of 26.92 t ha^{-1}, followed by G20 and G1, which yielded 25.46 and 25.09 t ha^{-1}, respectively. The lowest mean fresh root yield of 7.55 and 9.64 t ha^{-1} was recorded for G25 (variety Tula) and G21, respectively.

AMMI G x E for fresh root yield, based on IPCA1 scores, is presented in Table 4.9. Genotypes G4, G9, G11, G21 and G25 showed high positive interactions with environment while G1, G2, G6, G8, G17, G18 and G20 showed high negative interactions. Genotypes G3, G16, G19 and G23 had the lowest positive IPCA1 scores, while G10 had the lowest negative IPCA1 score (Table 4.9).

Table 4.9 AMMI adjusted mean fresh root yield (t ha^{-1}) and IPCA scores of sweetpotato genotypes evaluated across six environments

	Environments								
Genotypes ID	**Halaba**	**Kokate**	**Areka**	**Arbaminch**	**Hawassa**	**Dilla**	**Mean**	**IPCA1**	**IPCA2**
G1	29.36	11.84	15.23	54.04	19.16	20.93	25.09	-1.72	0.42
G2	19.67	11.72	12.91	48.65	18.58	20.42	21.99	-1.38	-1.00
G3	24.06	11.03	13.68	37.94	19.23	20.73	21.11	0.12	-0.34
G4	23.41	5.21	9.52	13.59	15.47	16.42	13.94	2.72	0.27
G5	19.22	9.93	11.55	42.28	17.31	19.01	19.88	-0.73	-0.85
G6	32.70	13.23	17.09	55.28	20.75	22.47	26.92	-1.63	0.70
G7	29.8	11.09	15.18	34.48	20.12	21.42	22.01	0.78	0.45
G8	23.13	11.47	13.42	54.44	18.17	20.07	23.45	-2.03	-0.42
G9	36.67	5.30	12.60	22.08	16.09	16.97	18.29	2.10	2.24
G10	1.81	7.98	6.09	30.66	14.72	16.51	12.96	-0.02	-3.15
G11	21.43	5.73	9.47	12.74	15.87	16.84	13.68	2.81	-0.10
G12	31.27	10.22	14.88	33.56	19.48	20.72	21.69	0.87	0.79
G13	20.49	9.89	11.78	44.49	17.20	18.93	20.46	-0.97	-0.64
G14	14.09	3.64	5.73	27.64	11.84	13.32	12.71	0.40	-0.74
G15	14.23	5.32	7.09	26.99	13.57	15.03	13.70	0.65	-0.98
G16	34.68	11.47	16.54	40.16	20.48	21.81	24.19	0.25	1.14
G17	27.39	9.50	12.93	53.60	16.69	18.49	23.10	-1.95	0.49
G18	23.50	7.62	10.58	51.16	14.67	16.50	20.67	-1.95	0.19
G19	31.08	8.73	13.58	37.78	17.62	18.98	21.30	0.17	1.02
G20	33.00	10.58	15.08	56.23	18.07	19.82	25.46	-1.99	1.15
G21	8.27	2.92	3.96	18.61	11.34	12.73	9.64	1.30	-1.54
G22	25.26	9.19	12.42	43.04	17.09	18.69	20.95	-0.68	0.15
G23	38.05	9.62	15.91	39.98	18.98	20.24	23.80	0.22	1.91
G24	27.99	11.44	15.06	32.95	20.43	21.72	21.60	0.95	0.13
G25	7.90	0.77	2.30	13.86	9.58	10.87	7.55	1.71	-1.30
Mean	**23.94**	**8.62**	**11.78**	**37.05**	**16.90**	**18.39**	**19.45**		

ID = identification, IPCA = interaction principal component axis.

Figure 4.2 Performance of sweetpotato genotypes at Kokate (a) and Arbaminch (b).

4.3.3 G x E and stability analysis using GGE bi-plot

4.3.3.1 Root dry matter content

GGE-biplot analysis of RDMC using PC1 and PC2 is presented in Figure 4.3. This figure shows which genotype performs best where or which is best for which environment. Accordingly, genotypes G11, G16, G3, G18 and G4, which had large positive PC1 scores, had the highest mean RDMC values, in that order. On the other hand, genotypes G25, G21, G15, G22 and G8, which had large negative PC1 scores, had low RDMC (Figure 4.3). Genotypes that had PC2 scores near zero such as G11, G3, G19, G23, G14 and G7 were relatively stable. Among these genotypes, only G3 and G11 had high RDMC.

Four environments, namely Halaba, Kokate, Arbaminch and Areka had larger PC1 scores and efficiently discriminated among the genotypes for RDMC. PC1 and PC2 accounted for 75.6% of the total PCs that sufficiently explained the GGE (Figure 4.3). Genotype G18 was the best performer at Halaba, Kokate, Hawassa and Dilla while G3 was the best performer at Arbaminch. Areka was not a good environment for any of the genotype for RDMC.

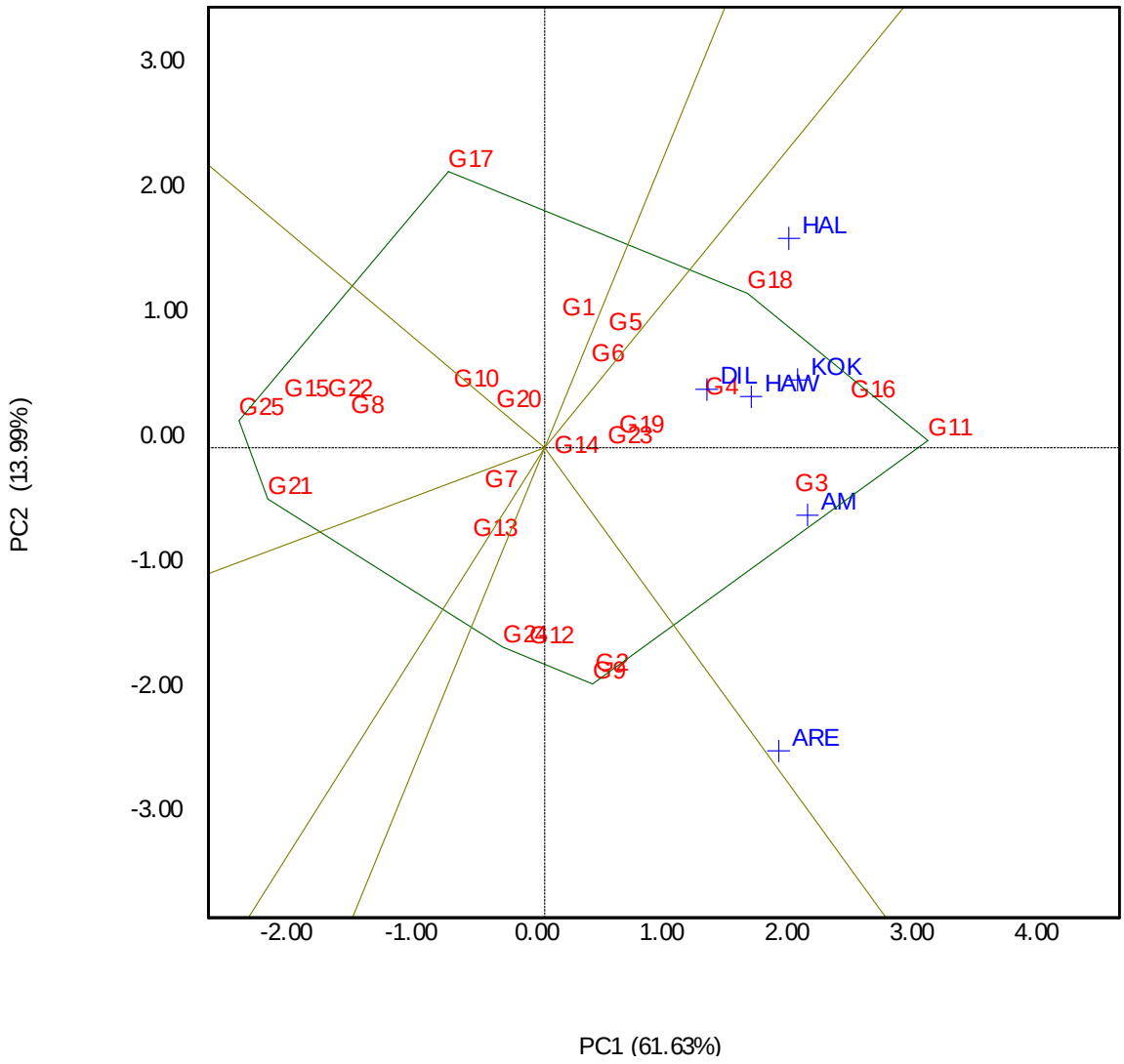

Figure 4.3 GGE-biplot showing environments and respective sweetpotato genotypes for RDMC.

Note: See Tables 4.1 and 4.2 for codes of environments and genotypes, respectively.

Figure 4.4 shows the stability of the genotypes across the test environments. Genotypes G11, G3, G19, G23 and G14 had shorter absolute length of projection and therefore they can be considered stable. The rank of the genotypes in the order of high to low RDMC is G11, G16, G3, G18, G4, G19 and G23. Genotypes G25 and G21 were poor performers for RDMC.

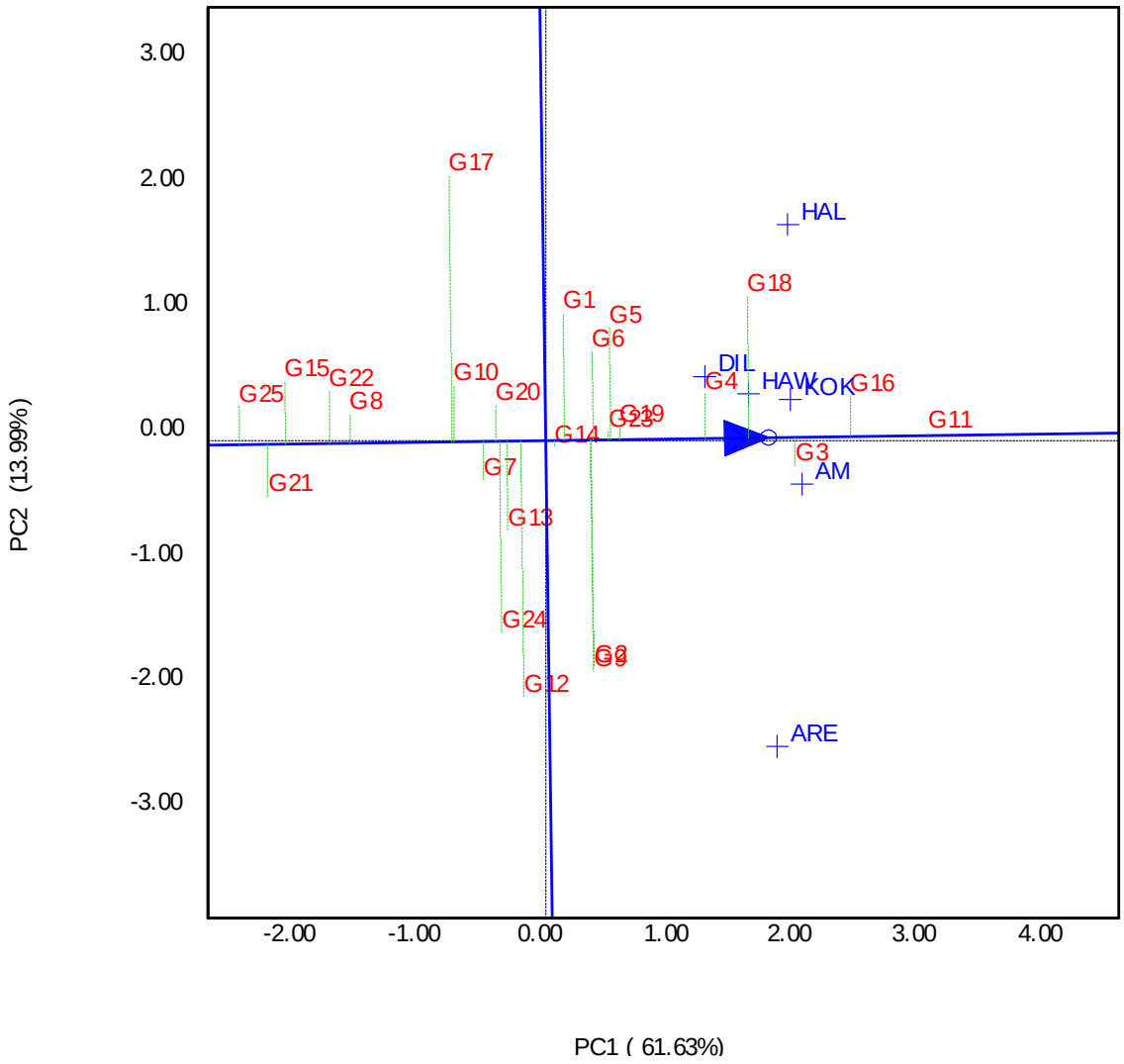

Figure 4.4 Genotypes mean performance and stability across environments for RDMC

Note: See Tables 4.1 and 4.2 for codes of environments and genotypes, respectively.

4.3.3.2 β-carotene content

GGE-biplot analysis of β-carotene content using PC1 and PC2 is presented in Figure 4.5. The genotypes G8, G15, G19, G20, G21, G22, G5, G6 and G7 had relatively larger PC1 values and had high average β-carotene content. All the genotypes that had no β-carotene were concentrated at a single point at the left end of the x-axis (Figure 4.5). The genotypes G8, G15, G12 and G13 had PC2 scores near zero. Among these genotypes, G8 and G15 had relatively higher β-carotene content.

Areka, Dilla, Kokate and Halaba were environments with relatively large PC1 scores and these environments better discriminated among genotypes for β-carotene content. Hawassa and Arbaminch had PC2 scores near zero and were more representative of an average environment (Figure 4.5). When the genotypes at the apex of each sector are considered, G19 and G24 were the best performers at Kokate and Areka while G8 was at Dilla and G6 was at Halaba.

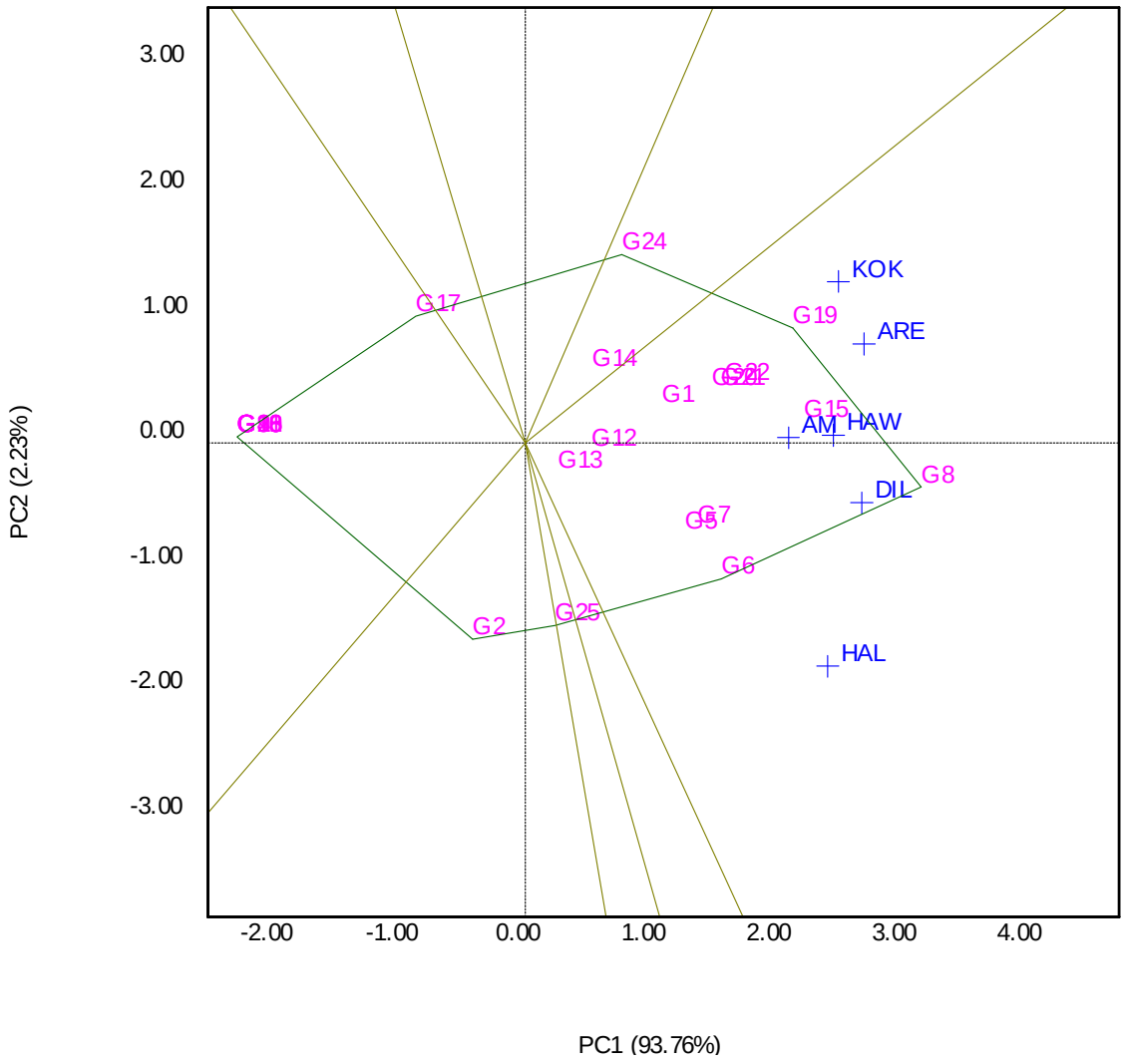

Figure 4.5 GGE-biplot showing environments and respective sweetpotato genotypes for β-carotene content.

Note: See Tables 4.1 and 4.2 for codes of environments and genotypes, respectively.

The stability of the genotypes across test environments is displayed in Figure 4.6. According to this Figure, genotypes G8, G15, G12 and G13 had shorter absolute projections and therefore they were stable across the test environments. Most of the genotypes had mean β-carotene

content that was above average since they were displayed at the right of the AEC *y*-axis. Only those genotypes that did not have any β-carotene and two genotypes with lower β-carotene content, namely G2 and G17 were displayed at the left of the AEC *y*-axis. These genotypes have mean β-carotene content values that were below average.

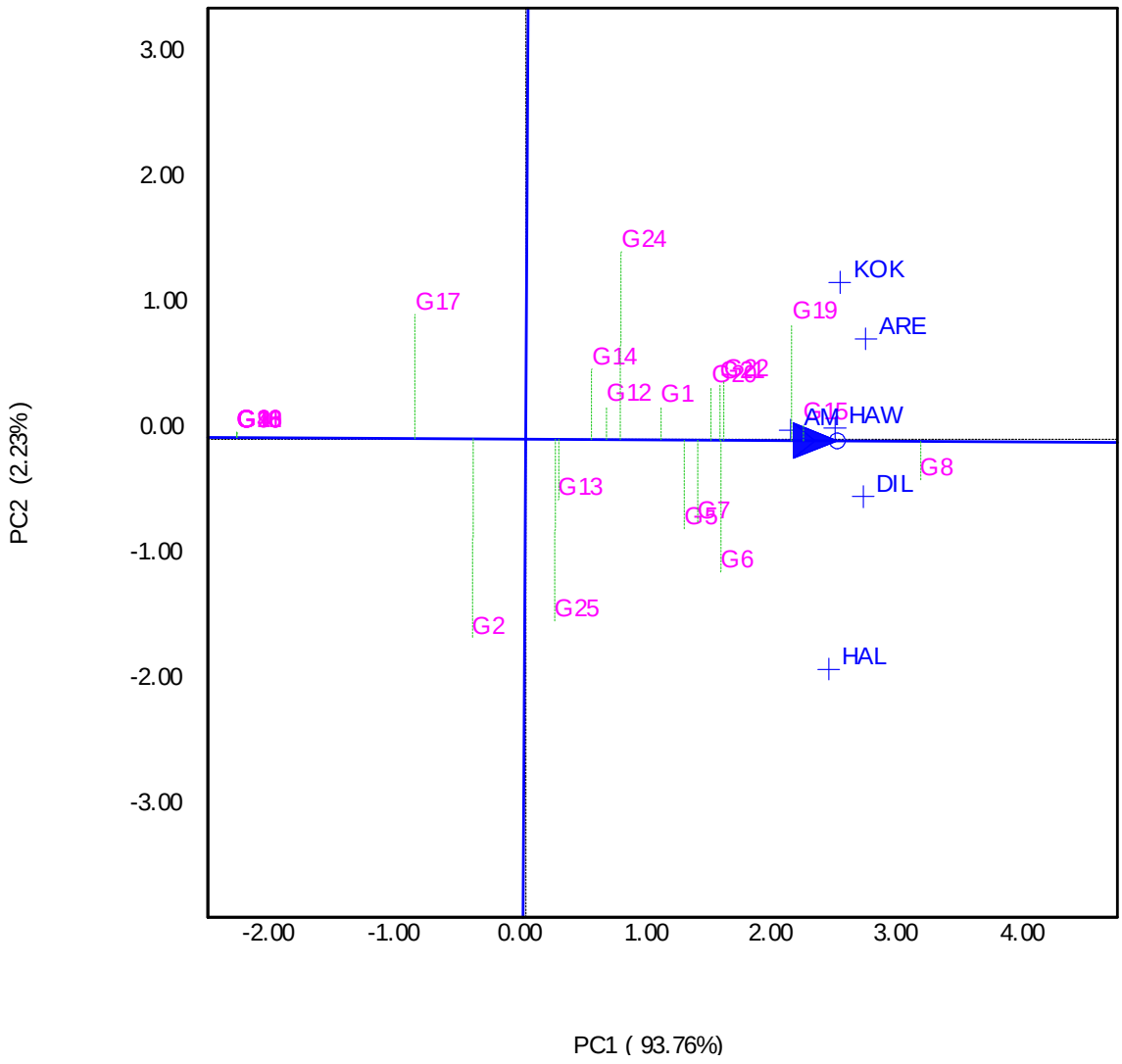

Figure 4.6 Genotypes mean performance and stability across environments for β-carotene content.

Note: See Tables 4.1 and 4.2 for codes of environments and genotypes, respectively.

4.3.3.3 Fresh root yield

Figure 4.7 displays the GGE-biplot analysis of fresh root yield. The genotypes G6, G20, G1, G17 and G8 had relatively higher PC1 values and had high average fresh root yield. On the other hand, the genotypes G25, G21, G11, G4, G10, G14, G15 and G9 had lower fresh root

yields that were below average. The genotypes G6, G20, G1, G22 and G3 had PC2 scores near zero. Among these genotypes, G1, G6 and G20 had relatively higher fresh root yields.

Arbaminch and Halaba had relatively large PC1 scores and hence they better discriminated among genotypes for fresh root yield. Kokate had PC2 scores near zero but was the worst performing environment for fresh root yield (Figure 4.7). When the genotypes at the apex of each sector were considered, genotypes G16 and G23 were best performers at Halaba and Areka while G2, G8, G17 and G18 were the best performers at Arbaminch.

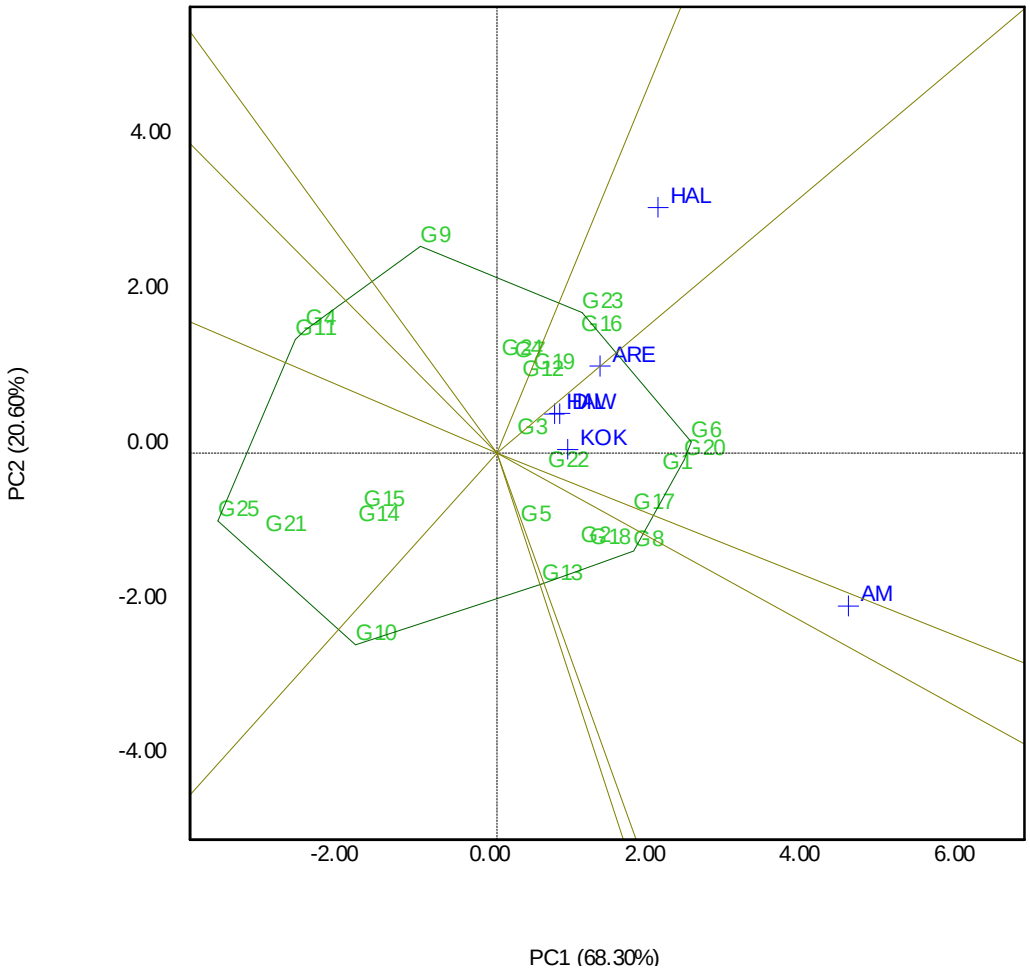

Figure 4.7 GGE-biplot showing environments and respective sweetpotato genotypes for fresh root yield.

Note: See Tables 4.1 and 4.2 for codes of environments and genotypes, respectively.

The stability of the genotypes across test environments for fresh root yield is displayed in Figure 4.8. Accordingly, genotypes G6, G20, G1 and G22 had shorter absolute projections and

therefore they were stable across the test environments. However, G22 had lower yield than the other three genotypes (G1, G6 and G20). Most of the genotypes had above average mean fresh root yield since they were displayed at the right of the AEC *y*-axis. G21 and G25 were the worst performing genotypes for fresh root yield.

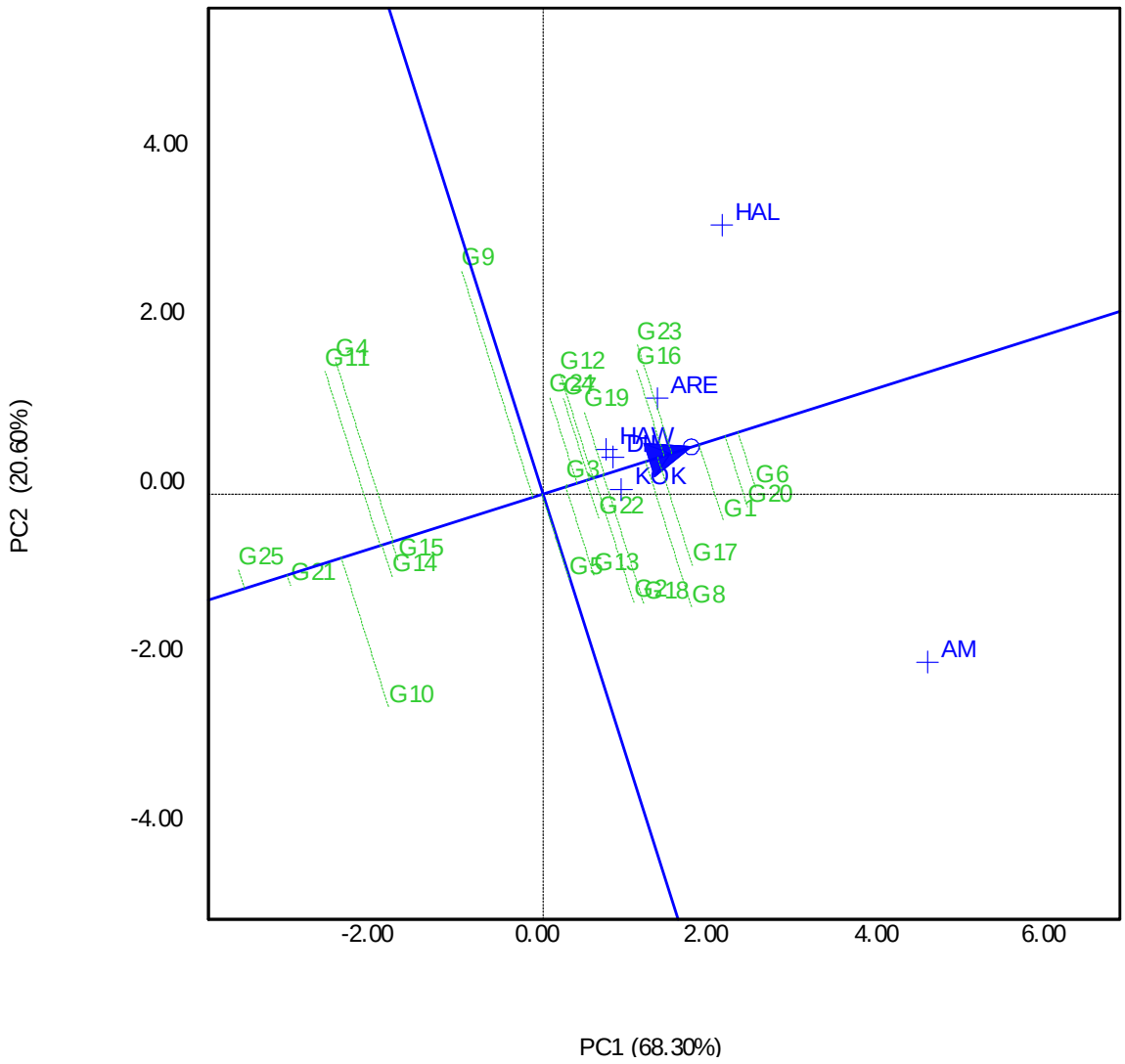

Figure 4.8 Genotypes mean yield performance and stability across environments for fresh root yield.

Note: See Tables 4.1 and 4.2 for codes of environments and genotypes, respectively.

4.4 Discussion

The significant genotypic difference across environments indicates the presence of genetic and environmental causes of variation among the tested genotypes. The presence of highly significant differences between the six test environments for the three traits indicates that the genotypes performed differently across environments. The significant genotype by environment interaction also indicates the significance of environmental effects in evaluating sweetpotato clones for the three traits. This result was similar to previous reports (Wolfgang et al., 2005; Tsegaye et al., 2007; Mbwaga et al., 2008; Chiona, 2009; Osiru et al., 2009; Moussa et al., 2011).

As revealed by AMMI ANOVA, genotypic effect accounted for the largest proportion of the total sum of squares for RDMC, followed by G x E interaction effects, whereas the environment effect contributed less. The dominant contribution of genotypic effects for RDMC suggests that environment had little effect on quality attributes. Similar results were reported by Manrique and Hermann (2001) who found small interaction effects for nutritional traits of sweetpotato tested across varied environments. Chiona (2009) reported a small G x E interaction effects for β-carotene, RDMC and HI and suggested that selection for these traits may be conducted in a few, well selected environments.

The first two IPCAs accounted for more than 58% of the total G x E interaction, indicating that the pattern of the interaction could be predicted based on the two IPCAs (Gauch, 1988; Gauch and Zobel, 1988; Yan et al., 2000). According to AMMI analysis, genotypes with large IPCA values (both positive and negative) are less stable while those with IPCA values close to zero are more stable (Gauch and Zobel, 1996). Accordingly, genotypes G19 and G23, which had the lowest positive IPCA1 scores and G11 and G14, which had the lowest negative IPCA1 scores, were the most stable and can be recommended for planting in similar agro-ecologies in Ethiopia. However, G11 and G23 had no β-carotene content, which limits their nutritional value.

The largest proportion of the total sum of squares for β-carotene content was accounted for by the genotypic effect. The result confirms that, generally, environment has little effect on quality attributes of sweetpotato (Manrique and Hermann, 2001; Chiona, 2009).

The first two IPCAs accounted for more than 56% of the total G x E interaction and therefore the two IPCAs can be used to predict the pattern of this interaction. Accordingly, the genotypes G1,

G8, G12, G13, G15, G20 and G21, which had lower IPCA1 scores, were more stable and can be recommended for wider adaptation. However, among these genotypes, G8, G15 and G23 had low RDMC values and therefore should not be considered.

Environment accounted for most of the total sum of squares for fresh root yield, which was 49.4%, followed by the G x E interaction effects (17.4%). Genotypic effect accounted for only 15%. The result indicates that root yield is more sensitive to environmental effects than quality attributes. Chiona (2009) reported similar results, indicating the presence of large G x E interaction effects for fresh root yield and vine fresh yield. The author suggested that these traits may require early testing in varied environments to select genotypes with either specific or wide adaptation. Manrique and Hermann (2001) also found large interaction effects on root yield related traits across environments.

For fresh root yield, only the first two IPCAs were significant and accounted for more than 83% of the total G x E interaction. Hence the two IPCAs can be used to predict the pattern of the interaction. According to AMMI result, genotypes with IPCA1 close to zero such as G3, G10, G16, G19 and G23 were more stable and can be considered for recommendation. However, among these genotypes, only G19 had β-carotene content.

According to Yan et al. (2000) and Yan (2001) large positive PC1 scores for genotypes indicate that those genotypes had relatively higher mean values. Yan (2001) also indicated that the line that passes through the bi-plot origin is called the average environment coordinate (AEC), and it separates genotypes with mean values below average and above average. Those genotypes to the right of this line are high yielders, while those to the left are low yielders for the trait of interest (Yan, 2001; Yan and Kang, 2003; Gurmu et al., 2012). Accordingly, the genotypes G11, G16, G3, G18 and G4 had high average RDMC values.

The AEC *y*-axis shows the stability of the genotypes. The stability of the genotypes is measured by their projection onto the AEC *y*-axis. When the absolute length of the projection of a genotype is higher, it means that a genotype was less stable or when the absolute length is shorter, a genotype was stable (Yan, 2001). In other words, genotypes with PC2 scores near zero are the most stable (Yan et al. 2000; 2001). Hence, the genotypes G11, G3, G19, G23, G14 and G7 had relatively low PC2 scores and can be considered relatively stable. Among the tested genotypes, G3 and G11 were the most stable genotypes with high RDMC and therefore can be recommended for wider production across similar environments. However, when the β-

carotene content of these genotypes is considered, both G3 and G11 have no β-carotene content. Similarly, G4 and G16, which had high RDMC and average stability, have no β-carotene content. This is one of the major challenges when breeding to improve the RDMC of the OFSPs due to the existence of negative correlations between the two traits (Simonne et al., 1993; Chiona, 2009; Cervantes-Flores et al., 2010). It is suggested that the simultaneous improvement of the two traits is a challenge in sweetpotato breeding unless the linkage can be broken. In this study, G19 was stable, with above average RDMC (33%) and high β-carotene content (16.3 mg 100 g^{-1}) and can be recommended for wider production. A similar result was obtained using AMMI analysis.

Environments with large PC1 scores are better in discriminating between the genotypes and those with PC2 scores near zero are more representative of an average environment (Yan et al., 2000; Yan, 2001). Four of the test environments, namely Halaba, Kokate, Arbaminch and Areka, efficiently discriminated between the test genotypes for RDMC and can be considered good environments for testing of sweetpotato genotypes for RDMC. Some of the genotypes showed specific adaption to some environments. Accordingly, G11, G16, G19 and G4 were the best performers at Halaba, Kokate, Hawassa and Dilla while G3 was the best performer at Arbaminch. Therefore, these genotypes can be recommended for adaptation to specific environments. However, among these genotypes, only G19 had β-carotene and was stable across environments. Areka was not a good environment for evaluating genotypes for RDMC.

Some of the genotypes, such as G8, G15, G19, G20, G21, G22, G5, G6 and G7 had relatively higher PC1 values and had high average β-carotene content. This is similar to the result presented in Table 4.7 using AMMI adjusted means. Genotypes G8, G15, G12 and G13 had PC2 scores near zero and were found to be stable. These genotypes were also identified as stable using AMMI analysis. Among these genotypes, G8 and G15 also had high β-carotene content. However, both of these genotypes had below average RDMC. G8 can be used as a parent for improvement of β-carotene content since it had the highest β-carotene content of all the genotypes studied, with a profuse flowering habit, although the RDMC was below average (27%).

Four environments: Areka, Dilla, Kokate and Halaba, better discriminated the genotypes for β-carotene content and were good test environments for evaluation of sweetpotato genotypes. Genotypes G19 and G24 can be recommended for Kokate and Areka while G8 for Dilla and G6

for Halaba. All of these genotypes, except G8, had RDMC that was greater than 30% and therefore can be recommended for specific adaptation to the listed environments.

Two test environments, namely Halaba and Arbaminch efficiently discriminated between the test genotypes for fresh root yield and can be considered as good test sites. These environments are relatively warm. Conversely, Kokate, which is relatively cool, was not a good test environment. Most of the genotypes showed stunted growth at this environment. Therefore, warmer environments with moderate temperature not exceeding 30^{o}C are ideal for improved yields of sweetpotato, as confirmed by a number of authors (Negeve et al., 1992; Belehu, 2003; DAFF, 2011).

Three genotypes: G1, G6 and G20, were stable with high mean fresh root yield. All these genotypes had RDMC greater than 30% and β-carotene content greater than 12 mg 100 g^{-1}. Therefore, these genotypes are ideal for recommendation as OFSPs, for wider production and commercialization.

Genotypes at the apex of each sector are the best performing in the environments included in that sector if the GGE is sufficiently approximated by PC1 and PC2 (Yan et al., 2000; Yan, 2001). The genotypes G16 and G23 can be considered for the Halaba and Areka areas due to their specific adaption. However, these genotypes had no β-carotene content. The genotypes: G2, G8, G17 and G18 were the best performers at Arbaminch. However, G18 had no β-carotene content and should not be considered for breeding to improve this trait.

4.5 Conclusions

G x E interactions were observed for all the three traits (RDMC, β-carotene content and fresh root yield) investigated, but with different magnitudes. Using both AMMI and GGE, genotypes G3 and G11 were stable with high RDMC but without β-carotene. On the other hand, G8 and G15 had high β-carotene content, but low RDMC. For fresh root yield, G19 was found to be stable using AMMI analysis. This genotype had above average RDMC and fresh root yield, and high β-carotene content. Using GGE, three genotypes, namely G1, G6 and G20 were identified as stable with high mean fresh root yield. These genotypes had high RDMC and β-carotene content. Therefore, these four genotypes are ideal for recommendation for large-scale production as OFSPs. Genotypes with high RDMC such as G3 and G11 can be used as breeding parents, in order to improve the RDMC of OFSP varieties. Similarly, G8, which had the

highest β-carotene content of all the genotypes studied, can be considered as parent for breeding aimed at enhancing the β-carotene content of sweetpotato varieties.

Arbaminch was identified as the best environment for sweetpotato screening in southern Ethiopia followed by Halaba, Dilla and Hawassa. The candidate clones did not perform well in Kokate, which was a relatively cool environment. Warmer environments with moderate temperatures are better for consistent performance of sweetpotato genotypes. Generally, the current study demonstrated that it is possible to breed sweetpotato varieties with combined high RDMC, β-carotene content and fresh root yield with either wide or specific adaptation.

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CHAPTER 5

Correlation and path-coefficient analyses of root yield and related traits among selected sweetpotato clones

Abstract

Fresh root yield is a key trait in sweetpotato, while other related traits contribute directly or indirectly towards its expression. The objective of this study was to assess associations between yield and yield related traits, and to identify the most efficient yield-predicting traits in sweetpotato for effective selection. Twenty five newly developed sweetpotato clones were evaluated across six environments (Halaba, Kokate, Areka, Arbaminch, Hawassa and Dilla) using a 5 x 5 simple lattice design. Data on root yield and yield related traits were subjected to analysis of variance and, correlation and path-coefficient analyses. Environment, genotype and genotype x environment interaction effects were significant ($p < 0.05$) for all traits, except for root girth and skin colour. Root yield was positively and significantly correlated with most traits studied, indicating that component characters should be simultaneously selected for improvement of sweetpotato. RDMC had significant negative correlation with root flesh colour ($r = -0.47$) and β-carotene content ($r = -0.40$). Conversely, β-carotene content and root flesh colour showed a highly positive correlation ($r = 0.76$), reflecting the importance of root flesh colour as an indirect selection criterion of high β-carotene content in sweetpotato. Path-coefficient analysis showed that individual root weight, number of roots per plant, RDMC and above ground fresh weigh had high positive direct effects of 0.821, 0.776, 0.276 and 0.410, respectively, on fresh root yield. These traits also had significant positive correlations with fresh root yield. Vine length and root length, which had highly significant positive correlations with fresh root yield, showed negative direct effects of -0.086 and -0.033, respectively. Similarly, root girth, which had a non-significant correlation with root yield, exerted the highest negative direct effect of -0.396 on fresh root yield. Therefore, path-coefficient analysis was more valuable in identifying the most influential traits than simple correlation analysis. Overall, individual root weight, number of roots per plant, RDMC, aboveground fresh weight and root length were identified as the most important characters determining fresh root yield in sweetpotato that can be recommended as indirect selection criteria.

Key words: Direct effect, fresh root yield, indirect effect, selection criteria

5.1 Introduction

The storage roots of sweetpotato are edible parts commonly used as staple food or as raw material for industrial products. The leaves are also consumed in some parts of Africa such as in Guinea, Sierra Leone, Liberia and some east African countries (Ebregt et al., 2004). The above ground parts including vines and leaves are used as animal feed. The vines are used as planting materials in sweetpotato production (Wilson, 1988; Belehu, 2003). Some key traits such as RDMC and β-carotene content have a direct impact on sweetpotato varietal development. The RDMC influences taste and the actual dry yield, while β-carotene content is a key nutritional trait and an excellent source of vitamin A. Root flesh colour, which may directly correlate with β-carotene content, also has significance in sweetpotato breeding, as it can be used as an indirect selection criterion for β-carotene content.

Information on the nature and magnitude of correlations of agronomically useful traits in sweetpotato is important for direct or indirect selection for improvement of the crop. It facilitates selection for complex traits with low heritability via other traits which are highly correlated with yield and have high heritability values (De Araujo et al., 2002). Martin and Rhodes (1983) suggested that significant correlations among traits influence the selection progress positively or negatively. Knowledge on the number of desired traits to be evaluated and magnitude of their correlations is important to breeders for simultaneous selection and to enhance selection gains. Furthermore, correlation analysis is the basis for establishing selection index during selection.

Simple correlation analysis involving some selected traits alone may not provide adequate information with regards to selection towards improved root yield. Often, there are indirect influences of one trait upon another which may reduce its contribution to yield. Therefore, understanding the interrelationships between several traits and their direct and indirect effects on root yield should be established. Path-coefficient analysis is a statistical tool helpful to quantify the relative contribution of causal sources of variance and covariance, given that there is a certain degree of interrelatedness between the variables (Lynch and Walsh, 1998). It is a standard partial regression coefficient that measures the direct influence of one variable upon others (Li, 1956; Dewey and Lu, 1959; Bhatt, 1973; Shimelis and Hugo, 2011).

Unlike simple correlation analysis, path-coefficient analysis is used to measure the direct influence of one variable on another and separates this correlation coefficient into components of direct and indirect effects (Diz. et al., 1994; Shimelis and Hugo, 2011). Each correlation

coefficient between a causal or independent variable and the response or dependent variable is partitioned. This provides components with the direct effect or path-coefficient for the predictor variable and indirect effects, which involve the product of a correlation coefficient between two predictor variables with the appropriate path-coefficient in the path diagram (Diz. et al., 1994; Shimelis, 2006). Therefore, a better understanding of both the direct and indirect effects of selecting for specific components can be attained by determining the interrelationships among yield components. This provides a comprehensive understanding of the relationship among a set of traits and how each trait affects or contributes to yield (Diz. et al., 1994; Akheter and Sneller, 1996; Board et al., 1997).

Some 25 potential sweetpotato clones were developed in Ethiopia with desirable genetic backgrounds with regards to high yield, dry matter and β-carotene contents. The candidate clones will be subjected to continuous selection with subsequent stability tests to develop and release farmers-preferred cultivars. Therefore, the objective of this study was to assess associations between yield and yield related traits, and to identify the most efficient yield-predicting traits in sweetpotato for effective selection.

5.2 Materials and methods

5.2.1 Study sites

The study was undertaken in six environments in the Southern Region of Ethiopia. The sites were the Halaba special district, Kokate and Areka in the Wolayita zone, Arbaminch in the Gamo Gofa zone, Hawassa in th Sidama zone and Dilla in the Gedeo zone. These sites represent diverse agro-ecologies that are suitable for sweetpotato production in Ethiopia (Tadesse et al., 2013; CSA, 2014; Mekonen et al., 2014; CSA, 2015; Gurmu et al., 2015b).

5.2.2 Plant materials and field establishment

The study used 24 clones selected from F1 families of a diallel cross based on a combination of desirable traits. High root yield was one of the criteria to select the clones. One locally released variety (Tula) was included as a comparative control in the study. The clones were evaluated in a 5 x 5 simple lattice design using four rows. The spacing between each row was 0.60 meter and between plants was 0.30 meter. The total number of plants per row and per plot was 10 and 40, respectively. No fertilizer was applied. Weeding was done as required. Two central rows were used for pre-harvest data recording and harvesting.

5.3.3 Data collection

Both qualitative and quantitative data were evaluated in the study. The qualitative data included: **SPVD,** recorded on singe plant basis, using a scale of 1 to 9, where 1 = No visible virus symptoms; 3 = Faint mosaic; 5 = Mosaic clear; 7 = Heavy mosaic and stunted; 9 = Necrosis (dead patches) (Hahn, 1979; Mwanga et al., 2002; Ndunguru et al., 2009); p**redominant skin colour,** recorded on a scale of 1-9 as described by Huaman (1991) and (1999), where 1 = White, 2 = Cream, 3 = Yellow, 4 = Orange, 5 = Brownish orange, 6 = Pink, 7 = Red, 8 = Purple red, 9 = Dark Purple; **predominant flesh colour,** recorded in scale of 1-9 as described by Huaman (1991) and (1999), where 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 anthocyanin.

The quantitative data included **RDMC,** expressed as percentage of root dry weight (g) to fresh roots weight (g). A 100-200 g samples were taken from roots of representative plants in a plot and the roots were cut in to smaller pieces and were dried in an oven at 80^{o}C for 48 hours; **β-carotene content** was analysed in Uganda at Namulonge Agricultural and Animal Production Research Institute (NAARI) using Near Infrared Reflectance Spectrometry (NIRS) and expressed in mg 100 g^{-1}; **Fresh root yield,** expressed as harvested fresh roots weight of two central rows converted to tonnes ha^{-1}; **days to 50% maturity,** recorded when leaves of 50% of the plants were turned yellow; **vine length (cm),** measured by taking the vertical length of the vine from the ground level to the tip of the main shoot of the plants; **vine internode length (cm),** measured on three internodes located in the middle section of the vine of ten randomly selected plants in a plot; a**boveground fresh weight (ton ha^{-1}),** measured as a weight of the above ground parts of the two central rows converted to ton ha^{-1}; **storage root length (cm),** recorded as a mean vertical length from the bottom to the tip of roots of ten randomly selected plants in a plot; **storage root girth (cm),** expressed as the mean diameter of the middle portion of roots of ten randomly taken plants in a plot and measured using a calliper; **number of storage roots per plant,** measured as a mean number of storage roots produced by the whole plant in a plot divided by the number of plants in the plot; **individual root weight (g),** estimated by dividing storage root weight per plant by the number of storage roots per plant of ten randomly taken plants in a plot; and **harvest index (HI),** measured as a ratio of fresh root weight to total weight (above ground fresh weight + fresh root weight). Ten plants were randomly sampled and tagged from each plot for recording the following data: vine length, vine

internode length, storage root length, storage root girth, individual root weight, β-carotene content, RDMC, skin colour and flesh colour.

5.2.4 Data analyses

Analysis of variance

ANOVA of qualitative data such as SPVD, skin colour and flesh colour was conducted after transforming the data using square root transformation for SPVD and log transformation for skin colour and flesh colour. For both qualitative and quantitative data sets, ANOVA of data from each environment and across environments was conducted using GenStat 14th edition (Payne et al., 2011) and SAS version 9.3 (SAS Institute Inc., 2003) statistical packages. The statistical models were described in Chapter 4, Section 4.2.5.

Correlation and path-coefficient analyses

The phenotypic correlation coefficients were determined according to the method suggested by Miller et al. (1958) and using Spearman's correlation, which is recommended for analysis of parametric and non-parametric data (Hauke and Kossowski, 2011). SAS was used for the analysis. Path-coefficient analysis was computed with the method suggested by Dewey and Lu (1959) using Microsoft Excel 2010.

5.3 Results

5.3.1 Mean performance of the clones

The combined ANOVA indicated presence of significant effects of genotype x environment interaction affecting all traits except root girth and skin colour (Table 5.1).

The mean response of clones for RDMC, β-carotene content and fresh root yield is discussed in Chapter 4 Section 4.3.2. The overall mean across the six environments for additional twelve traits is presented in Table 5.2. For SPVD, the lowest scores were 1.2, 1.0 and 1.3, recorded for the genotypes G1, G11 and G16, respectively. The highest SPVD scores were recorded for the genotypes G9, G14 and G15 with scores of 5.2, 6.0 and 5.7, respectively, reflecting their susceptibility. The genotype designated as G8 had the lowest days-to-maturity of 132 days, while G21 had the longest days-to-maturity (145 days). The genotype G21 had the longest vine of 213.9 cm with internode length of 7.3 cm, while G25 had the shortest vine and internode

lengths of 65.0 and 2.0 cm, respectively. Above ground fresh weight ranged between 6.8 and 26.7 t ha^{-1}. These values were recorded for G25 and G10, respectively. Genotype G25 had the shortest root length of 13.0 cm, while the longest root was recorded for G13 of 18.9 cm. The lowest values of root girth (4.0 cm) was recorded for G21, number of roots per plant (1.1) for G25, individual root weight (85.1 g) for G8, harvest index (0.30) for G10 and G21, and skin colour (2.3) for G4. The lowest score of flesh colour of 2.0 was recorded for the genotypes G3, G4, G9, G10 and G11. Conversely, the highest mean root girth (6.2 cm) was recorded for G6, number of roots per plant (7.6) for G8, individual root weight (211.5 gm) for G18, HI (0.7) for G12 and G20, skin colour (8.6) for G3 and flesh colour (8.0) for G8 and G21 (Table 5.2).

Table 5.1 Analysis of variance of 12 traits of sweetpotato genotypes evaluated across six environments in Ethiopia

Source of variation	df	Mean square and significant tests											
		SPVD	DTM	VL	INL	AGFW	RL	RG	NRP	IRW	HI	SC	FC
Environment (E)	5	2.1**	1830.9**	78613.7**	60.0**	5816.4**	178.1**	30.0**	222.6**	206945.1**	0.325**	0.04*	0.02*
Block (B)	9	0.16ns	59.5ns	519.04ns	0.35ns	56.8ns	8.1ns	1.9*	3.2ns	2187.2ns	0.012ns	0.03ns	0.01ns
Replication (R)	5	0.41*	20.8ns	263.05ns	0.63*	102.3*	23.4*	1.9*	20.4*	76087.6*	0.021ns	0.03ns	0.003ns
Genotype (G)	24	1.5**	95.4*	12710.4*	13.6**	298.0*	28.1*	2.3*	23.3*	15359.6*	0.085*	0.37**	0.71**
G x E	120	0.23*	70.8*	2386.8*	1.48*	82.6*	9.6*	0.5ns	5.9*	8211.1*	0.017*	0.01ns	0.01*
Error	136	0.09	44.4	308.25	0.22	47.9	6.9	0.6	2.8	2498.3	0.009	0.02	0.003

* and ** denote significant differences at $p < 0.05$ and $p < 0.01$ probability level, respectively, df = degrees of freedom, ns = not significant, G x E = genotype by environment interaction; SPVD = sweetpotato virus disease, DTM = days to 50% maturity, VL = vine length, INL = internode length, AGFW = above ground fresh weight, RL = root length, RG = root girth, NRP = number of roots per plant, IRW = individual root weight, HI = harvest index, SC = skin colour, FC = flesh colour.

Table 5.2 Combined mean values of 25 sweetpotato genotypes evaluated across six environments in Ethiopia

Genotypes ID	Genotypes	Traits											
		SPVD	DTM	VL	INL	AGFW	RL	RG	NRP	IRW	HI	SC	FC
G1	Ukrewe x Ejumula- 10	1.2	144.2	134.5	5.2	20.3	17.7	5.5	4.0	158.8	0.5	4.0	7.0
G2	Ukrewe x Ejumula - 13	2.7	141.7	140.9	4.3	14.4	15.0	4.8	6.0	97.0	0.6	6.8	7.0
G3	Ukrewe x PIPI-1	1.8	143.3	98.9	3.4	19.0	17.9	5.3	4.1	137.3	0.5	8.6	2.0
G4	Ukrewe x NASPOT-1	1.8	137.5	92.8	3.4	22.0	16.6	5.2	2.6	146.2	0.4	2.3	2.0
G5	Ukrewe x Ogansagan-5	4.0	142.9	130.8	3.9	22.3	18.4	5.8	3.2	171.7	0.5	4.5	7.5
G6	Resisto x Ejumula -7	1.7	138.8	134.2	4.5	22.1	18.4	6.2	4.1	184.0	0.6	3.3	7.3
G7	Resisto x PIPI-1	3.8	133.3	81.9	3.1	11.8	16.3	4.6	7.5	76.4	0.6	5.8	6.8
G8	Resisto x PIPI-2	2.0	131.7	182.2	5.9	12.6	14.4	4.3	7.6	85.1	0.6	6.5	8.0
G9	Resisto x PIPI-4	5.2	137.1	113.5	4.1	11.0	17.8	5.0	3.5	117.0	0.5	2.8	2.0
G10	Resisto x PIPI-14	2.3	140.8	134.4	4.2	26.7	14.4	4.6	3.7	196.8	0.3	2.8	2.0
G11	Resisto x Temesgen -10	1.0	143.8	91.6	3.2	19.8	16.5	5.3	2.1	174.9	0.4	8.2	2.0
G12	Resisto x Temesgen -12	1.7	135.0	159.2	5.7	11.0	16.4	5.2	6.5	107.1	0.7	5.9	7.1
G13	Resisto x Temesgen -14	1.8	143.8	151.3	5.3	21.4	18.9	5.7	3.3	163.2	0.5	3.8	6.8
G14	Resisto x Temesgen -17	6.0	140.4	106.0	3.5	12.5	15.4	5.7	2.8	169.3	0.5	2.5	7.3
G15	Resisto x Temesgen-23	5.7	139.6	126.4	4.0	9.8	14.3	5.8	2.8	156.0	0.6	6.2	7.7
G16	Resisto x Ogansagen-5	1.3	141.7	93.8	3.5	20.8	17.7	5.3	4.0	155.8	0.5	7.6	3.5
G17	Resisto x Ogansagen-16	2.0	134.2	151.9	5.1	14.8	14.4	4.9	6.7	87.4	0.6	6.5	7.7
G18	Resisto x Ogansagen-20	1.8	138.3	93.4	3.2	22.9	16.9	5.5	2.6	211.5	0.5	2.7	2.2
G19	Resisto x Ogansagen-23	2.0	141.7	132.5	4.5	16.9	18.7	5.0	3.2	194.3	0.6	4.3	7.5
G20	Ejumula x PIPI-10	3.7	136.7	112.5	3.6	14.0	17.3	5.3	6.5	102.0	0.7	7.2	7.7
G21	Ejumula x PIPI-18	3.3	145.0	213.9	7.3	19.9	14.3	4.0	4.4	124.4	0.3	4.5	8.0
G22	Ejumula x PIPI-19	4.0	139.2	164.9	5.3	15.1	14.8	4.5	5.5	105.0	0.6	6.6	7.8
G23	Ejumula x Temesgen-15	2.0	142.9	124.2	4.6	21.9	17.1	5.0	3.2	198.1	0.6	2.8	2.2
G24	Ejumula x Ogansagen-17	2.3	138.8	135.7	4.6	23.1	18.3	4.6	3.4	164.8	0.5	4.3	7.7
G25	Tula	1.7	136.3	65.0	2.0	6.8	13.0	5.0	1.1	146.7	0.6	2.8	6.6
Mean		2.7	139.5	126.7	4.3	17.3	16.4	5.1	4.2	145.2	0.5	4.9	5.7
LSD (0.05)		0.8	5.4	14.2	0.4	5.6	2.1	0.6	1.4	40.4	0.08	1.0	0.5
CV (%)		19.7	4.8	13.9	10.9	39.9	15.9	15.3	39.7	34.4	17.7	19.5	7.9
R^2 (%)		87.6	78.6	96.0	96.6	88.0	76.7	79.2	88.3	89.7	83.9	85.6	98.0

ID = Identification, SPVD = sweetpotato virus disease, DTM = days to 50% maturity, VL = vine length (cm), INL = internode length (cm), AGFW = above ground fresh weight (ton ha^{-1}), RL = root length (cm), RG = root girth (cm), NRP = number of roots per plant, IRW = individual root weight (g), HI = harvest index, SC = skin colour (1-9), where 1 = white, 2 = cream, 3 = yellow, 4 = orange, 5 = brownish orange, 6 = pink, 7 = red, 8 = purple red, 9 = dark purple, FC = flesh colour (1-9), where 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 anthocyanin.

5.3.2 Simple correlation analysis

The result of phenotypic correlation among the fourteen traits is presented in Table 5.3. Fresh root yield had significant positive correlations with most of the traits except with SPVD (r = -0.29) and days-to-maturity (r = 0.30). This trait had non-significant correlations with β-carotene content, root girth, skin colour and flesh colour. RDMC was negatively and significantly correlated with β-carotene content, SPVD, vine length, internode length, above ground fresh weight and flesh colour. It had relatively high negative correlation with β-carotene content (r = -0.40) and root flesh colour (r = -0.47). Figure 5.1 shows the simple negative association between RDMC and β-carotene content. The highest positive correlation was observed between vine length and vine internode length (r = 0.81). The second highest positive correlation was observed between β-carotene content and root flesh colour (r = 0.76), which is depicted in Figure 5.2. Number of roots per plant and individual root weight were negatively and significantly correlated (r = -0.48). Similarly, aboveground fresh weight and harvest index were negatively and significantly correlated (r = -0.47).

Skin colour did not show correlation with most of the traits, while flesh colour showed positive correlation with some of the traits and negative correlations with a few traits.

Table 5.3 Spearman's correlation coefficients showing pair-wise associations of 14 traits of sweetpotato genotypes evaluated across six environments in Ethiopia

Traits	BCC	FRY	SPVD	DTM	VL	INL	AGFW	RL	RG	NRP	IRW	HI	SC	FC
RDMC	-0.40***	0.16**	-0.20***	0.03ns	-0.14**	-0.23***	-0.28***	0.26***	0.18**	0.05ns	0.10ns	0.14*	0.02ns	-0.47***
BCC		-0.02ns	0.22***	-0.01ns	0.18**	0.20***	-0.19**	-0.15**	-0.04ns	0.11ns	-0.11ns	0.19**	0.12ns	0.76***
FRY			-0.29***	-0.30***	0.39***	0.37***	0.53***	0.54***	0.04ns	0.46***	0.48***	0.42***	0.12ns	0.04ns
SPVD				0.04ns	-0.12ns	-0.16**	-0.37***	-0.24***	-0.10ns	-0.02ns	-0.28**	0.08ns	-0.03ns	0.24***
DTM					-0.21***	-0.09ns	-0.12ns	-0.20**	-0.09ns	-0.28***	0.05ns	-0.13*	-0.04ns	-0.06ns
VL						0.81***	0.46***	0.18**	0.12ns	0.37***	0.06ns	-0.05ns	0.03ns	0.23***
INL							0.31**	0.13*	-0.05ns	0.22***	0.18**	0.06ns	0.04ns	0.27***
AGFW								0.42***	0.25***	0.29***	0.26***	-0.47***	-0.04ns	-0.16*
RL									0.23***	0.24***	0.30***	0.11ns	-0.08ns	-0.16*
RG										0.22***	0.19**	-0.20**	-0.01ns	-0.05ns
NRP											-0.48***	0.18**	0.31***	0.21***
IRW												0.23***	-0.16**	-0.14*
HI													0.16**	0.22***
SC														0.20**

*,**, and *** denote significant correlations at 0.05, 0.01 and 0.001 probability levels, respectively; ns = not significant, RDMC = root dry matter content, BCC = β-carotene content, FRY = fresh root yield, SPVD = sweetpotato virus disease, DTM = days to maturity, VL = vine length, INL = internode length, AGFW = above ground fresh weight, RL = root length, RG = root girth, NRP = number of roots per plant, IRW = individual root weight, HI = harvest index, SC = skin colour, FC = flesh colour.

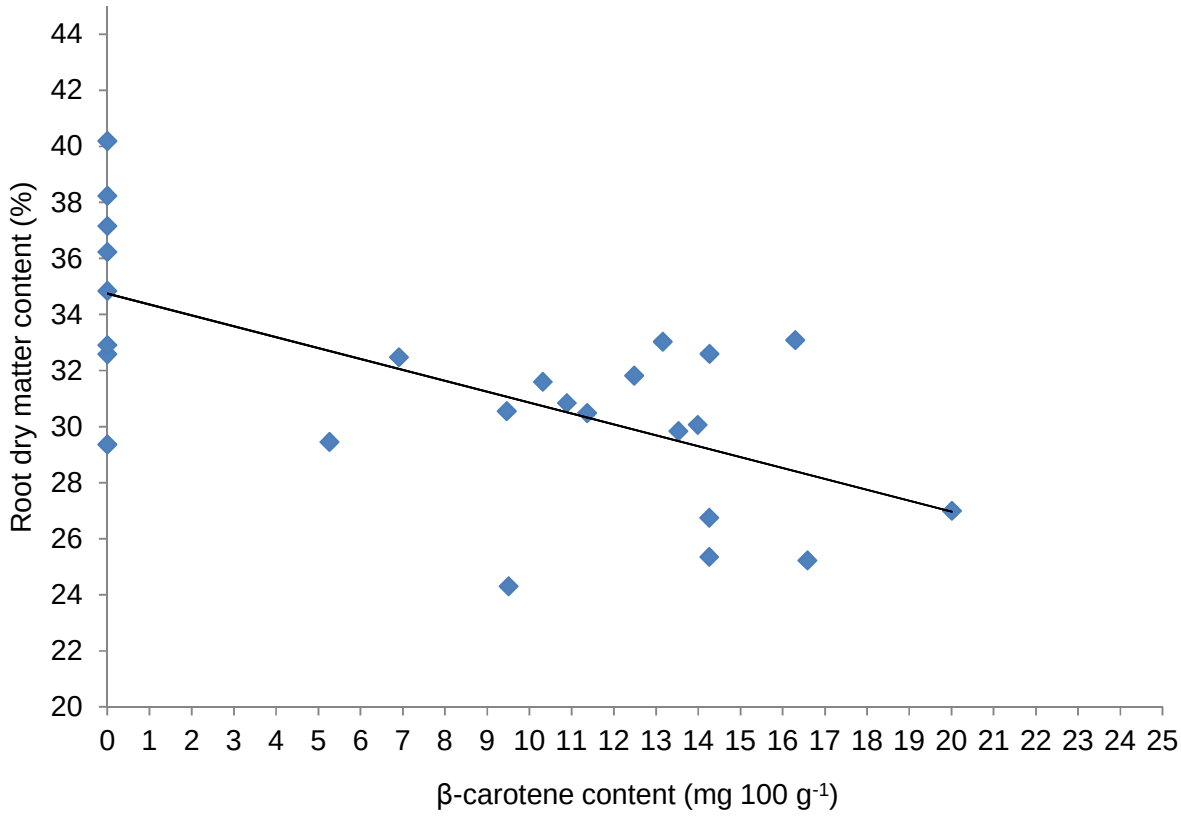

Figure 5.1 Simple linear relationship between root dry matter and β-carotene contents of sweetpotato genotypes tested across six environments

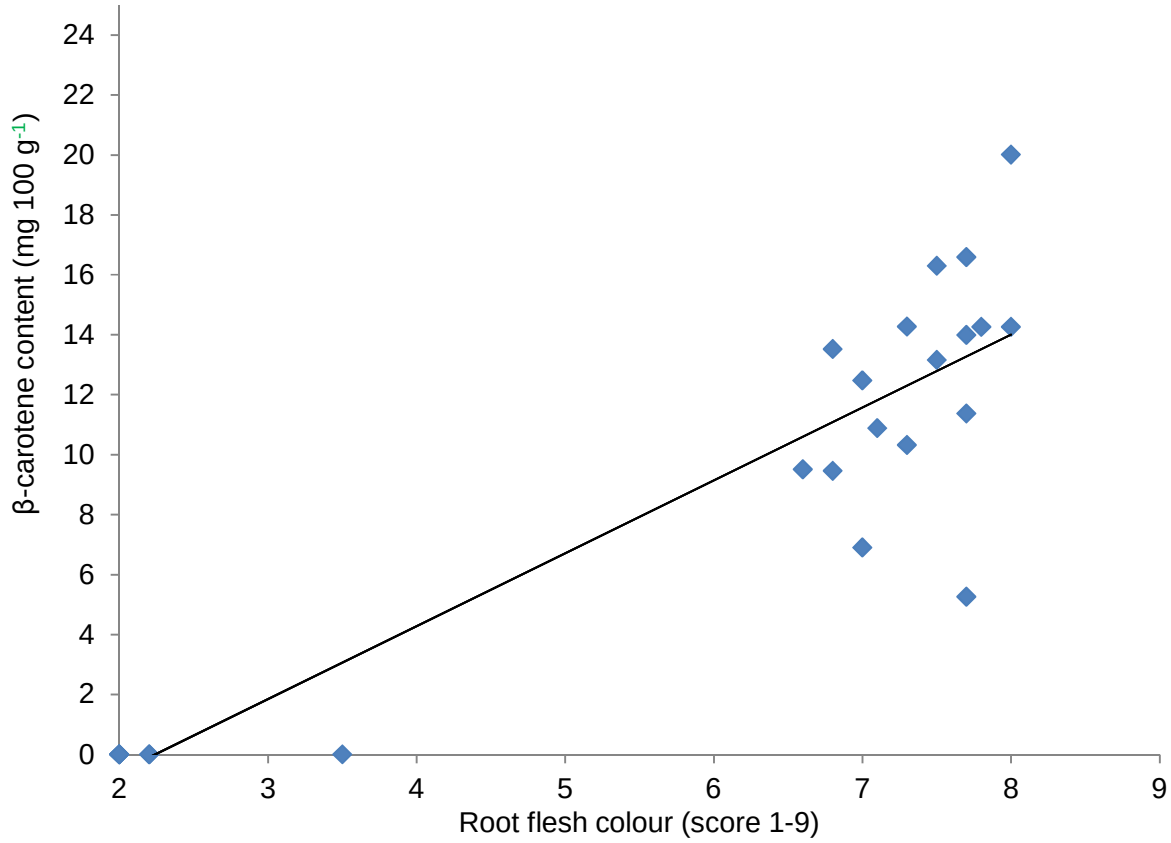

Figure 5.2 Simple linear relationship between β-carotene content and root flesh colour of sweetpotato genotypes tested across six environments

5.3.3 Path-coefficient analysis

The interrelationship among twelve agronomic traits (predictor variables) and their direct and indirect effects on fresh root yield (response variable) is presented in Table 5.4. The result of path-coefficient analysis showed that number of roots per plant and individual root weight had the highest positive direct effects of 0.776 and 0.821, respectively, on fresh root yield. Other traits that exerted high positive direct effects on fresh root yield were RDMC and above ground fresh weigh with path-coefficients of 0.276 and 0.410, respectively. Root girth had a high negative direct effect of -0.396 on fresh root yield (Table 5.4).

Number of roots per plant had an indirect negative effect on fresh root yield through individual root weight (-0.373) and days to maturity (-0.217). This traits also had significant negative correlations with individual root weight and days-to-maturity with correlation coefficients of r = -

0.48 and r = -0.28, respectively. Similarly, above ground fresh weight had an indirect negative effect of -0.193 on fresh root yield through harvest index. Individual root weight had an indirect negative effect of -0.230 on fresh root yield through SPVD. Other traits: vine length, internode length, root length, root girth and HI all exerted indirect positive effect on fresh root yield through the number of roots per plant and individual root weights (Table 5.4).

Table 5.4 Direct (bold diagonals) and indirect effects of 12 sweetpotato traits on fresh root yield of sweetpotato genotypes

Traits	RDMC	BCC	SPVD	DTM	VL	INL	AGFW	RL	RG	NRP	IRW	HI	r_p
RDMC	**0.276**	-0.050	-0.015	-0.004	0.012	-0.002	-0.115	-0.009	-0.071	0.039	0.082	0.017	0.16
BCC	-0.111	**0.126**	0.016	0.001	-0.015	0.002	-0.078	0.005	0.016	0.085	-0.090	0.022	-0.02
SPVD	-0.055	0.028	**0.074**	-0.005	0.010	-0.002	-0.152	0.008	0.040	-0.016	-0.230	0.009	-0.29
DTM	0.008	-0.001	0.003	**-0.129**	0.018	-0.001	-0.049	0.007	0.036	-0.217	0.041	-0.015	-0.30
VL	-0.039	0.023	-0.009	0.027	**-0.086**	0.008	0.188	-0.006	-0.048	0.287	0.049	-0.006	0.39
INL	-0.064	0.025	-0.012	0.012	-0.069	**0.010**	0.127	-0.004	0.020	0.171	0.148	0.007	0.37
AGFW	-0.077	-0.024	-0.027	0.015	-0.039	0.003	**0.410**	-0.014	-0.099	0.225	0.213	-0.056	0.53
RL	0.072	-0.019	-0.018	0.026	-0.015	0.001	0.172	**-0.033**	-0.091	0.186	0.246	0.013	0.54
RG	0.050	-0.005	-0.007	0.012	-0.010	0.000	0.102	-0.008	**-0.396**	0.171	0.156	-0.024	0.04
NRP	0.014	0.014	-0.001	0.036	-0.032	0.002	0.119	-0.008	-0.087	**0.776**	-0.394	0.021	0.46
IRW	0.028	-0.014	-0.021	-0.006	-0.005	0.002	0.106	-0.010	-0.075	-0.373	**0.821**	0.027	0.48
HI	0.039	0.024	0.006	0.017	0.004	0.001	-0.193	-0.004	0.079	0.140	0.189	**0.118**	0.42

RDMC = root dry matter content, BCC = β-carotene content, SPVD = sweetpotato virus disease, DTM = days to maturity, VL = vine length, INL = internode length, AGFW = above ground fresh weight, RL = root length, RG = root girth, NRP = number of roots per plant, IRW = individual root weight, HI = harvest index, r_p = phenotypic correlation coefficient.

5.4 Discussion

The significant genotypic difference observed across environments in the traits studied indicates the presence of considerable genetic variation among the tested genotypes. The results show that most traits in sweetpotato are sensitive to G x E interaction. This is in agreement with the reports of various authors (Janssens, 1983; Collins et al., 1987; Nasayao and Saladaga, 1988; Manrique and Hermann, 2001; Wolfgang et al., 2005). More than two-third of the studied genotypes showed resistance to SPVD, and three genotypes, G1, G11 and G16, exhibited the best SPVD resistance with relatively very low SPVD scores of 1.2, 1.0 and 1.3, respectively. On the other hand, three genotypes, namely G9, G14 and G15, were relatively susceptible to SPVD with disease scores of 5.2, 6.0 and 5.7, respectively. The genotype G8 was relatively early maturing while G21 was late maturing.

The genotype G21 had the highest mean vine length and internode length as revealed by the combined analysis. Genotype G25 (Tula), had the lowest length of vine and internode of 65.0 and 2.0 cm, respectively. This variety had a stunted growth habit in almost of the test environments. Furthermore, G25 had the lowest above ground fresh weight and number of roots per plant owing to its bushy growth habit. Genotype G10 had the highest above ground fresh weight of 26.7 t ha^{-1}, indicating its potential as a source of animal feed. The lowest mean root girth (4.0 cm) was recorded for G21, which had very small roots. G12 and G20 had the highest harvest index (HI) of 0.7. These genotypes had low above ground fresh weight. Therefore, the high HI values were not only due to their high fresh root yield but also due to their low above ground fresh weight. This suggests that high correlation between yield and HI does not necessarily imply that HI could be an effective selection criterion for high yield in all situations, as suggested by Labana et al. (1993).

The lowest skin colour score of 2.3 was recorded for G4. This genotype had a creamy skin colour, while the highest mean skin colour score of 8.6 was recorded for G3 with a purple skin colour. The genotypes G3, G4, G9, G10 and G11 had the lowest flesh colour of 2.0, which was cream. These genotypes had no β-carotene content which was revealed by results of β-carotene analysis presented in Table 4.7 of Chapter 4. On the other hand, the genotypes G8 and G21 had the highest root flesh colour scores of 8.0, displaying deep orange flesh colour that reflected their high β-carotene content.

Fresh root yield had a significant positive correlation with most of the traits except SPVD, days-to-maturity, β-carotene content, root girth, skin colour and flesh colour. Ofuape et al. (2011) reported similar results where all the traits included in their study, except stand count at harvest, showed positive and significant correlations with fresh root yield of sweetpotato. Root dry matter content was negatively and significantly correlated with most of the traits studied. The existence of slight negative correlations between RDMC and β-carotene content has been reported by several authors (Simonne et al., 1993; Chiona, 2009; Cervantes-Flores et al., 2010). Figure 5.1 shows the negative correlation of RDMC with β-carotene content in which the RDMC of genotypes decreases with increasing β-carotene content. RDMC was positively and highly correlated with fresh root yield. Fresh root yield was positively and highly correlated with most of the traits studied. The positive correlation between fresh root yield and other traits suggests that the traits could be used as selection criteria for high storage root yield (Lin et al., 2007; Gasura et al., 2008). This might be associated with higher photosynthetic leaf area leading to high root yield and dry matter accumulation. Jha (2012) reported that root yield per plant had positive correlations with biological yield per plant, harvest index and root diameter. The author suggested that selection for component traits may increase the root yield of sweetpotato.

The negative correlation observed between fresh root yield and SPVD was expected as SPVD is a damaging disease complex of sweetpotato in Ethiopia (Mekonen et al., 2014). β-carotene content and root flesh colour showed a high positive correlation as it can also be seen in Figure 5.2, where increases in flesh colour intensity (from cream to deep orange) correlated with increased values of β-carotene. The existence of a strong positive correlation between flesh colour and β-carotene content in sweetpotato has been reported by several authors (Cervantes-Flores, 2006; Mcharo and LaBonte, 2007; Gasura et al., 2008; Burgos et al., 2009; Vimala and Hariprakash, 2011). Takahata et al. (1993) studied the relationship between β-carotene content and root flesh colour in sweetpotato varieties and found a high positive correlation of $r = 0.89$, which is close to the current result. Therefore, root flesh colour can be used as a selection criterion of sweetpotato clones for high β-carotene content. This is especially useful at the beginning of a screening work where large numbers of progeny need to be evaluated and analysis of β-carotene content for each plant is not feasible. To this effect, a colour chart (Burgos et al., 2009) that correlates root flesh colour with the levels of β-carotene content in the roots can be used to select clones with high β-carotene content.

The negative correlation between number of roots per plant and individual root weight indicates that an increase in number of roots per plant appears to result in competition between roots of a

plant and this may result in many, small sized, unmarketable roots, as also reported by Tsegaye et al. (2006).

Generally, traits that showed strong positive correlation with fresh root yield such as vine length, internode length, above ground fresh weight, storage root length, number of roots per plant, individual root weight and HI could be useful as indirect selection criteria for storage root yield in a sweetpotato improvement program. However, path-coefficient analysis is recommended to confirm which trait can be used as a primary trait to select for better fresh root yield. Further, path analysis shows direct and indirect effect(s) of traits on the selection for fresh root yield.

In analysing the interrelationship among the traits and in isolating their direct and indirect effects on fresh root yield, root yield was considered as a dependent variable while other traits were considered as independent variables. Number of roots per plant and individual root weight had high positive direct effect on fresh root yield. These traits also had high correlation coefficients with fresh root yield indicating that the two traits were the best predictors of fresh root yield of sweetpotato. Similar results have been reported by other authors (Kamalam, 1977; Alam et al., 1998; Hossain et al., 2000; Tsegaye et al., 2006). RDMC and above ground fresh weigh were other traits that exerted high positive direct effect on fresh root yield. These traits also had high positive correlations with fresh root yield, and could be used as selection criteria for fresh root yield.

Number of roots per plant exerted indirect negative effects on root yield via individual root weight and days to maturity. This trait also had significant negative correlations with individual root weight and days to maturity, in agreement to the report of Tsegaye et al. (2006). As the number of roots increased, their individual weight tends to decrease due to competition for nutrient resources among the roots. Similarly, above ground fresh weight had an indirect negative effect on fresh root yield through harvest index, where the two traits were also significantly and negatively correlated. SPVD, which was negatively correlated with individual root weight, had an indirect negative effect on fresh root yield through individual root weight. Vine length, internode length, root length and root girth exerted indirect positive effects on fresh root yield through the number of roots per plant.

Traits that have positive correlations with yield might exert negative direct effect on it. Conversely, traits that have negative correlations or no correlations with yield might exert positive direct effect on it. In this study, vine length and root length, which had high significant

positive correlations with fresh root yield, showed negative direct effects of -0.086 and -0.033, respectively. Similarly, root girth, which had a non-significant correlation with root yield, exerted the highest negative direct effect of -0.396 on fresh root yield. Therefore, path-coefficient analysis could be a more valuable method to identify influential traits than simple correlation analysis.

Generally, the number of roots per plant and individual root weight, which had the highest positive direct effect and also positive indirect effect via positively influencing most of the traits, can be used as indirect selection criteria for fresh root yield. Moreover, RDMC, above ground fresh weight and root length, which had relatively high positive direct effect on fresh root yield, could be used as a means of indirect selection for fresh root yield.

5.5 Conclusions

Correlation and path-coefficient analyses are important statistical procedures to detect the interrelationship among different traits and to identify the direct and indirect effects of traits on fresh root yield. This in turn helps to identify traits that can be used as indirect selection criteria for fresh root yield during recurrent selection among large number of genotypes.

In this study, based on the path-coefficient analysis, individual root weight, number of storage roots per plant, RDMC, aboveground fresh weight and root length were the most important characters that impact on storage root yield. Therefore, these traits could be used for indirect selection of sweetpotato clones for increased fresh root yield in sweetpotato improvement programs.

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CHAPTER 6

Evaluation of newly developed orange fleshed sweetpotato clones for nutritional traits

Abstract

Micro-nutrient deficiency currently affects nearly two billion people worldwide, especially in low income countries of the world and in poor communities. Micro-nutrient deficiencies increase susceptibility to other diseases. Sweetpotato, notably the OFSP, is considered to be a cheap food source that is rich in many macro- and micro-nutrients. Information on the nutrient contents of newly developed OFSP varieties is required in order to make recommendation to growers and the food industry. Therefore, the objectives of this study were to determine the nutritional value of newly developed OFSP clones and to establish the associations between β-carotene content and micro-nutrients for targeted large scale production to alleviate nutrient deficiencies. Seventeen OFSP and eight white/cream fleshed sweetpotato clones were evaluated across six diverse environments (Halaba, Kokate, Areka, Arbaminch, Hawassa and Dilla) in southern Ethiopia using a 5 x 5 simple lattice design. Nutritional traits data were collected and subjected to analysis of variance and correlation analyses. Environment, genotype, and genotype x environment interaction effects were highly significant ($p < 0.01$) for all parameters measured. A newly developed genotype, designated G8, had the highest contents of β-carotene (20.01 mg 100 g^{-1}), protein (7.08%), iron (2.55 mg 100 g^{-1}), zinc (1.42 mg 100 g^{-1}), fructose (4.45%), glucose (5.34%) and sucrose (16.20%). The genotypes G15 and G19 performed relatively well for the above nutritional traits. β-carotene content had significant positive correlations with iron ($r = 0.27$, $p < 0.001$), zinc ($r = 0.14$, $p < 0.05$), fructose ($r = 0.1$, $p < 0.05$), glucose ($r = 0.12$, $p < 0.05$) and sucrose ($r = 0.36$, $p < 0.001$). This reflects the potential to breed for OFSP varieties enriched with the important micro-nutrients. Overall, the candidate OFSP clones, G8 (Resisto x PIPI-2), G15 (Resisto x Temesgen-23) and G19 (Resisto x Ogansagen-23) were good sources of nutritional traits such as vitamin A, iron zinc, protein, sucrose, glucose and fructose. The selected genotypes can be recommended for large-scale production, food processing or further sweetpotato improvement to alleviate nutrient deficiencies in Ethiopia or similar environments in sub-Saharan Africa.

Key words: β-carotene, correlation analysis, nutrient deficiencies, micro-nutrients

6.1 Introduction

Micro-nutrient deficiency is a global health problem, especially in low income countries of the world, affecting the health of the poor communities (Welch, 2002; Knez and Graham, 2013). Deficiency of micro-nutrients such as vitamin A and minerals, especially iron (Fe) and zinc (Zn), affects nearly two billion people worldwide (Allen et al., 2006; Tulchinsky, 2010). The deficiencies increase susceptibility to other diseases. Pregnant and lactating mothers, and young children, are greatly affected by nutrient deficiencies since they need relatively high levels of vitamins and minerals (Nabakwe and Ngare, 2004; WHO, 2009b). Vitamin A deficiency is the major health problem worldwide that leads to blindness, retarded growth and death, particularly in developing countries. It largely affects pre-school children, pregnant and lactating mothers, and the rural poor (WHO, 2009a; Gurmu et al., 2015a). Fe deficiency is another global health problem with approximately two billion people in the world being reported to be anemic (Frossard et al., 2000; WHO, 2009b; Singh et al., 2013). Fe is required for proper functioning of the immune system, the blood system, protein synthesis, cell reproduction and wound healing. Furthermore, this micro-nutrient plays a major role in fertility and conception (Singh et al., 2013). Zn is another essential element. Over one-third of the world's population is estimated to have a Zn deficiency (WHO, 2009b, 2011, 2012). According to Black (2003), nearly 800,000 and 700,000 deaths per year can be attributed to Fe and Zn deficiencies, respectively. The author reported that more than 2% of global disease problems are attributable to vitamin A, Fe and Zn deficiencies.

Different strategies have been used to combat the problem of nutrient deficiencies. One of the strategies is multiple vitamin and mineral supplements for pregnant and lactating mothers, and for young children aged below 5 years. However, this approach is not sustainable. It is expensive, and also difficult to deliver to all mothers and children that are at risk, especially in remote rural areas (Anderson et al., 2007). Therefore, consumption of food items naturally rich in vitamins and minerals is more reliable strategy. The food items are vegetables such as kale, tomatoes, yellow pepper, carrot, broccoli, spinach, squash and pumpkin, fruits such as cantaloupe, apricot, mango and papaya, and root crops such as sweetpotato (Toenniessen, 2000; Mwanga et al., 2003; Kapinga et al., 2005; Anderson et al., 2007; Gurmu et al., 2015a). Among these food items, sweetpotato is the cheapest food source that is rich in many of the macro and micro-nutrients (Woolfe, 1992; Courtney et al., 2008; Grüneberg et al., 2009a; Betty et al., 2015).

Sweetpotato [*Ipomoea batatas* (L.) Lam] is an important food crop that is grown primarily by smallholder farmers of the developing countries. The crop is used as a substitute for starchy staples such as rice, wheat, maize and potato and is mainly consumed by poor communities. Sweetpotato roots are important sources of carbohydrates, vitamin C, vitamin B6, copper, potassium, iron, and fiber (Woolfe, 1992). It contains a significant level of vitamins, minerals, and other nutrients (Woolfe, 1992). It also contains moderate quantities of zinc, sodium, magnesium and manganese (Suda et al., 1999; Antia et al., 2006).

Some sweetpotato varieties, especially those with orange and purple flesh, are rich in β-carotene, anthocyanins, phenolics, dietary fibre, vitamin C, folic acid and minerals (Woolfe, 1992; Bovell-Benjamin, 2007). OFSP is an effective, low-priced, sustainable source of β-carotene (pro-vitamin A) (Low et al., 2001; Mwanga et al., 2003; Tumwegamire et al., 2004; Gurmu et al., 2015a). β-carotene is converted to vitamin A in the human body (Low et al., 2001; Mwanga et al., 2003; Kapinga et al., 2005). Roots of some dark-orange fleshed sweetpotato varieties can contain up to 20,000 µg 100 g^{-1} of β-carotene on a fresh weight basis (Woolfe, 1992; Takahata et al., 1993; Kapinga et al., 2010). The leaves of sweetpotato also serve as nutritious vegetable for humans (Woolfe, 1992). Sweetpotato leaves are good sources of protein, β-carotene, some of the B vitamins, iron, and other minerals. Therefore, using sweetpotato as a dietary source to combat nutrient deficiency related health problems is a key strategy, especially for smallholder and poor communities.

Twenty four candidate sweetpotato clones with improved root dry matter, β-carotene content, and fresh root yield were selected from a family of crosses constituting seven parents. Information on the nutrient contents of the newly developed OFSPs is crucial for strategic recommendation to growers, the food industry or to government or non-government scientists. Therefore, the objectives of this study were to determine the nutritional value of newly developed OFSP clones and to establish the associations between β-carotene content and micro-nutrients for targeted large scale production to alleviate nutrient deficiencies in Ethiopia.

6.2 Materials and methods

6.2.1 Study sites

Six sites with varying climatic conditions were used to undertake the study. The sites were Halaba, Kokate, Areka, Arbaminch, Hawassa and Dilla in the SNNPRS of Ethiopia. The details

of the sites are described in Chapter 4, Section 4.2.1. Across the sites sweetpotato is widely grown by smallholder farmers for food security and market.

6.2.2 Plant materials, experimental design and field establishment

The study used 25 sweetpotato genotypes: 24 were F1 clones selected recently (Chapter 4, Section 4.2.2), with one check variety currently grown in Ethiopia. Among these genotypes, 17 were OFSPs and eight were white/cream fleshed sweetpotato clones. A 5 x 5 simple lattice design was employed for the plant layout with four rows per plot of 3m for each genotype. The spacing between rows and plants was 0.60 and 0.30m, respectively. This resulted in a total of 10 plants per row and 40 plants per plot. The spacing between blocks and replications was 1m and 2m, respectively. All necessary agronomic practices were followed as per the recommendation for sweetpotato production in the study sites.

6.2.3 Data collection

Roots from the two central rows of each plot were harvested and representative samples of five medium sized roots were taken from each plot for nutritional analysis. The roots were washed with tap water, peeled, and each root was cut longitudinally into four sections. Two opposite sections of each of the sectioned roots were taken to prepare a 100 g composite sample that was placed in a transparent polythene bag and freeze-dried at -31 °C for 72 hours, following the method described by Tumwegamire et al. (2011). The freeze dried samples were kept in light proof black polythene bags and sent to the International Potato Center (CIP)-Uganda for analysis. Eight nutritional traits were analysed namely, β-carotene content (expressed in mg 100 g^{-1}), protein (expressed in %), iron (mg 100 g^{-1}), zinc (mg 100 g^{-1}), starch (%), glucose (%), fructose (%) and sucrose (%) using Near Infrared Reflectance Spectrometry (NIRS).

6.2.4 Statistical analyses

Analysis of variance

ANOVA of the data across environments was conducted using GenStat 14th edition (Payne et al., 2011) and SAS version 9.3 (SAS Institute Inc., 2003) statistical packages. The statistical models were described in Chapter 4, Section 4.2.5.

Correlation analysis

Correlation analyses were performed to describe the pattern of association between the nutritional traits. Correlation coefficients were determined using the Pearson's procedure in the SAS program (SAS Institute Inc., 2003).

6.3 Results

6.3.1 Variation in sweetpotato genotypes for nutritional traits

The combined ANOVA was conducted which indicated that environment, genotype, and genotype x environment interaction effects were highly significant ($p < 0.01$), influencing all the traits studied (Table 6.1).

The performance of the clones for the eight nutritional traits is presented in Table 6.2. The mean β-carotene content of the genotypes ranged between 0.0 and 20.01 mg 100 g^{-1}. Genotype G8 expressed the highest β-carotene content of 20.01 mg 100 g^{-1}, whilst eight genotypes, G3, G4, G9, G10, G11, G16, G18 and G23, had no β-carotene content. For protein content, the lowest mean was recorded for the genotype G12, with 5.06%. The highest protein content was recorded for the genotype G18 at 7.83%. Six genotypes, G1, G5, G8, G14, G18 and G19, had mean protein contents of > 7%. The lowest and highest mean Fe contents were found in the genotypes G4 and G8 at 1.62 and 2.55 mg 100 g^{-1}, respectively. About half of the tested genotypes had Fe content > 2.0 mg 100 g^{-1} (Table 6.2).

The lowest and the highest mean Zn content was 0.71 and 1.42 mg 100 g^{-1} for the genotypes G25 and G8, respectively (Table 6.2). Most genotypes had mean Zn content close to 1.0 mg 100 g^{-1}. The highest starch content was recorded for the genotypes G16 and G23, with 68.0 and 67.4%, respectively. Conversely, the lowest starch values were recorded for the genotypes G8 and G25 at 47.1 and 50.8%, respectively. Ten genotypes had a starch content that was > 60.0%. Genotype G15 and G25 had the highest fructose content of 5.23 and 5.1%, respectively. Six genotypes, G8, G12, G13, G15, G17 and G25, had fructose contents > 4.0%. Nine genotypes had fructose content of < 3.0% (Table 6.2).

The local check sweetpotato variety 'Tula', designated as G25, had the highest glucose content of 7.49%, while the genotype G23 had < 3.0%. About 60% of the genotypes had a glucose content of > 4.0%. Six genotypes, namely G7, G8, G15, G21, G22 and G25, had a sucrose

content exceeding 10%, with G8 producing 16.20% sucrose. The lowest sucrose content was recorded for G16 at 2.71%. Only five genotypes had sucrose content < 5.0% (Table 6.2).

Table 6.1 Combined analysis of variance of eight nutritional traits for 25 sweetpotato genotypes evaluated across six environments in Ethiopia

Source of variation	df	Traits and mean squares							
		β-carotene	Protein	Iron	Zinc	Starch	Fructose	Glucose	Sucrose
Environment (E)	5	23.07***	317.20***	12.18***	6.41***	371.08***	4.55***	22.46***	347.80***
Replication (R)	5	0.09ns	0.3n0s	0.04ns	0.01ns	6.46*	0.18ns	0.12ns	1.73ns
Block (B)	9	0.46ns	0.10ns	0.16**	0.04ns	4.67ns	0.11ns	0.13ns	0.99ns
Genotype (G)	24	489.45***	5.90***	0.64**	0.25**	271.78***	6.08***	12.60***	108.98***
G x E	120	8.61***	4.10***	0.19**	0.12**	89.27**	5.40***	11.70***	36.80***
Error	136	0.81	0.30	0.05	0.03	2.52	0.14	0.14	0.71

df = degrees of freedom; *,** and *** = significant at $p < 0.05$, $p < 0.01$ and $p < 0.001$ probability level, respectively; ns = not significant, G x E = genotype by environment interaction.

Table 6.2 Mean performance of sweetpotato genotypes for eight nutritional traits evaluated across six environments

Genotypes ID	Pedigree/Name	Traits							
		β-carotene (mg 100 g^{-1})	Protein (%)	Iron (mg 100 g^{-1})	Zinc (mg 100 g^{-1})	Starch (%)	Fructose (%)	Glucose (%)	Sucrose (%)
G1	Ukrewe x Ejumula-10	12.48	7.43	2.27	1.04	59.23	2.70	3.70	6.54
G2	Ukrewe x Ejumula-13	6.91	6.27	1.96	0.94	58.19	3.15	3.88	8.67
G3	Ukrewe x PIPI-1	0.00	5.51	1.59	0.76	64.50	3.83	4.81	3.95
G4	Ukrewe x NASPOT-1	0.00	5.52	1.62	0.86	63.19	3.36	4.23	6.54
G5	Ukrewe x Ogansagan-5	13.16	7.28	2.09	1.06	62.61	2.47	3.03	5.42
G6	Resisto x Ejumula-7	14.27	6.99	2.05	1.01	59.31	3.08	4.12	5.99
G7	Resisto x PIPI-1	13.53	6.24	1.85	0.84	57.78	3.74	4.58	12.42
G8	Resisto x PIPI-2	20.01	7.08	2.55	1.42	47.07	4.45	5.34	16.20
G9	Resisto x PIPI-4	0.00	6.84	1.84	1.01	59.03	3.70	4.16	8.81
G10	Resisto x PIPI-14	0.00	6.58	1.83	1.04	62.58	3.37	4.25	5.09
G11	Resisto x Temesgen-10	0.00	6.13	1.72	0.92	65.40	2.96	4.19	4.16
G12	Resisto x Temesgen-12	10.89	5.06	1.79	0.74	57.89	4.23	4.80	9.80
G13	Resisto x Temesgen-14	9.46	6.69	2.08	1.08	55.65	4.40	5.80	5.61
G14	Resisto x Temesgen-17	10.32	7.48	2.07	1.09	59.32	3.49	4.88	7.08
G15	Resisto x Temesgen-23	16.59	5.48	1.90	0.97	53.16	5.23	6.42	10.07
G16	Resisto x Ogansagen-5	0.00	6.44	1.81	1.00	67.95	2.04	2.62	2.71
G17	Resisto x Ogansagen-16	5.26	6.44	2.16	1.14	52.14	4.67	5.79	9.87
G18	Resisto x Ogansagen-20	0.00	7.83	2.10	1.06	64.32	2.79	3.19	4.37
G19	Resisto x Ogansagen-23	16.30	7.81	2.20	1.07	58.66	2.97	3.71	6.55
G20	Ejumula x PIPI-10	13.99	6.39	2.09	1.01	60.32	2.92	3.54	8.98
G21	Ejumula x PIPI-18	14.26	6.10	2.18	0.93	55.87	3.32	3.75	11.38
G22	Ejumula x PIPI-19	14.26	6.46	2.12	1.05	55.15	3.75	4.65	10.60
G23	Ejumula x Temesgen-15	0.00	5.73	1.64	0.87	67.37	2.58	2.74	4.67
G24	Ejumula x Ogansagen-17	11.37	6.64	2.06	1.07	60.32	2.94	3.63	5.94
G25	Tula	9.51	5.49	1.74	0.71	50.76	5.14	7.49	13.44
Mean		8.47	6.48	1.97	0.99	59.11	3.49	4.37	7.79
LSD (0.05)		0.73	0.47	0.17	0.14	1.28	0.30	0.30	0.68
CV (%)		5.50	8.90	10.97	17.27	2.69	10.78	8.59	10.81
R^2 (%)		99.20	98.03	94.06	93.14	98.33	97.82	98.99	98.98

ID = identification.

6.3.2 Relationship among nutritional traits in sweetpotato

Correlation coefficients describing pair-wise association of the eight nutritional traits of 25 sweetpotato genotypes are presented in Table 6.3. β-carotene content had significantly high positive correlation with most of the traits except with protein content and starch. It had a non-significant correlation with protein content and negative correlation (r = -0.43) with starch content. Protein content had significantly positive correlations with the mineral contents Fe and Zn, with correlation coefficients of r = 0.80 and 0.79, respectively. On the other hand, it had high negative correlations with starch and sucrose contents, with r = -0.16 and -0.27, respectively. This trait had non-significant correlations with β-carotene, fructose and glucose. Fe content had a significantly high positive correlation of r = 0.83 with Zn content. Starch content had strong and significantly negative correlations with all the studied nutritional traits. Fructose and glucose showed the highest positive correlation of r = 0.92. Fructose, glucose and sucrose had strong positive relationships.

Table 6.3 Correlation coefficients describing pair-wise association among seven nutritional traits of sweetpotato genotypes evaluated across six environments in Ethiopia

Traits	Protein	Iron	Zinc	Starch	Fructose	Glucose	Sucrose
β-carotene	0.10ns	0.27***	0.14*	-0.43***	0.12*	0.12*	0.36***
Protein		0.80***	0.79***	-0.16**	-0.11ns	-0.10ns	-0.27***
Iron			0.83***	-0.45***	0.10ns	0.11ns	-0.06ns
Zinc				-0.29***	-0.01ns	0.01ns	-0.22**
Starch					-0.70***	-0.72***	-0.66***
Fructose						0.92***	0.41***
Glucose							0.38***

*,** and *** = denote significant correlations at 0.05, 0.01 and 0.001 probability levels, respectively, ns = not significant.

6.4 Discussion

The results indicate the presence of genetic variation among the tested genotypes for the nutritional traits. The results also suggest that most sweetpotato nutritional traits are influenced by G x E interaction effects (Nasayao and Saladaga, 1988; Manrique and Hermann, 2001; Grüneberg et al., 2005; Osiru et al., 2009)

Eight out of the 25 genotypes had no β-carotene content. These genotypes had cream to white flesh colour. The remaining 17 genotypes had varying levels of β-carotene content, most of which would provide the recommended daily allowance (RDA) of vitamin A. A 100 g OFSP per day in a meal can provide more than the RDA required to prevent vitamin A deficiency (Hagenimana et al., 2001; Christina, 2007; Tanumihardjo et al., 2010). Therefore, depending upon the colour intensity of the OFSP variety used, and taking into account losses of β-carotene during cooking (approximately 20% loss through boiling), a quarter to one cup of boiled and mashed sweetpotato meets the RDA of vitamin A of a young child (Prakash, 1994; van Jaarsveld et al., 2006; Fleshman et al., 2011; Gurmu et al., 2015a) Among the tested genotypes, G8 had the highest β-carotene content (20.01 mg 100 g^{-1}) of the genotypes included in the study and therefore can be recommended as a good source of pro-vitamin A.

The protein content of the clones ranged between 5.06 and 7.83%. Similar results were reported by Tumwegamire et al. (2011) in 90 sweetpotato accessions evaluated in Uganda with protein content ranging between 5.3 and 8.4%. In the current study, the genotypes G18 and G19 had the highest protein content of 7.83 and 7.81%, respectively. About 50% of the studied genotypes had Fe content > 2.0 mg 100 g^{-1}. The genotype, G8, had the highest Fe content of 2.55 mg 100 g^{-1} and Zn content of 1.42 mg 100 g^{-1}. This genotype also had the highest β-carotene content as described above. Therefore, G8 is the best genotype that can be recommended as a breeding parent for the improvement of sweetpotato for micro-nutrient contents. However, its starch content was exceptional low and needs improvement.

Most of the white/cream fleshed sweetpotatoes had high starch content, the highest being recorded for G16 and G23 with 67.95 and 67.37%, respectively. Conversely, the OFSPs had lower starch contents. Accordingly, the lowest starch content was recorded for the OFSP genotype G8 (47.07%) which had the highest β-carotene content. This shows the presence of an inverse relationship between β-carotene and starch contents in sweetpotato. Most of the OFSPs had high fructose content. Among these, two genotypes, G15 and G25 had the

highest fructose content of 5.23 and 5.14%, respectively. In addition, four genotypes, namely G8, G12, G13 and G17, had a fructose content > 4.0%.

Genotype G25 (Tula), a locally grown check variety, had the highest glucose content of 7.49%. This variety also had the second highest fructose and sucrose contents. Sucrose content of the genotypes ranged between 3.95 and 16.20%, which is similar to the range reported by Tumwegamire et al. (2011). The authors reported sucrose content ranging between 2.5 and 15.7% for 90 sweetpotato accessions evaluated in Uganda. In the present study, the genotype G8 expressed the highest sucrose content of 16.20%. Similarly, six OFSP genotypes, namely G7, G8, G15, G21, G22 and G25, had a high sucrose content >10%.

Generally, the OFSPs had higher levels of nutritional characters than the white/cream fleshed sweetpotato clones included in the study. A similar result was reported by Aywa et al. (2013) from their study on the nutrient contents of coloured sweetpotato varieties. They reported that OFSPs contained high levels of Fe, Cu, K, vitamin A and vitamin C, confirming the value of this crop as a rich source of organic and mineral dietary nutrients. Amagloh et al. (2013) compared sweetpotato- and maize-based complementary foods and reported that the former, on average, had significantly higher maltose, sucrose, free glucose and fructose, and total dietary fibre. The authors concluded that sweetpotato-based formulations have significant advantages as complementary foods.

Usually sweetpotato cultivars with high level of sugars and low starch contents tending to reduce the viscosity, increase the solubility and convey desirable sensory characteristics. Hence, it potentially avoids the loss of excessive energy and nutrients (Amagloh et al., 2013). A study by Truong et al. (1995) on texture of sweetpotato puree indicated that OFSPs are more suited for making this product since they have a moist texture after cooking, producing purees that are viscous, but flowable, and can be handled in various processing operations. Therefore, OFSP can be recommended as a source of pro-vitamin A and as a source of other important micro-nutrients (Woolfe, 1992; Courtney et al., 2008; Grüneberg et al., 2009a; Betty et al., 2015).

Correlation analysis showed that β-carotene content had a positive association with most traits studied except protein and starch content. β-carotene content has a strong positive association with the levels of Fe and Zn. The presence of positive correlations between β-carotene content and mineral contents has also been reported by other authors, suggesting the possibility of an indirect improvement of mineral content through selection for higher β-carotene content (Grüneberg et al., 2009b; Tumwegamire et al., 2011). However, β-carotene content had a negative correlation with starch content suggesting that OFSPs have less

starch than to white fleshed sweetpotatoes, as reported by Truong et al. (1995) and Tumwegamire et al. (2011). Fe content had a high positive correlation of r = 0.83 with Zn content, implying the possibility of concurrent improvement of the two quality traits. Starch content had a strong negative correlation with all the other nutritional traits studied. As expected, a high starch content is not a characteristic of OFSPs. Higher starch content was recorded for cream fleshed sweetpotatoes. According to Woolfe (1992), white and cream fleshed sweetpotatoes usually have high starch content with 50 to 80% of dry matter, and sugar levels ranging from 5 to 15% of dry matter. The OFSPs have a lower starch content, with approximately 45 to 55% of dry matter and a higher sugar content of 10 to 20% of dry matter. Tumwegamire et al. (2011) also reported that a number of white fleshed farmer varieties had higher dry matter, higher starch, and lower sucrose contents than a OFSP variety used as a control.

6.3 Conclusions

Sweetpotato is a potential source of many of the macro- and micro-nutrients that are required by human body. In the current study, among the tested genotypes, G8 had the highest nutritional levels except for starch. The genotypes G15 and G19 were also among promising genotypes for the nutritional traits.

β-carotene content had a positive association with most of the traits studied, suggesting the potential to develop OFSP varieties enriched with important micro-nutrients that are essential for human health. The tested OFSPs are good sources of minerals such as Fe and Zn, and other nutritional traits such as protein, sucrose, glucose and fructose.

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CHAPTER 7

Thesis Overview

7.1 Introduction

Sweetpotato [*Ipomoea batatas* (L.) Lam] is among the food security crops supporting about 20 million people in the eastern, southern and south-western Ethiopia. The OFSPs are rich sources of β-carotene and therefore could play a crucial role in prevention of vitamin A deficiency (VAD) in Ethiopia. VAD leads to blindness and, death of mothers and pre-school children in many developing countries. In addition, OFSPs are a good sources of minerals such as Fe, Zn, Ca and Mg. However, due to the low RDMC of the OFSPS, they are not widely accepted and adopted by farmers. This requires development of OFSP varieties with improved RDMC for sustainable sweetpotato production and to ensure food and nutrition security in Ethiopia. A strategic breeding of OFSP clones with enhanced RDMC, β-carotene content and fresh root yield, and a good balance of micronutrients, is an overriding consideration to select best clones for further breeding and release. This chapter highlights the study objectives and summary of the core findings with respect to each objective. Moreover, it summarises the implications of the findings towards breeding for sweetpotato varieties with enhanced RDMC, β-carotene content and fresh root yield in Ethiopia.

The objectives of the study were as follows:

- To assess and document the major constraints affecting production, pre- and post-harvest handling, and farmers' preferences for sweetpotato in Ethiopia.
- To determine the combining ability, type of gene action and heritability of RDMC and β-carotene content, and yield related traits of selected sweetpotato clones, for further evaluation and breeding.
- To estimate the magnitude of G x E interactions and to select stable and high yielding candidate sweetpotato clones for root dry matter content, β-carotene content and fresh root yield, and to identify the most discriminating and representative test environments in Ethiopia.
- To assess associations between yield and yield related traits, and to identify the most efficient yield-predicting traits in sweetpotato for effective selection.

- To determine the nutritional value of newly developed OFSP clones and to establish the associations between β-carotene content and micro-nutrients for targeted large scale production to alleviate nutrient deficiencies.

7.2 Summary of the major research findings

A participatory rural appraisal (PRA) study was conducted in a total of six districts from three major sweetpotato growing administrative zones in the SNNPR of Ethiopia involving 183 farmers. The results of the study indicated that:

- Five crops: maize, enset, common bean, sweetpotato and potato were mainly grown in the study areas, and sweetpotato was the most important among root and tuber crops.
- The major pre-harvest production constraints were considered to be heat and drought at 21.6%, shortage of planting materials (20.1%), a shortage of land (15.7%), diseases (10.0%), insect pests (9.4%), a lack of draft power (8.1%) and a shortage of money to cover input costs (7.9%).
- Poor access to markets at 22.6%, poor market prices (19.1%), low yields (14.2%), low root dry matter content (13.6%), a lack of knowledge on processing (11.7%), a lack of processing equipment (11.1%) and transportation problem (7.7%) were identified as the major post-harvest constraints.
- Resistance to heat and drought at 19.6%, RDMC (16.4%), taste (14.3%), root yield (13.6%) and, resistance to disease and insect pests (13.3%) were identified as the major farmers' selection criteria for sweetpotato varieties.
- There should be a strategic breeding program to address the above problems and to develop varieties according to the farmers' criteria, which should be reinforced by the government actions to facilitate access to infrastructure, transportation, markets, credit and land.

Crosses were performed at Hawassa, Ethiopia, using seven sweetpotato parents (three orange, two yellow and two white fleshed genotypes). A total of 28 genotypes: 21 crosses resulted from a 7 x 7 half diallel mating design and 7 parents were evaluated at four locations (Hawassa, Wondogenet, Arbaminch and Dilla) in Ethiopia using a 7 x 4 alpha lattice design with two replications. The main findings of this study were:

- There was significant difference ($p < 0.01$) among genotypes across the four test environments for root dry matter, β-carotene, sweetpotato virus disease, fresh root yield and harvest index.

- The GCA and SCA mean squares were significant ($p < 0.01$) for all traits.
- The GCA to SCA variance ratios were 0.96, 0.94, 0.74, 0.96 and 0.97 for RDMC, β-carotene content, SPVD, fresh root yield and HI, respectively, indicating that the inheritance of the traits was controlled mainly by additive genes.
- The following parents were identified with good GCA effects for the three traits: Ukrewe and PIPI for RDMC; Ukrewe, Resisto and Ejumula for β-carotene content; and Resisto and NASPOT-1 for fresh root yield.
- Progenies of crosses involving Ukrewe x Ejumula, Ukrewe x PIPI, Resisto x PIPI and Ejumula x PIPI exhibited high level of positive heterosis for RDMC. Similarly, progenies of crosses including Resisto x PIPI and Resisto x Ogansagan had higher positive heterosis for fresh root yield, confirming the breeding value of these parents.
- Generally, early clones selected from cross combinations of Ukrewe x Resisto, Resisto x Ogansagan, Ejumula x PIPI and NASPOT-1 x Temesgen exhibited high RDMCs of 36.6, 37.5, 38.2 and 37.2%, and β-carotene contents of 9844.7, 10590.3, 4685.6 and 5153.4 µg 100 g^{-1}, respectively. These genotypes also had medium to high mean fresh root yields.
- Therefore, the experimental clones from these families were identified and maintained for further selection and breeding for high RDMC, β-carotene content and root yield.

A total of 24 experimental clones selected based on their SCA effects for root dry matter and β-carotene contents, and fresh root yield, along with one local check variety, were evaluated across six sweetpotato growing environments (Halaba, Kokate, Areka, Arbaminch, Hawassa and Dilla) in southern Ethiopia using a 5 x 5 simple lattice design. G x E and stability analyses were conducted using AMMI and GGE biplot methods. The results of the study indicated that:

- Environment, genotype and G x E interaction variances were significant ($p < 0.01$) for RDMC, β-carotene and fresh root yield.
- The magnitude of environment and G x E interaction effects was higher for fresh root yield at 66.8% than for RDMC (44.0%) or β-carotene content (7.6%).
- Four candidate clones, designated as G1 (Ukrewe x Ejumula-10), G6 (Resisto x Ejumula-7), G19 (Resisto x Ogansagen-23) and G20 (Ejumula x PIPI-10) with above average RDMCs of 31.82, 32.60, 33.09 and 30.06%; high β-carotene contents of 12.48, 14.27, 16.30 and 13.99 mg 100 g^{-1}; and, stable, high fresh root yields of 25.09, 26.92, 21.30 and 25.46 t ha^{-1}, respectively, were selected for finishing off and recommendation. Arbaminch was identified as the best environment for sweetpotato

testing or production in Ethiopia, providing high mean RDMC of 32.9%, a mean β-carotene of 7.2 mg 100 g^{-1} and the highest mean fresh root yield of 37.1 t ha^{-1}.

Twenty five sweetpotato clones were evaluated across six environments (Halaba, Kokate, Areka, Arbaminch, Hawassa and Dilla) using a 5 x 5 simple lattice design in the SNNPR of Ethiopia. Fifteen quantitative traits were recorded and subjected to correlation and path analysis. The results revealed that:

- Root yield was positively and significantly correlated with most traits studied, indicating that component characters should be simultaneously selected for improvement of sweetpotato.
- Path-coefficient analysis showed that individual root weight, number of roots per plant, RDMC and above ground fresh weight had high positive direct effects of 0.821, 0.776, 0.276, and 0.410, respectively, on fresh root yield.
- Vine length and root length displayed high significant positive correlation with fresh root yield, showed negative direct effect of -0.086 and -0.033, respectively. Similarly, root girth, which had a non-significant correlation with root yield, exerted the highest negative direct effect of -0.396 on fresh root yield.
- Therefore, path-coefficient analysis was a more valuable tool to identify the most influential traits than simple correlation analysis.
- Four traits: root weight, number of roots per plant, RDMC and above ground fresh weigh were the most important characters determining fresh root yield and therefore they can be used for indirect selection to improve root yield.

Seventeen OFSP and eight white/cream fleshed newly developed sweetpotato clones were evaluated across six diverse environments (Halaba, Kokate, Areka, Arbaminch, Hawassa and Dilla) in southern Ethiopia. Nutritional traits data were collected including β-carotene content, protein content, iron, zinc, starch, fructose, glucose and sucrose. Results indicated that:

- Environment, genotype, and G x E interaction effects had highly significant effect on all the parameters measured.
- The newly developed clone designated as G8 (Resisto x PIPI-2), was nutritionally superior, with the highest contents of β-carotene (20.01 mg 100 g^{-1}), protein (7.08%), iron (2.55 mg 100 g^{-1}), zinc (1.42 mg 100 g^{-1}), fructose (4.45%), glucose (5.34%) and sucrose (16.20%) followed by the genotypes G15 (Resisto x Temesgen-23) and G19 (Resisto x Ogansagen-23).

- β-carotene content showed significant positive correlations with iron, zinc, fructose, glucose and sucrose, but it had strong negative correlation with starch content ($r = -0.43$, $p < 0.001$).
- The above candidate OFSP clones (G8, G15 and G19) are good sources of vitamins and minerals such as vitamin A, iron and zinc with high levels of protein and soluble sugars including sucrose, glucose and fructose.
- These genotypes can be recommended for food processing or for breeding to develop varieties with high nutritional contents to alleviate nutrient deficiencies in Ethiopia.

7.3 Implications of findings in breeding for enhanced root dry matter and β-carotene contents, and fresh root yield.

- The participatory rural appraisal study identified heat and drought, shortage of planting materials, low root dry matter contents of the OFSPs, low root yield, sweetpotato viruses, and weevils as the major pre- and post-harvest production constraints of sweetpotato in Ethiopia. Most of the above problems can be addressed through designed breeding program. However, the other problems mentioned by the farmers such as problems related to shortage of land, poor access to markets, poor market prices, less access to agricultural inputs and transportation problems need the intervention of policy makers.
- The combining ability and heterosis study revealed that the inheritance of root dry matter, β-carotene and root yield is controlled mainly by additive genes. The following parents were considered good general combiners: Ukrewe and PIPI for RDMC; Ukrewe, Resisto and Ejumula for β-carotene content and; Resisto and NASPOT-1 for fresh root yield. The best specific combiners were selected from the crosses of Ukrewe x Resisto, Resisto x Ogansagan, Ejumula x PIPI and NASPOT-1 x Temesgen. The new families are valuable genetic resources for sweetpotato breeding for improved RDMC, β-carotene content, root yield and yield components.
- Superior and stable candidate clones, and suitable environments were identified using AMMI and GGE biplot methods. Accordingly, four candidate clones designated as G1, G6, G19 and G20 were identified as high yielding and stable genotypes for RDMC, β-carotene content and fresh root yields. Among the test environments, Arbaminch was identified as the best environment for sweetpotato testing or production in Ethiopia. Therefore, environments having similar agro-ecologies with

Arbaminch can be represented by this site for cost-effective, efficient and effective selection.

- Path-coefficient analysis showed that individual root weight, number of roots per plant, RDMC and above ground fresh weigh had high positive direct effects on fresh root yield. These traits can be used as indirect selection criteria to improve root yield.
- The candidate OFSP clones designated as G8, G15 and G19 are good sources of nutritional traits such as vitamin A, iron and zinc, protein, sucrose, glucose and fructose. These genotypes can be recommended for large-scale production, food processing or sweetpotato improvement to alleviate nutrient deficiencies in Ethiopia.

In summary, the present study assessed the major sweetpotato production constraints, developed novel sweetpotato families with high combining ability and heterosis for RDMC, β-carotene content and fresh root yield. Four traits including individual root weight, number of roots per plant, RDMC and above ground fresh weight were identified for indirect selection to improve root yield. Finally, the study found that the newly developed candidate OFSP clones are good sources of vitamins and minerals such as vitamin A, iron and zinc with high levels of protein and soluble sugars including sucrose, glucose and fructose.