DEVELOPMENT OF END-USER PREFERRED SWEETPOTATO VARIETIES IN GHANA

BY

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DECLARATION

I hereby declare that except for references to works of other researchers, which have been duly cited, this work is my original research and that neither part nor whole has been presented elsewhere for the award of a degree.

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ABSTRACT

Studies were undertaken to identify the constraints to increase sweetpotato utilization in Ghana and to develop end-user preferred varieties that would increase utilization in Ghana and beyond. A survey was conducted using Focus Group Discussion (FGD) followed by administration of Semi-Structured Questionnaire. This was done in some selected communities in Ghana where sweetpotato is popular in February 2012. Sweetpotato germplasm was also collected from farmers' field in these areas, and from National Agricultural Research Stations of Ghana as well as the International Potato Centre (CIP) research station at Fumesua, Ghana in 2010. The germplasm was evaluated at two locations in the major and minor cropping seasons in 2011 for beta-carotene, dry matter and sugar contents as well as other agronomic and quality traits. Crosses among four genotypes, two with low sugar, high dry matter, low beta-carotene contents, and the other two with high sugar, low dry matter and high beta-carotene contents, were made to determine gene action influencing these three traits and other quality traits from 2012 to 2013. Four superior genotypes with low sugar content and five with high beta-carotene content were selected as parents for the development of low sugar and high beta-carotene populations, respectively, from 2012 to 2013. The survey showed that consumers in Ghana desire non-sweet, high dry matter sweetpotatoes with low or moderate beta-carotene content. Agro-morphological and physico-chemical descriptors revealed high variation among the sweetpotato accessions and it was confirmed by the SSR markers. Much of the genetic variation identified among the sweetpotato genotypes was additive in nature. Sufficient useful genetic variation was present in the germplasm and was exploited for improvement on beta-carotene, dry matter and sugar contents. There was significant heterosis for beta-carotene, dry matter and sugar contents. Fifteen percent of the low sugar population developed had sugar content less than 12% (non-sweet staple types) whilst the remaining 85% had sugar content of 12 – 20% (low sugar).

Fourteen percent of the high beta-carotene population developed were low sugar (12 – 20%) genotypes. Seven non-sweet (preferred staple types) hybrids, 30 low sugar hybrids, 16 high beta-carotene and moderate dry matter content hybrids, and 18 high yielding hybrids were identified. There is a high potential for identifying hybrids that combine all the preferred traits and so further testing needs to be done multi-locational for potential release to farmers.

DEDICATION

To Esther my dear wife, our lovely children Adwoah, Kwabee and Nana Yaw, and to my inspiring sister Kate and niece Amono. Thank you all for everything.

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LIST OF ABBREVIATIONS

AEA = Agricultural Extension Agent

AFLP = Amplified Fragment Length Polymorphism

AGRA = Alliance for a Green Revolution in Africa

AVRDC = Asian Vegetable Research and Development Centre

CIP = International Potato Centre

CRI = Crops Research Institute

CSIR= Council for Scientific and Industrial Research

DNA = Deoxyribonucleic Acid

FAO = Food and Agriculture Organization of the United Nations

FGD = Focus Group Discussion

HPLC = High Performance Liquid Chromatography

IBPGR = International Board for Plant Genetic Resources

ICRISAT = International Crops Research Institute for the Semi-Arid Tropics

IRRI = International Rice Research Institute

METASIP = Medium Term Agriculture Sector Investment Plan

MoFA = Ministry for Food and Agriculture

NIRS = Near-infrared Reflectance Spectroscopy

PRA = Participatory Rural Appraisal

SAS = Statistical Analysis System

SPSS =Statistical Package for the Social Sciences

SSR = Simple Sequence Repeat

SSQ = Semi-Structured Questionnaire

CHAPTER ONE

1.0 GENERAL INTRODUCTION

1.1 Introduction

Sweetpotato (*Ipomoea balatas* (L) Lam) is a dicotyledonous plant of the botanical family Convolvulaceae, which consists of 55 genera and over 1000 species (Watson and Dallwitz, 2000). In this family, only *Ipomoea batatas* is of economic importance as a source of food (Woolfe, 1992; Onwueme and Charles, 1994). Sweetpotato is one of the most important root crops in the world with more than 133 million tonnes produced worldwide annually (Joel *et al.*, 2011). It is a major staple crop, particularly in numerous tropical countries (Lebot, 2009). The crop is rich in dietary fibre, minerals, vitamins and antioxidants such as phenolic acid, anthocyanins, tocophenols and beta-carotene (Ray and Tomlins, 2010). It has tremendous flexibility of utilization as food, feed for livestock and industrial raw material for various products. Its importance as a health food is recognized in terms of high nutritive content with its anti-carcinogenic and cardiovascular disease-preventing properties (Hill *et al.*, 1992). Sweetpotato storage roots and leaves are good sources of antioxidants (Teow *et al.*, 2007), fibre, zinc, potassium, sodium, manganese, calcium, magnesium, iron, vitamin C (Antia *et al.*, 2006), and vitamin A (Woolfe, 1992). Despite its name "sweet", it may be a good food for diabetics as it helps to stabilize blood sugar levels and lower insulin resistance (Kusano and Abe, 2000; Ray and Tomlins, 2010).

Sweetpotato is a crop with great potential for Ghana as a food security and income generation crop, as well as, raw material for industry. The crop has proven in Ghana to have versatility to be used in various food preparations in place of rice, cassava, yam, plantain and other well-

integrated staples (Adu-Kwarteng *et al.*, 2001; Ellis *et al.*, 2001; Meludu *et al.*, 2003; Zuraida, 2003). In spite of its great potential to alleviate food insecurity, malnutrition and poverty, it has remained an untapped resource in Ghana. It is currently not well integrated into the average Ghanaian diet as its level of utilization is very low as compared to the other root and tuber crops (Adu-Kwarteng *et al.*, 2002). This is because, it is uncommon to find sweetpotato being served in Ghanaian restaurants, workers canteens, and schools (Sam and Dapaah, 2009). In addition to flavour which is a primary determinant in consumer acceptance (Kays *et al.*, 1999), storage root yield, root morphology, sugar content, dry matter content, beta-carotene content, and resistance to diseases and pests are the major end-user traits mainly required. Consumers in Ghana prefer sweetpotatoes with dry mealy flesh, low sugar content, and high nutritive value (Sam and Dapaah, 2009). However, locally available clones have very sweet taste, which limits their consumption as a staple food (Missah and Kissiedu, 1994). Recently introduced orange-flesh sweetpotatoes, which possess the vitamin A precursor to combat vitamin A deficiency at relatively cheaper cost, have low dry matter content. High dry matter is one of the important attributes that affects consumer preferences in most of Sub-Saharan Africa (Tumwegamire *et al.*, 2004). These factors may have led to the very low adoption rate of the thirteen improved varieties released in Ghana. These cultivars either have low dry matter content and/or sweet taste (non-bland pleasant taste) which need to be improved. Improvement on these traits will make sweetpotato attain increased status as a food security, health, income generating and industrial crop in Ghana.

National Agricultural Research Systems (NARS) over the years have solely depended on introductions of elite clones without adequate adjustment of breeding objectives, and selection procedures to cater for stakeholders' need for non-sweet, high dry matter and high

beta-carotene contents of sweetpotato storage roots. Even though it is an under-exploited crop based on its breeding initiatives (Rees *et al.*, 2003), studies conducted elsewhere have shown that substantial variation in flavour and sweetness exist in its gene pool (Mclaurin and Kays, 1992; Morrison *et al.*, 1993). Similarly, significant variation can be found for dry matter and beta-carotene contents. However, breeding programmes in Ghana for decades have not exploited this diversity. Therefore, there is the need to exploit both local and exotic germplasm to develop non-sweet (staple type), high dry matter sweetpotatoes in Ghana. This is because the need to identify and incorporate local genotypes with desirable traits in breeding programmes has long been recognized (Rees *et al.*, 2003). Preferences for sweetpotato are known to vary with ethnic background and geographic location (Kays and Horvat, 1983). Hence, in meeting the quality needs, it is also important to consider farmers' and/or consumers' opinion when developing and selecting sweetpotato varieties. This is addressed through participatory plant breeding, participatory variety selection (Gibson *et al.*, 2007; Gasura *et al.*, 2008), and/or participatory rural appraisal.

The objectives of this study were to:

a) Ascertain stakeholders' knowledge, perceptions, and preferences on sweetpotato end-user-traits in Ghana.

b) Assess genetic variation of sweetpotato genotypes in Ghana using agro-morphological, physico-chemical and SSR markers.

c) Assess self- and cross-compatibility among sweetpotato genotypes.

d) Determine the gene action involved in the control of beta-carotene, dry matter and sugar contents of storage roots.

e) Determine level of heterosis for beta-carotene, dry matter and sugar contents of sweetpotato storage roots.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Botany, Origin, Distribution and Evolution of sweetpotato

2.1.1 Botany

The genus *Ipomoea* to which sweetpotato belongs also contains several garden flowers called morning glories. Sweetpotato is a herbaceous perennial vine predominantly bearing alternate heart-shaped or palmately lobed leaves and medium-sized sympetalous flowers. It is grown from vines or underground storage roots. The leaves and flowers are variable in shape, size and colour. The storage roots also vary enormously in taste, size, shape, and texture, although all are smooth-skinned. Its flesh can be white, orange, yellow, reddish or purple (Lebot, 2010). The skin colour also varies from yellow, red, orange, to brown. Varieties with pale yellow- or white-flesh are less sweet and moist than those with orange-flesh. The former also have little or no beta-carotene and higher levels of dry matter, and therefore, their textures are drier and mealier and they stay firmer when cooked. The orange-flesh types are particularly high in beta-carotene, the vitamin A precursor. In developed countries, where the crop is used more as a vegetable or in sweet dishes, the red- or orange-flesh types are preferred because of their moist flesh and sweet flavour. The edible storage roots develop to form usually four to ten storage roots per plant (Thottappilly, 2009).

According to Lebot (2010), from a marketing point of view, there are three broad groups of cultivars. These are those intended for processing (traditional or industrial) which are often very high in dry matter and starch content and have a white flesh; those for the fresh (table) roots market for daily consumption in developing countries, with high dry matter content and

low sugars; those for the US market, the "moist" North American types of cultivars, which have low dry matter content, high sugar and high beta-carotene contents. The quality standards are not the same for the three groups. In the United States, varieties are classified into dry-flesh and moist-flesh and surprisingly this classification is not based on the moisture content of the root but rather on the characteristics of the solids in cooked roots (Smith *et al.*, 2009). Moist-flesh varieties convert starch into sugars more efficiently when cooked and are sweeter than the dry-flesh varieties. The moist-flesh types are incorrectly referred to in the US as "yams"(Carpena, 2009).

2.1.2 Origin

Sweetpotato is native to the tropical parts of South America and was domesticated over 5000 years ago (CIP, 2000; Pickersgill, 2007; Roullier *et al.*, 2013b). According to Roullier *et al.* (2013b), the botanical origin of sweetpotato, the timing and geographic location(s) of its domestication remain unclear. This is because on one hand, its center of origin is between the Yucatán Peninsula of Mexico and the mouth of the Orinoco River in Venezuela (Austin, 1988; Zhang *et al.*, 1998). Zhang et al. (1998), on the other hand, considered the much lower diversity found in Peru–Ecuador as secondary center of diversity. Using molecular markers (Huang and Sun, 2000), and (Zhang *et al.*, 2001) found the highest diversity in Central America supporting (Austin, 1988), and reemphasising (Zhang *et al.*, 1998). According to Roullier *et al.* (2013b), wild tuber bearing populations of sweetpotato may have been domesticated independently in South America and the Caribbean/Central America, two gene pools that have secondarily come into contact along human movements.

Sweetpotato was grown in Polynesia before western exploration and current thinking is that it was brought to Central Polynesia possibly by Polynesians who had traveled to South America and back and it was spread across Polynesia to Hawaii and New Zealand (Van Tilburg, 1994). It is possible however, that South Americans brought it to the Pacific. The theory that the plant could have spread by floating seeds across the ocean is not supported by evidence because cultivated *Ipomoea batatas* in Polynesia is generally spread by vine cuttings and not seeds (Botgard, 2010). Other secondary centres of genetic diversity where the crop evolved separately from its American ancestors have also been reported. These include Papua New Guinea, and other parts of Asia (CIP, 2000), and East Africa (Tumwegamire *et al.*, 2011), where many types of sweetpotato can be found and are genetically distinct from those found in the American area of origin. This may largely explain why inhabitants of the Pacific islands today and East Africans are among the largest per capita consumers of sweetpotato in the world.

2.1.3 Distribution

Sweetpotato was widely cultivated throughout Central and South America before the first European contact. Its introduction to the Pacific Islands apparently occurred in prehistoric times (Yen, 1982). It was introduced into Europe in 1492 by Columbus, and the Portuguese explorers of the 16th century took it to Africa, India, Southeast Asia and East Indies (Loebenstein, 2009; Lebot, 2010). Spanish ships brought it from Mexico to the Philippines in the 16th century. By the mid-nineteenth century, the crop was grown from Zanzibar to Egypt in Africa (Lebot, 2010). Because of its hardy nature and broad adaptability, and because its planting material can be rapidly multiplied from very few roots, it spread through Asia, Africa, and Latin America during the 17th and 18th centuries. Sweetpotato is now grown in

more developing countries than any other root crop (CIP, 2000). The crop has been widely grown in the Gold Coast (now Ghana) during the latter part of the seventeenth century (Doku, 1984), and it is currently the number four root crop produced in Ghana after cassava, yam, and cocoyam.

2.1.4 Evolution

Sweetpotato is a member of the Genus *Ipomoea* and section Batatas, and is the only hexaploid (6x = 90) in the section (Firon *et al.*, 2009). *I. batatas*, a 'cultigen', is not found in the wild and no direct ancestor has been positively identified (Woolfe, 1992). However, the section Batatas continues to undergo revision and contains about 12 other species, most of which are diploid (2n = 30), with a few tetraploids (4x = 60) collected in the wild (Bohac *et al.*, 1993). There is a hypothesis that *Ipomoea trifida* and wild Mexican tetraploids are putative ancestors of the cultivated sweetpotato (Jarret *et al.*, 1992). This is because several sections of Batatas species (*I. batatas var apiculata*) found in Mexico were established to have putative linkages to domesticated sweetpotato (Mcdonald and Austin, 1990). Genetic studies found Mesoamerica (Guatemela, Mexico, Nicaragua, Panama, and El Salvador) to possess the most allelic diversity, hence justifying consideration as the primary source of genetic diversity in sweetpotato (Zhang *et al.*, 2001). Species in the section *Batatas* contain unreduced gametes which could results in hexaploid development (Bohac and Austin, 1994). But, according to Firon et al. (2009), the derivation of the hexaploid sweetpotato remains unknown. A number of authors have put forward different theories to explain the evolution of *I. batatas.* Some consider it an autopolyploid derivative of *I. trifida* (Shiotani, 1988), but, others favour an allopolyploid origin involving *I. trifida* and an unidentified tetraploid parent (Foulkes *et al.*, 1978). Tetrasomic segregation patterns in SSR primers was found to be

consistent with an allopolyploid origin (Buteler *et al.*, 1999). Tetrasomic patterns of inheritance in sweetpotato were also observed by Zhang *et al.* (2000). The most compelling evidence for the origin of an allopolyploid was based on cytological data (Magoon *et al.*, 1970). The meiotic patterns of various pairing configurations among the chromosomes show duplicates, triplicates and quadrivalents suggesting that *I. batatas* consists of two related and a third more distant genome (Firon et al., 2009). However, using a broad sample of cultivated sweetpotatoes and its diploid and polyploid wild relatives, for noncoding chloroplast and nuclear intergenic spacer (ITS) sequences, and nuclear SSRs, Roullier *et al.* (2013a), did not support an allopolyploid origin for *I. batatas*. According to the authors, *I. trifida* and *I. batatas* are closely related although they do not share haplotypes. They therefore, supported an autopolyploid origin of sweetpotato from the ancestor it shares with *I. trifida*, which might be similar to currently observed tetraploid wild *Ipomoea* accessions.

Autopolyploidy (genome duplication with a single progenitor species) has been distinguished from allopolyploidy (hybridization and genome doubling of highly divergent parental species) (Otto, 2007). However, there is a continuum between the two (Roullier *et al.*, 2013a). Autopolyploid complexes often have multiple independent origins, sometimes involving crosses between the same species as another organism (conspecific), but still substantially differentiated populations (Parisod *et al.*, 2010). Also polyploidization often triggers genomic re-patterning and gene expression changes (Otto, 2007), which could explain the sudden appearance of new phenotypes that diverge from those of their diploid parents in numerous traits (Roullier *et al.*, 2013a). Although these genetic changes are probably more rapid and extensive in allopolyploids, they may also affect autopolyploids

over the longer term (Parisod *et al.*, 2010). Furthermore, polyploids may be reproductively isolated from their parents, and often can adapt to new ecological niches (Otto, 2007).

2.2. Uses of Sweetpotato

In developing countries, sweetpotato is ranked fifth in economic value, sixth in dry matter production, seventh in energy production, and ninth in protein production (Gregory, 1992). It has tremendous flexibility for utilization as food, feed for livestock and industrial raw material for various products such as starch, flour, glucose and alcohol. It is important as a health food because of its high nutritive content with its anti-carcinogenic and cardiovascular disease-preventing properties (Hill *et al.*, 1992; Chen *et al.*, 2003; Aina *et al.*, 2009).

2.2.1. Human Food

The potential of sweetpotato in food security and global well-being has been well recognized (Van Hal, 2000). It is a staple food for millions of people and the seventh most abundant crop globally after wheat, rice, maize, potato, barley, and cassava (Bouvelle-Benjamin, 2007). Sweetpotato produces more biomass and nutrients per hectare than any other food crop in the world (Loebenstein, 2009). They are nutritious, low in fat and protein, but rich in carbohydrates (Betty, 2010). The sweetpotato is a versatile plant offering various products and diverse uses ranging from consumption of fresh leaves or roots to processing into starch, flour, noodles, natural colorants, candy and alcohol (Lebot, 2010). The storage roots can be boiled, steamed, baked, fried, or roasted. It can also be canned or dried and made into flour and noodles. It is used in sweet dishes such as puddings, cakes, biscuits, pies, and desserts. In the United States, sweetpotatoes are best known for their use in pies and as a candied

vegetable. The smaller storage roots are canned. Storage roots of good size are sold fresh and any that are too large are generally processed into baby food. Sweetpotatoes are also a traditional accompaniment to “Thanksgiving dinner” and often appear on the menu at other festival times, such as Christmas and Easter (Thottappilly, 2009). The pale varieties can be substituted for regular potatoes in most recipes.

Sweetpotato is the number one food crop in Papua New Guinea, where it is estimated that about 5000 cultivars are grown, but varieties with low moisture content are preferred (Bourke, 2006). In Indonesia, sweetpotato is utilized mainly as food whereas in Vietnam, it is used both for food and as animal feed (Carpena, 2009). Most of the sweetpotatoes (50%) produced in Japan are used as food (Komaki and Yamakawa, 2006). In Brazil, it is the fourth most consumed vegetable. It is a food of high energy value and is rich in carbohydrates (Loebenstein, 2009). The greens of the crop are edible and provide an important source of food in Africa, especially in Guinea, Sierra Leone and Liberia, as well as in East Asia (Scott *et al.*, 2000a; Scott *et al.*, 2000b). Across East Africa’s semi-arid densely populated plains, thousands of villages depend on sweetpotato for food security. it has become the staple of communities living in the highlands of Uganda, Rwanda, and Burundi (Lebot, 2010). Dried pieces of sweetpotatoes are also ground into flour, which when rehydrated is eaten as quick porridge known as *atapa* in Uganda (Thottappilly, 2009). In the densely populated, semi-arid plains of Eastern Africa, sweet potato is called *cilera abana*, "protector of the children". This title alludes to the vital role it fulfils in thousands of villages, where people depend on the crop to combat hunger (Baafi *et al.*, 2011).

Sweetpotato has a long and unique history of saving lives in relief famine and for providing food security. Because of its relatively early maturity and its nutrient rich content, it is often the first crop planted after a natural disaster, providing abundant food for otherwise starving populations (Thottappilly, 2009). Sweetpotato was an important staple food during the American Revolutionary and Civil Wars. It was also an important part of the diet of the slave population in the Southern States. The National Aeronautics and Space Administration (NASA) of the United States of America also included sweetpotato as a food for long term space missions because of its nutrition and versatility (Hill *et al.*, 1992). In the year 1994, when a huge area of crops was destroyed resulting in famine, the governor of Fujian ordered farmers to grow sweetpotatoes extensively, in order to starve off famine (Zhang *et al.*, 2009). The Japanese also used it when typhoons demolished their rice fields (Thottappilly, 2009).

2.2.2. Animal Feed

All parts of the sweetpotato are used as animal feed (CGIAR, 2005; Thottappilly, 2009). Nearly half of the sweetpotatoes produced in Asia are used for animal feed (CGIAR, 2005). For example, 70% of sweetpotato output in China goes to animal feed, principally to pigs (Bottema, 1992). Sweetpotato production in Vietnam also goes primarily with pig production. In addition to China and Vietnam, sweetpotato-pig systems play an important role in the rural economy of many parts of Asia. This includes the Philippines, India, Korea, Taiwan, some eastern islands of Indonesia (Bali and Irian Jaya), and Papua New Guinea. This is also practiced, to a lesser extent, in Latin America and Africa (Scott, 1991). Sweetpotato is also used as livestock feed in the southern US (Huntrods, 2008). On the coast of Peru, where desert conditions restrict agriculture to irrigated valleys with little or no pasture land, sweetpotato foliage is the major source of animal feed (Woolfe, 1992). There, cultivars are

selected by farmers for two qualities: good root production and abundant foliage. According to Lin *et al.* (1985), the crop also plays an important role in animal production in Japan.

Economic considerations in feeding beef cattle with sweetpotatoes revealed that 12% of the storage roots which had no commercial value could be used together with the forage to produce a profit of 38%, thus providing a new alternative feed for the livestock producer (Backer *et al.*, 1980). The chemical composition of the sweetpotato forage shows dry matter contents of 12 - 17% and dry matter digestibility of greater than 70% (Foulkes *et al.*, 1978). Replacing traditional energy sources such as maize with dried storage roots of sweetpotato for beef production in the temperate zones produced weight gains of up to 1 kg/head/day (Darlow *et al.*, 1950). Increases in vitamin A content in milk and increased milk production of up to 0.79 kg/cow/day was also recorded when sweetpotato storage roots were fed to dairy cattle (Massey *et al.*, 1976).

2.2.3. Industrial Uses

In third world countries sweetpotatoes are processed into starch, noodles, candy, desserts, and flour, which allow the farm household to extend the availability of the crop. In some countries storage roots are processed to produce starch and fermented to make alcohol (Thottappilly, 2009). In China, for example, sweetpotato starch production has become an important cottage industry. Also sweetpotatoes are sliced and dried in Uganda to increase keeping quality up to five months and can be ground into flour. The cooked mashed sweetpotatoes are also used to replace some of the wheat flour in breads, cakes, muffins, and cookies. In Japan, 20% of sweetpotatoes produced are used for starch production (Katatayama *et al.*, 2006). The juice of red sweetpotatoes is combined with lime juice in

South America to make a dye for cloth; and every shade from pink through purple to black can be obtained (Verrill, 1937).

2.3.4. Health Benefits

The crop is rich in carbohydrates, vitamins, minerals, dietary fibre, and antioxidants such as phenolic acids, anthocyanins, tocopherol and beta-carotene (Ravindran *et al.*, 1995; Liu *et al.*, 2010; Ramesh *et al.*, 2012). Sweetpotatoes were selected as one of the foods tested for long-term space travel because of their nutritional qualities (Wilson *et al.*, 1998). Besides simple starches, sweetpotatoes are rich in complex carbohydrates, dietary fiber, beta carotene, vitamin C, B_2, B_6 and E, potassium, copper, manganese and iron, and they are low in fat and cholesterol (Miranda, 2002; CGIAR, 2005; Thottappilly, 2009). The yellow-and orange-flesh types are excellent sources of vitamin A. These sweetpotatoes are being used in a number of African countries to combat the widespread Vitamin A deficiency that results in blindness and even death of 250,000-500,000 African children a year (CGIAR, 2005). Both beta-carotene and vitamin C are very powerful antioxidants that work in the body to eliminate free radicals. Free radicals are chemicals that damage cells and cell membranes and are associated with the development of conditions like atherosclerosis, heart disease and colon cancer. The white-skinned sweetpotato is also used as a traditional medicine in Minas Gerais, Brazil (Noda *et al.*, 1992). It is high in carbohydrates and can produce more edible energy per hectare per day than wheat, rice or cassava (CGIAR, 2005). Sweetpotato anthocyanins could scavenge free radicals (Saigusa *et al.*, 2005), attenuate liver dysfunction (Han *et al.*, 2007), enhance memory function (Wu *et al.*, 2008), decrease blood sugar (Ray and Tomlins, 2010), lower insulin resistance (Kusano and Abe, 2000), and inhibit cancer cell growth (Hayashi *et al.*, 2003; Wang *et al.*, 2006).

The roots and leaves are used in folk remedies to treat illnesses as diverse as asthma, night blindness, and diarrhoea. Also because they digest easily, they are good for eliminative system, and also bind heavy metals to detoxify the system (Thottappilly, 2009). According to the author, a patent has been granted for the production of bread from 100 percent sweetpotato flour in the United States that will appeal to consumers who are allergic to grain breads and flours. Also scientists in the USA have developed genetically modified sweetpotatoes containing edible vaccines. One of the vaccines works against hepatitis B and the other against the Norwalk virus found in food that has not been stored correctly. Edible vaccines such as these may provide cheap protection for some of the poorest people in the world.

2.3. End-User Traits of Sweetpotato

Many sweetpotato clones are maintained by the gene bank of various National Agricultural Research Systems (NARS) all over the world but, only a few clones dominate major producing areas in producing countries. This is because the choice of clone to grow depends on anticipated utilization. The choice of varieties to grow appears to depend largely on whether the roots are used as food either directly or in processed form as food component, or as sources of industrial starch (Carpena, 2009). The preferences seem to vary among and even within countries. For example, the North American market prefers high sugar, orange flesh dessert types while low sugar types generally predominate in the tropics (La Bonte and Picha, 2000). Currently in Ghana, the indispensable user traits in addition to storage root yield, earliness, and disease and pest tolerance are low sugar content/staple type (bland pleasant taste), high beta-carotene content, and high dry matter content.

2.3.1. Beta-Carotene Content

Beta-carotene is a constituent of the carotenoid pigments which are responsible for the cream, yellow or orange flesh colouration of sweetpotato storage roots. Carotenoids are a group of more than 700 phytochemicals with a broad range of structures and polarities (Sherry *et al.*, 2010). About 50 carotenoids can cleave to vitamin A, but only three represent major sources in human diet. These are β-carotene, α-carotene, and β-cryptoxathin. The depth of sweetpotatoes storage root flesh colour is largely a function of the concentration of beta-carotene (Woolfe, 1992). Hence, the yellow- and orange-flesh sweetpotatoes have higher amount of beta-carotene (pro-vitamin A). The storage root pigmentation in addition to its health benefit as source of vitamin A, may be exploited in sweetpotatoes to introduce attractive colour into foods to which they are added. White-fleshed cultivars contain no beta-carotene (Bradbury and Holloway, 1988). Cultivars with cream or light yellow flesh also may contain traces of beta-carotene (Garcia *et al.*, 1970).

Though sources of provitamin A carotenoids are plentiful in the world, vitamin A deficiency (VAD) affects over 250 million people globally and is one of the most prevalent nutritional deficiencies in developing countries, resulting in growth, vision, reproduction, and immunity impairments (WHO, 1995). Although the problem of vitamin A deficiency has to be tackled by multiple means, one approach is to encourage the production and consumption of foods rich in provitamin A, such as yellow- or orange-fleshed sweetpotatoes (Woolfe, 1992). However, according to Thottappilly (2009), even though it has been shown that even small amounts of these varieties as a regular part of the diet will eliminate vitamin A deficiency in adults and children, African countries have traditionally grown white-fleshed sweetpotatoes, which are low in vitamin A. This is because, traditionally, the provitamin A varieties usually

don't meet the food preparation standards of African countries due to their low dry matter content and relatively high sugar levels. Because of this, Woolfe (1992), proposed that a goal which should be pursued by plant breeders is selection of varieties with a moderately dry mouthful, high satiety value, a bland pleasant taste, and containing provitamin A carotenoids in sufficient quantities to contribute significantly to dietary requirements. The author encouraged breeders that, in spite of the reported significant negative correlation between sugar and dry matter contents, coupled with strong positive correlation between sugar and beta-carotene in sweetpotatoes, it is possible to develop a low-sugar, high dry matter sweetpotato which still retains a satisfactory level of beta-carotene.

2.3.2. Dry Matter Content

Dry matter content of the storage root is the remaining part of the edible root after its water has been completely drained away. Carbohydrates constitute most of the dry matter in sweetpotatoes (Picha, 1987). These carbohydrates exist in the form of starch, sugar and non-starch polysaccharides. Starch is quantitatively the most important component of sweetpotato storage root dry matter (Woolfe, 1992). This is because compounds produced as a result of photosynthesis in the leaves are translocated to the fleshy roots and eventually transformed into starch. On the average, starch constitutes 60 - 70% of dry matter (Woolfe, 1992). Sweetpotato starch granules are made up of amylopectin and amylose molecules in variable ratio but generally in 3:1 or 4:1. These ratios affect the mealiness of the roots since low amylose: high amylopectin ratio has been linked to the 'moist', sticky texture of roots when cooked. Amylopectin is a large, highly branched polymer of alpha-1, 4-linked glucose chains branching through alpha-1, 6-glucose links. The amylose molecule is a smaller, unbranched straight-chained polymer with its glucose subunits joined by alpha-1, 4-links.

The compounds classified together as non-starch polysaccharides include the pectic substances, hemicelluloses and cellulose, which are found in the middle lamella (Woolfe, 1992). These are also referred to as dietary fibre, and play an essential role in the nutritional value of sweetpotatoes. In addition to their contribution to dietary fibre, the pectic constituents play a key role in textural attributes in the utilization of the storage root. These include firmness, moistness or dryness. However, most sweetpotato varieties currently cultivated in Sub-Saharan Africa have a dry matter (DM) content that is too low (25-30%) to be used as raw material in the processing industry, which prefers DM >35% (Lu and Sheng, 1990). Among the root and tuber crops, dry matter content has been used extensively as a selection index for traits such as starch content and cooking quality. According to Woolfe (1992), a highly significant positive correlation (r=0.926) was found between dry matter content and starch content for Taiwanese sweetpotato cultivars, indicating that the dry matter content of storage roots can be used to evaluate their starch content. This makes the determination of dry matter content indispensable in sweetpotato breeding.

2.3.3. Sugar Content (Taste)

Sugars and organic acids are the primary contributors to the taste in the sweetpotato (Kays *et al.*, 1999). The high levels of sweetness and strong flavour associated with many cultivars of sweetpotatoes may have reduced its popularity as a staple food, and made it difficult to combine with other foods in a variety of dishes (Woolfe, 1992). These factors have reduced the esteem of sweetpotato in the eyes of the consumer. Variability in sugars among varieties of sweetpotato is very high and has been recorded as high as 38.3% of dry matter in American cultivars (Lebot, 2010). According to the author, although not thoroughly been

investigated, the hundreds of cultivars found in Papua New Guinea and Island Melanesia, are low in sugars, allowing an important daily consumption. A local variety of Vanuatu presents total sugar content as low as 1.49% of dry matter (Lebot *et al.*, 2009). The major sugars occurring in raw storage roots are sucrose, glucose and fructose (Woolfe, 1992). However, low concentrations of maltose in raw storage roots have been reported (Truong *et al.*, 1986; Bradbury and Holloway, 1988). Sugars that are present in the uncooked roots (principally sucrose, fructose, and glucose) and maltose, which is formed during baking, are responsible for the sweetness (Kays *et al.*, 2001). The concentration of maltose increases significantly during cooking due to starch hydrolysis (Woolfe, 1992). According to Truong et al. (1986), for cultivars analysed raw, the concentration of sucrose exceeded the other sugars. In some cultivars the concentration of glucose is higher than that of fructose; in others they are present in approximately equal amounts (Woolfe, 1992). The amount of oligosaccharides including raffinose, stachyose and verbascose in the sweetpotatoes has also been studied in relation to their perceived effect of flatulence. For example, small amounts of raffinose apparently found in raw Filipino and American samples using High Performance Liquid Chromatography (HPLC) analysis (Truong *et al.*, 1986) were largely accounted for as maltotriose with no stachyose or verbascose detected.

The sweetpotato contains many enzyme systems, which catalyse individual synthetic and degradative processes within the tissues (Woolfe, 1992). The most important enzymes from a viewpoint of quality in both cooked and processed roots are the amylases (alpha- and beta-amylases), originally known as diastase. These enzymes hydrolyse starch to shorter chain molecules. Freshly harvested sweetpotatoes contain relatively little alpha-amylase, but the level increases greatly during storage, unlike beta-amylase which initially has higher

concentration but changes little and erratically during storage. Baking converted more starch to sugars than boiling, but boiled roots were higher in percent total sugars, starch, hemicellulose, and cellulose, and lower in water soluble pectins (Sistrunk, 1977). According to Kays *et al.* (2001), very low levels of endogenous sugars and extremely low activity of the amylase system, accounts for the exceptionally low hydrolysis of starch to maltose during cooking.

2.3.4. Laboratory Determination of Beta-carotene and Sugar Content

Reliable High performance Liquid Chromatography (HPLC) procedures for quantitative analysis of sugars in raw and baked sweetpotatoes (Picha, 1985) have been developed. Other methods that have been used for sugar determination include refractive index (Walter, 1992) and near infrared transmittance (Lu and Sheng, 1990; Katayama *et al.*, 1996). Also Bushway (1986) and Simonne *et al.* (1993) used HPLC for determination of beta-carotene content. Due to the tedious nature of the HPLC methodology, a quicker method that links beta-carotene content and the intensity of the orange flesh colour of the sweetpotato was developed (Takahata *et al.*, 1993). In recent years, significant advances have been made in the precision of quantitative measurements for individual sugars and beta-carotene in the sweetpotatoes. These include the Nuclear magnetic resonance (NMR) spectroscopy, and the use of Near-infrared reflectance Spectroscopy (NIRS).

Chemical analysis costs are so high that unless a simple screening tool is available, it is difficult to include the root quality traits for routine screening (Lebot, 2010). Major storage root quality traits can now be quantified using NIRS (Lebot *et al.*, 2009), and this technique

is used by the International Potato Centre (CIP) and other scientists in sweetpotato breeding. This is because sweetpotato improvement requires the analysis of several thousand samples each year through screening and evaluation and, fewer samples can be analysed per day by a chemical method such as HPLC (8-10 samples for ß-carotene per day). There are also associated problems with chemical waste disposal and high cost of chemical analysis. The NIRS is a technique based on correlations between chemical properties, as determined by defined reference methods, and absorption of energy at different wavelengths in the near infrared region of the electromagnetic spectrum. Thus, the absorption of energy (near-infrared light) by different molecules is measured. In the near-infrared wavelength area, C-H, C-O, N-H and O-H bonds absorb specific energy. The absorbed energy produces spectra which are interpreted to produce results on a computer connected to the NIRS.

2.4. Genetic Variation in Sweetpotatoes

The intervention of humans through domestication and artificial selection as well as the occurrence of natural hybridization and mutations have resulted in the existence of a very large number of cultivars of sweetpotato. There is more diversity in the sweetpotato than in cassava, yam or cocoyam (Woolfe, 1992). All attempts made to structure the existing morphological variation found within cultivated *I. batatas* into meaningful varietal groups have failed because there is a continuum of variation (Lebot, 2010). The many descriptors for morphological traits of sweetpotato (CIP/AVRDC/IBPGR, 1991; Huaman, 1991), also indicates that there exist a number of varieties of this crop species in the world (Carpena, 2009). Over 6000 accessions of landraces, breeding lines, and advanced cultivars of sweetpotato are held by CIP in its gene-bank (Rossel *et al.*, 2007). This collection is just a small fraction of the available varieties in the world (Carpena, 2009). Variation may occur in

storage root shape and size, storage root skin colour, flesh colour, depth of rooting, root orientation in the soil, maturity period, dry matter content, sugar content, beta-carotene content, texture of the cooked roots, resistance/tolerance to diseases and pests, and utilization. Beyond the CIP collections, a number of National Agricultural Research Systems (NARS) or National Programmes have collections as well. For example, sweetpotato is the number one food crop in Papua New Guinea, where it is estimated that about 5000 cultivars are grown which, vary in root flesh and skin colour (Bourke, 2006). Also sweetpotato varieties grown in Brazil are highly diverse, at least phenotypically and no single varieties seem to dominate cultivation (Bressan *et al.*, 2005; Veasey *et al.*, 2007).

2.5 Determination of Genetic Variation

Characterization helps to document the genetic variability that exists in a population (Pérez De La Vega, 1993). This is an important activity in crop improvement since the amount of genetic diversity within populations determines the rate of adaptive evolution and extent of response in traditional breeding through selection. Selectable and neutral genetic markers are commonly used to assess genetic diversity among populations and accessions (Turyagyenda *et al.*, 2012). They facilitate and speed up selection in crop improvement by serving as genetic markers.

2.5.1 Agro-morphological Characterization

The usual approach to characterization and evaluation of populations using agro-morphological descriptors involves cultivation of sub-samples and assessing their morphological and agronomic description (Pérez De La Vega, 1993). The International Plant

Genetic Resources Institute (IPGRI) has developed descriptors for quantitative as well as qualitative characters to ensure precise, accurate and uniform identification of genotypes (Chavez, 1990). In addition, Principal Component Analysis (PCA) is a descriptive technique which reveals the pattern of character variation among individual clones (Mwirigi *et al.*, 2009). It brings a set of multivariate data into components that account for meaningful amount of variation in a population. Cluster analysis on the other hand decreases the number of individual variable units by classifying such variation into groups which are translated into a dendrogram using the coefficient of similarity (Sneath and Sokal, 1973; Tatineni *et al.*, 1996).

2.5.2 Molecular Characterization

The most precise tool for studying genetic variation is the application of molecular markers which is referred to as genotyping. Selectable markers (agro-morphological traits) respond to selection pressure and change after several years of natural and/or artificial selection (Yong-Jin *et al.*, 2009). On the contrary, neutral genetic markers are least subjected to selection pressure and can accurately infer genetic diversity among populations and accessions (Chakravarthi and Naravaneni, 2006; Raji *et al.*, 2009). For this tool, deoxyribonucleic acid (DNA) samples are quantified and used. Different approaches and techniques have been used over the years by different authors. Amplified Fragment Length Polymorphism (AFLP) has been used for studying the historic dispersal of sweetpotato (Zhang *et al.*, 2004) and also for assessing the genetic diversity of cultivars and landraces (Zhang *et al.*, 2000; Fajardo *et al.*, 2002). Inter-simple sequence repeat (ISSR) and restriction analysis of chloroplast DNA have been used to investigate the genetic relationships between cultivated sweetpotato and its wild relatives (Huang and Sun, 2000; Hu *et al.*, 2003). Chloroplast and nuclear microsatellite have also been used to study the origin and dispersal of sweetpotato (Roullier *et al.*, 2011; Roullier

et al., 2013a; Roulliera *et al.*, 2013b). For now the SSR markers appear to be the ones for assessing genetic variation in sweetpotatoes. This is because microsatellite or simple sequence repeats (SSR) markers exhibit relatively high levels of polymorphism, and several such markers have been developed for sweetpotato genotyping (Jarret and Bowen, 1994; Buteler *et al.*, 1999; Hu *et al.*, 2004). These markers have successfully been used to determine the genetic relationships between cultivars derived from hybrid or polycross breeding programs (Hwang *et al.*, 2002), and also for analysing the genetic diversity of sweetpotato landraces (Zhang *et al.*, 2001; Gichuru *et al.*, 2006). SSR markers remain competitive because they are multi-allelic, highly polymorphic, co-dominant and highly reproducible, and provide rich genetic information with good genome coverage (Kawuki *et al.*, 2009; Sree *et al.*, 2010). They are also affordable and amenable to most breeding procedures and, thus, applicable in public breeding programmes which may not be able to afford expensive diversity assessment techniques (Turyagyenda *et al.*, 2012). Genotypes are scored for the presence (1) or absence (0) for each fragment, and carrying out an Analysis of Molecular Variance (AMOVA) also helps to quantify the genetic variation and relationship levels between and within the genotypes or a population. It can also provide information on the genetic distances between different populations as well.

2.6 Sweetpotato Breeding

The sweetpotato can be reproduced by three means (Woolfe, 1992). Asexually they can reproduce and colonize an area by production of storage roots which subsequently sprout to give new plants. Alternatively, they may allocate major resources to producing vines which may form roots at the node producing daughter plants. Of least importance, except for breeding, is sexual reproduction in the form of seed. Flowers are borne singly or on inflorescences that grow vertically upward from the leaf axils, and are trumpet shaped. A

mature flower opens before dawn, stays open only a few hours and wilts before noon on the same day. Pollination is by insects, but can be assisted by man. As flowers are open and receptive for a very short time, the chances of failure of pollination are quite high.

Two major difficulties have been encountered in the development of scientific breeding methods (Lebot, 2010). Firstly, because of its polyploidy, sweetpotato is a difficult species for Mendelian genetics and segregation ratios are quite complex unless a single dominant allele is involved. Secondly, sweetpotato is almost always self-incompatible. Variation in stamen height with respect to the style also complicates self-pollination mechanism. It is therefore, very difficult to produce seeds by self-pollination and hand pollination can produce often only one or two seeds per capsule. Sterility problems are also common, probably as a result of the high polyploidy. The practical consequences of these setbacks have been recognized by different researchers in different countries (Martin, 1988a; Wilson *et al.*, 1989; Mihovilovich *et al.*, 2000). Cross-incompatibility also exists. Some sweetpotatoes are day length sensitive and clones differ in this respect. Some flower readily in any season, others flower in short days. Short days promote flowering and storage root growth (Lam *et al.*, 1959; Porter, 1979; Martin, 1988b). There are some clones that do not flower at any season and flowering may have to be induced through grafting, girdling, wounding or the use of hormones like 2,4-D. Incompatibility (self-incompatibility and occasional cross-incompatibility) exists and restricts the chances that pollination will result in fertilization and seed production (Woolfe, 1992).

However, despite these practical constraints, one of the first modern breeding programmes was implemented by the Louisiana State University in the 1920s (Lebot, 2010). Since the 1950s, breeding programmes have been implemented, mostly in temperate climates, in the

United States (South Carolina), China, Japan, and the subtropical Taiwan. In the United States, successes in breeding were achieved in the years following the Second World War (Lebot, 2010). The leading variety, Beauregard is a polycross selection released by the Louisiana State University and occupied about 65% of the area planted annually (Smith *et al.*, 2009). The GA90-16 is also an open-pollinated seedling selection from a polycross nursery in 1990 of which the female parent was 'HiDry'. The exact parentage of 'HiDry' is not known; however, it was a 4th generation open pollinated selection from MK-14 in mass selection population J. MK-14. Population J. MK-14 was a selection from open-pollinated seeds of 'Minamiyutuka' from the Kyushu Agricultural Experiment Station, Japan (Hamilton *et al.*, 1985). GA90-16 is a sweetpotato breeding line that was developed jointly by the University of Georgia and the U.S. Dept. of Agriculture (USDA), and the U.S. Vegetable Laboratory in Charleston, S.C (Kays *et al.*, 2001). The major distinguishing traits for the line are exceptionally low endogenous sugar and maltose content, reduced aroma, and firm texture in the cooked product. The composite effect is a cooked product with a flavour (taste and aroma) similar to potato, and much lower flavour intensity, similar to cassava and rice. It has excellent potential for developing commercial cultivars with low flavour impact for use as a staple or for blending with conventional sweetpotatoes or other foods to broaden the flavour potential of processed sweetpotato products (Kays *et al.*, 2001).

In China, the variety Xushu 18 was developed by the Institute of Agriculture of Xuzhou in 1972 and is currently the leading variety with an annual area of 1.5 Mha (Lebot, 2010). The variety Nanshu 88 was also released in 1988 by the Nanchong Institute of Agriculture, in Sichuan, and is mainly used for food as fresh tuber and feed processing (Zhang *et al.*, 2009). Also in Japan, the leading table variety, Beniazuma was released by the National Institute of Crop Science in 1981. In Uruguay, polycross population breeding combined with recurrent

selection which started in 1988 and allowed substantial progress for most traits and cultivars adapted to diverse regions and uses were released in 2002 (Lebot, 2010). One of the varieties INLA Arapey is grown over 75% of the area and spreading to Brazil and Argentina. Similar progress is found in Ghana. Thirteen (13) varieties namely Histarch, Otoo, Apomuden, Ogyefo, Okumkom, Sauti, Faara, Santompona, Ligri, Danayuie, Bohye, Patron (by the CSIR-CRI), and Teksantom (by the Kwame Nkrumah University of Science and Technology) have been released to farmers in Ghana. Many of such success stories may be found elsewhere. This is because according to Lebot (2010), since the early 1980s thanks to the leadership of CIP, various programmes are now being conducted in the tropics and are releasing improved varieties. Successful breeding has been achieved in Colombia, India, the Philippines, Indonesia, and Vietnam. Many improvement programmes in Africa (especially in Burundi, Mozambique, Nigeria, Rwanda, Uganda) have received CIP material in tissue culture and true seed form. When tested in local environmental conditions, some of them outperform local varieties and are released to farmers.

2.7 Participatory Breeding

Even though it has been shown that even small amounts of the orange-flesh varieties as a regular part of the diet will eliminate vitamin A deficiency in adults and children, African countries have traditionally grown white-fleshed sweetpotatoes, which are low in vitamin A (Thottappilly, 2009). This is because, traditionally, the provitamin A varieties usually don't meet the food preparation standards of most African countries due to their low dry matter content and sweetness. The high levels of sweetness and strong flavour associated with many cultivars of sweetpotatoes may have reduced its popularity as a staple food, and made it difficult to combine with other foods in a variety of dishes (Woolfe, 1992). These factors

have reduced the esteem of sweetpotato in the eyes of many consumers. As a result of this perception and preference for sweetpotato varies with ethnic background and geographic location (Kays and Horvat, 1983).

Sweetpotato is grown in all the agroecozones of Ghana, but is more popular in the Upper East Region, Southern part of Volta Region, Central Region, Northern Region (during lean season), and some parts of Greater Accra, Eastern and Brong Ahafo Regions. In spite of its nutritional attributes with a good complement of energy, vitamins, and minerals, consumers have not accepted sweetpotato as a staple food in Ghana for decades and this needs to be addressed. Addressing issues such as this effectively requires gathering knowledge and opinions of stakeholders involved. One effective way of obtaining information on the perception, knowledge and the opinion of stakeholders on the constraints to increase sweetpotato utilization is Participatory Rural Appraisal (PRA) (Chanbers, 1997).

PRA is an active research tool that involves community members or stakeholders with the aim of tapping their indigenous knowledge to solve local concerns. PRA has been popularly used by NGO's and other agencies over the past decade (Cornwall *et al.*, 2001). Participatory Rural Appraisal (PRA) can take many forms. These include participatory plant breeding and participatory varietal selection (Gibson *et al.*, 2007; Gasura *et al.*, 2008). Participatory Plant Breeding (PPB) (Sperling *et al.*, 1993), and Participatory Varietal Selection (PVS) (Witcombe *et al.*, 1996), are widely use, especially for food crops and by NGO-led projects. These usually require farmers, scientists and perhaps other stakeholders to collaborate (Sperling *et al.*, 1993), in a decentralized approach (Ashby and Sperling, 1994; Berg, 1997), and skills are transferred to local farmers and other local stakeholders (Humphries *et al.*,

2005). These approaches recognize that it is the stakeholders (farmers mainly) that decide traits to incorporate into an existing clone or select. Focus Group Discussion (FGD) is a form of group interview that capitalises on communication and interactions among participants in order to generate data (Kitzinger, 1995). It makes use of a wide range of techniques which include secondary data review, direct observation, semi-structured interviewing, matrix scoring and ranking (preference ranking and scoring), pair-wise ranking and wealth ranking. FGDs can be a powerful research tool which provides valuable spontaneous information in a short period of time and at relatively lower cost. Depending on the topic, it may be risky to use FGDs as a single tool. This is because in group discussions, people tend to centre their opinions on the most common ones, or on social norms. In reality, opinions and behaviour may be more diverse. Therefore it is advisable to combine FGDs with at least some key informant and in-depth interviews. PRA is not like a formal survey that is based on a written questionnaire. Yet it can produce data that can be analysed graphically and statistically. Participatory breeding in sweetpotato has been reported (Bashaasha *et al.*, 1985; Gibson *et al.*, 2007). It has also been reported for cassava breeding in Ghana (Manu-Aduening et al., 2006).

CHAPTER THREE

3.0. STAKEHOLDERS' PERCEPTIONS AND PREFERENCES FOR SWEETPOTATO AND IMPLICATIONS FOR BREEDING IN GHANA

3.1. Introduction

The decision to adopt a new cultivar is complexly related to field and yield performance as well as consumer taste acceptability (Sugri *et al.*, 2012). Consumer taste, preference and acceptance are critical in determining the degree of suitability of sweetpotato cultivars to any locality (Tomlins *et al.*, 2004; Kwach *et al.*, 2010). Food preferences may vary among individuals, age groups, gender and sometimes cultures as well as geographical locations (Sugri *et al.*, 2012). Traits to select during crop improvement therefore, depend on the target beneficiaries (Sugri *et al.*, 2012). It is believed that some cultivars that have been released were not adopted because of lack of sufficient consideration of farmers' (Derera *et al.*, 2006), and other stakeholders' preferences in the process of their development. Breeders fail to consider the special preferences of farmers (Toomey, 1999; Banziger and Cooper, 2001), possibly because they are unaware of them (Derera *et al.*, 2006). Breeding programmes must therefore adjust breeding objectives and selection procedures to meet client needs. Effective breeding should be based on clear identification of stakeholders perceived constraints and preferences. These can be addressed through participatory plant breeding (PPB), participatory varietal selection (PVS) (Gibson *et al.*, 2007; Gasura *et al.*, 2008) and/or participatory rural appraisal (PRA).

The main aim of the survey was to become familiar with stakeholders' knowledge and perceptions on sweetpotato end-user-traits and the implications on sweetpotato improvement in Ghana. The specific objectives were to:

a) Assess the role of sweetpotato in the farming and food systems of Ghana

b) Identify sweetpotato utilization constraints and opportunities

c) Ascertain the current patterns of sweetpotato consumption

d) Establish general baseline data for future impact assessment of sweetpotato production and utilization in Ghana.

3.2. Materials and Methods

The study was conducted using Focal Group Discussions (FGD) followed by administration of a Semi-Structured Questionnaire (SSQ) in 2012.

3.2.1. Focal Group Discussions (FGD)

3.2.1.1. Study area

The study was conducted in seven communities (Table 3.1), which span all the five agroecological zones of Ghana. The areas covered latitude 4^0 30' to 11^0 north of the equator, and longitudes 1^0 12'east to 3^0 15'west. The communities were the major sweetpotato production, marketing and utilization areas in Ghana.

Table 3.1 List of study communities

Community	District	Region	Ecozone
Fiaso	Techiman	Brong Ahafo	Transition
Komenda	KEEA	Central	Coastal savanna
Aseja	Fanteakwa	Eastern	Forest
Sege	Dangme East	Greater Accra	Coastal Savanna
Woriborgu-kukuo	Tolon	Northern	Guinea Savanna
Natugnia	Kassena-Nankana	Upper East	Sudan Savanna
Agorve	Ketu-North	Volta	Coastal Savanna

3.2.1.2. Nature of Participants

District Agricultural Extension agents (AEAs) were actively involved in the identification and selection of respondents through random sampling. Participants were selected from sweetpotato stakeholders, namely consumers, farmers, marketers, and processors. In all, 79 participants were involved. These included 50 males and 29 females (Table 3.2).

Table 3.2 Group characteristics

Region	Females	Males	Total
Brong Ahafo	2	6	8
Central	1	11	12
Eastern	8	4	12
Greater Accra	6	6	12
Northern	4	7	11
Upper East	4	8	12
Volta	4	8	12
Total	**29**	**50**	**79**

3.2.1.3. Data collection and analysis

The team was composed of a facilitator/moderator and two recorders. In communities where language was a barrier, an interpreter was hired. An open-structured questionnaire guided by a checklist (variety grown, source of planting material, uses, gender, and farming systems) was used for the interaction. General description of the group dynamics was also recorded.

The study was done in February, 2012. The data were converted to numerical values, standardized (Etzkorn, 2011), and analysed using Principal Component Analysis (PCA). The analyses were done using Genstat (Released 9.2.0.152) Computer package (Genstat, 2007).

3.2.2. Administration of Semi-structured Questionnaire (SSQ)

3.2.2.1 Study area

The survey was conducted in eight communities (Table 3.3) which also span all the five agroecological zones of Ghana. These communities with the exception of Kumasi were the major sweetpotato production and marketing areas in Ghana.

Table 3.3 List of Study communities

Community	District	Region	Ecozone
Fiaso	Techiman	Brong Ahafo	Transition
Kumasi	Kumasi	Ashanti	Forest
Komenda	KEEA	Central	Coastal savanna
Aseja	Fanteakwa	Eastern	Forest
Sege	Dangme East	Greater Accra	Coastal Savanna
Woriborgu-kukuo	Tolon	Northern	Guinea Savanna
Natugnia	Kassena-Nankana	Upper East	Sudan Savanna
Agorve	Ketu-North	Volta	Coastal Savanna

3.2.2.2. Respondents

In all, 178 people involving 52% female and 48% males were interviewed. The structure of respondents is presented in Figure 3.1. There were 160 consumers of sweetpotato, 123 sweetpotato farmers, 40 sweetpotato traders and 18 sweetpotato processors. Among them were 24 traders who were also consumers, 93 farmers who were consumers, 11 people who were consumers and processors and one person who was a farmer and a trader. Out of the 178 respondents, 15, 12, 3 and 2 of the respondents were consumers, farmers, traders, and

processors only, respectively. The number of respondents per community is presented in Table 3.4.

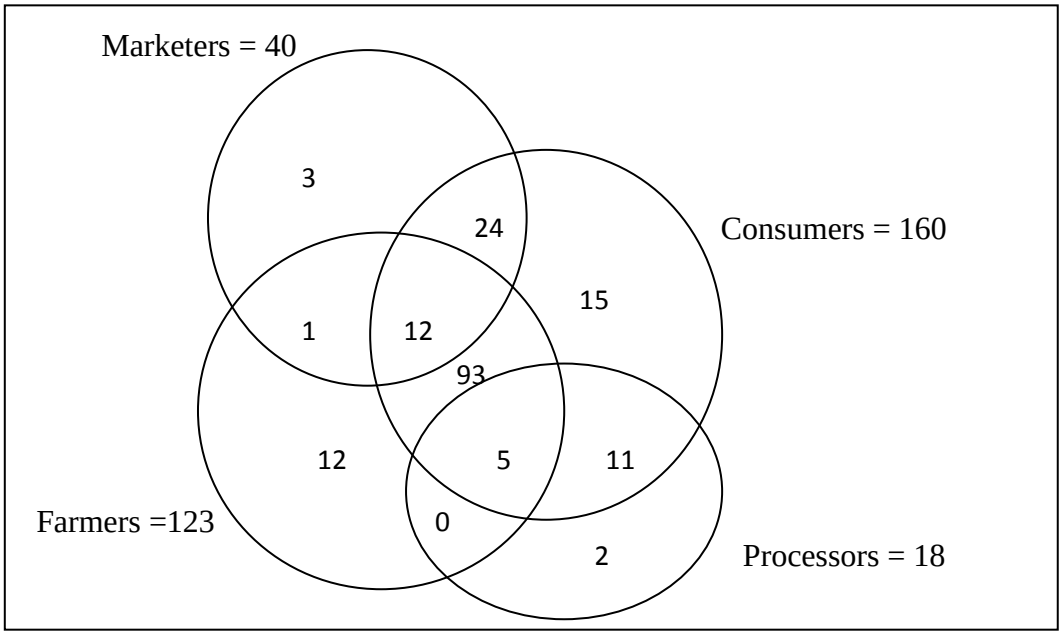

Figure 3.1 Euler diagram of respondents

Table 3.4 Frequency of respondents per community (Region)

Community (Region)	Respondents		
	Number of participants	Percent	Cumulative Percent
Ashanti	13	7.3	7.3
Brong Ahafo	17	9.6	16.9
Central	28	15.7	32.6
Great Accra	19	10.7	43.3
Upper East	30	16.9	60.1
Volta	40	22.5	82.6
Northern	17	9.6	92.1
Eastern	14	7.9	100
Total	178	100.0	

3.2.2.3. Data collection and analysis

Planned interviews were employed in the data collection. District Agricultural Extension Agents (AEAs) were involved in the identification and selection of respondents by random sampling. The Semi-structured Questionnaire (SSQ) was developed using a checklist which included gender, kind of stakeholder, crop enterprise and food consumption pattern, and sweetpotato preference. Sweetpotato root-flesh colour chart was used to estimate the beta-carotene content of the storage root. In the colour chart, white-flesh represented low beta-carotene content, yellow-flesh represented moderate beta-carotene content and orange-flesh represented high beta-carotene content. The survey was done in February, 2012, as a follow-up to the FGD. Data were analysed using Statistical Package for Social Sciences (SPSS Release 16.0) Computer software (SPSS, 2007). Results were summarized into frequencies and percentages and represented in tables and graphs.

3.3. Results

3.3.1. Role of sweetpotato in farming and food systems

Fifteen variables (questions) were discussed (Table 3.5) with each group. The first five principal components (PCs) with Eigen values greater than 1.0 together explained 96.33% of the total variation in the data set (Table 3.5). Scores for method of storage and emotional aspect of participants were not significantly associated with any of the components. Scores on the first two PCs accounted for 58.75% of the dissimilarity, and were related to all the questions except for sex and source of planting material which were related to PCs 3 and 5.

Table 3.5 Principal Component Analysis of the 15 questions used for the Focal Group Discussion

Variables	PC1	PC2	PC3	PC4	PC5
Total participants	**-0.327**	-0.080	-0.200	-0.191	**0.437**
Sex	-0.148	0.048	**0.599**	0.037	-0.243
Crop calendar	**0.315**	0.121	-0.201	0.215	**0.496**
Crop enterprise	**-0.420**	-0.048	-0.019	0.025	0.170
Rank of sweetpotato	**-0.303**	0.200	0.063	**-0.474**	0.114
Variety grown	**-0.325**	-0.225	**-0.377**	-0.026	-0.119
Planting material source	-0.234	0.171	0.270	0.034	**0.494**
Source of sweetpotatoes eaten	**-0.329**	0.179	**-0.303**	**-0.317**	-0.005
Ways sweetpotato is eaten	0.119	**-0.427**	0.091	**-0.525**	0.192
Storage	0.000	0.000	0.000	0.000	0.000
Other uses	-0.079	**-0.305**	0.288	**0.515**	**-0.200**
Constraints to consumption	0.232	**-0.495**	-0.052	0.202	0.102
Perception on health	-0.236	**-0.502**	0.121	-0.080	0.200
Emotional aspect of participants	0.000	0.000	0.000	0.000	0.000
Group dynamics	**0.325**	0.225	**0.377**	0.026	0.119
Latent roots (Eigen values)	5.183	2.454	2.198	1.518	1.170
Variance (%)	39.87	18.88	16.91	11.67	9.00
Cumulative (%)	39.87	58.75	75.66	87.33	96.33

***Values in bold indicate the most relevant characters (>0.3) that contributed most to the variation of the particular component.**

The distribution produced by PCs 1 and 2 is shown in Figure 3.2. Brong Ahafo Region is separately classified in group 1, Volta and Eastern Regions are in group 2. Groups 3 and 4 are composed of Upper East and Central Regions, and Greater Accra and Northern Regions.

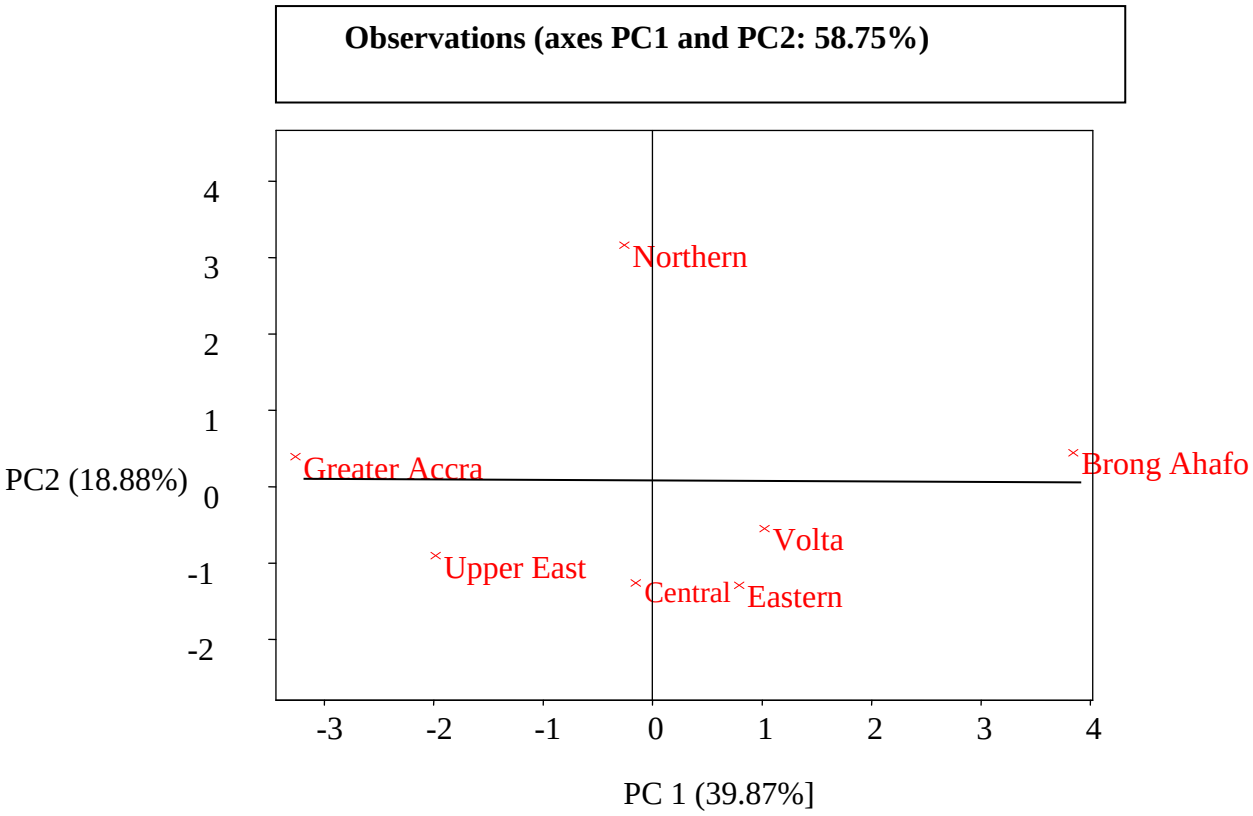

Figure 3.2 A biplot of PC1 and PC2 showing the distribution of communities involved in the focus group discussion

The hierarchical clustering (Fig. 3.3) illustrates the relationship between responses among the communities. The communities were separated with Euclidean similarity distance from 1.00 to 0.75. All the communities, except the Northern region, were similar at about 0.75 level of similarity. However, they were all distinct at 0.87 level. Four main clusters, A, B, C, and D, were identified at similarity level 0.76. Cluster B was composed of the Volta and the Eastern Regions, whilst Brong Ahafo Region and the Northern Region were found in cluster A and D, respectively. Cluster C was composed of Central, Upper East and the Greater Accra Regions.

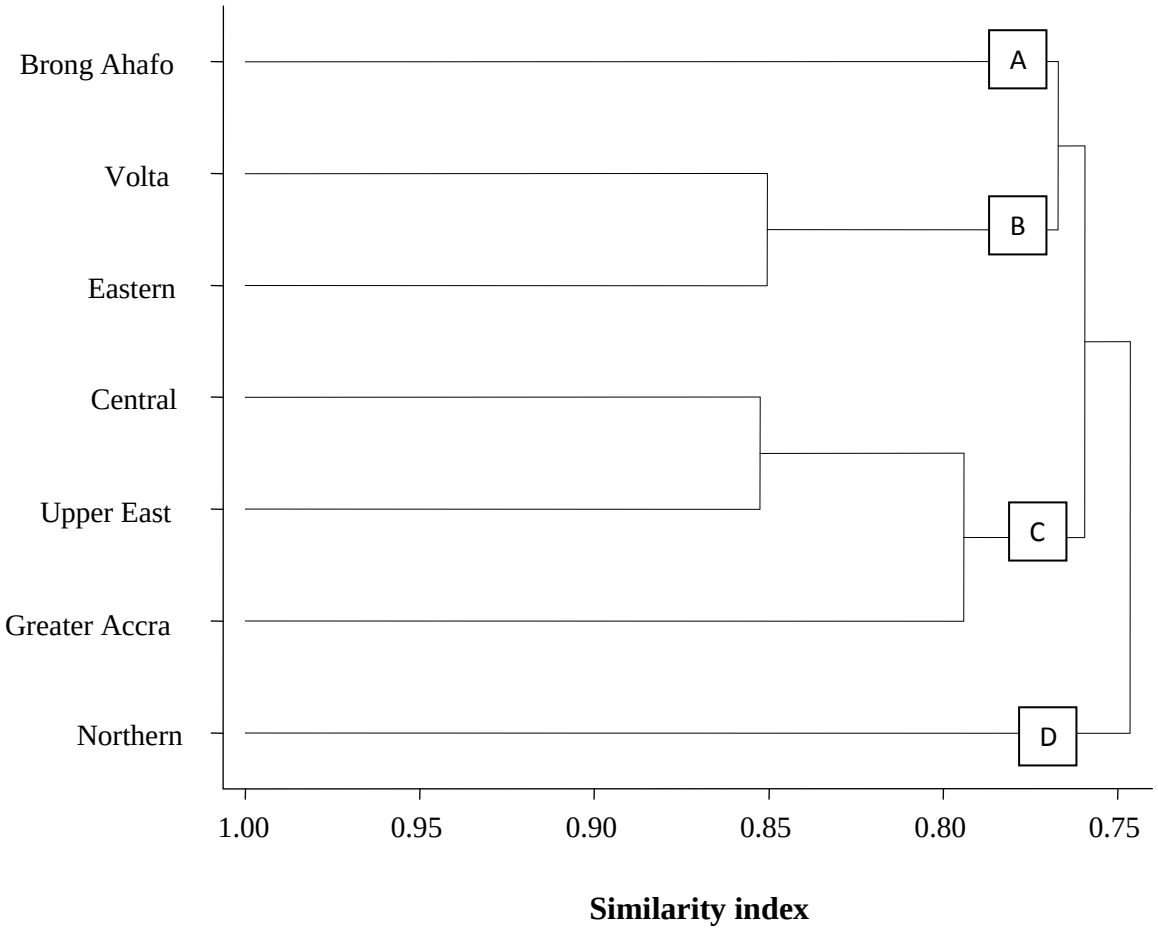

Figure 3.3 Dendrogram showing response of communities involve in the Focal Group Discussion

3.3.1.3. Crop enterprise of the community

In all, 24 crops were cultivated and produced by the communities (Table 3.6). Brong Ahafo Region cultivated the least (9) whilst Greater Accra cultivated the highest (12). The range of crops cultivated includes roots and tubers (sweetpotato, cassava, yam, cocoyam and frafra potato), cereals (maize, millet and rice), legumes (cowpea, groundnut, bambara groundnut/beans and soybean), horticultural crops (tomato, okra, watermelon, onion, eggplant, cabbage, pepper and eggplant), and others – plantain, sugarcane and tiger nuts. Sweetpotato was ranked between first and tenth among the communities. It was ranked first in Brong Ahafo and Central Regions but, tenth in the Greater Accra Region.

Table 3.6 Crop enterprise ranking within the seven communities involved in the focus group discussion

	Region						
Rank Position	**Brong Ahafo**	**Central**	**Eastern**	**Greater Accra**	**Northern**	**Upper East**	**Volta**
1	Sweetpotato	Sweetpotato	Sweetpotato	Pepper	Maize	Millet	Maize
2	Maize	Maize	Cassava	Tomato	Yam	Maize	Sugarcane
3	Yam	Cassava	Maize	Cassava	Rice	Rice	Cassava
4	Cassava	Watermelon	Plantain	Okra	Sweetpotato	Groundnut	Sweetpotato
5	Watermelon	Tomato	Cocoyam	Maize	Cowpea	Sweetpotato	Rice
6	Cowpea	Pepper	Pepper	Watermelon	Cassava	Frafra potato	Pepper
7	Pepper	Okra	Yam	Cowpea	Groundnut	Bambara beans	Okra
8	Egg plant	Egg plant	Tomato	Groundnut	Pepper	Cowpea	Tomato
9	Onion	Groundnut	Okra	Egg plant	Soybean	Soybean	Groundnut
10		Tiger nut	Cowpea	Sweetpotato	Bambara groundnut	Pepper	Cowpea
11		Yam		Cabbage	Tomato	Egg plant	
12				Onion			

3.3.2. Pattern of sweetpotato preferences and utilization

3.3.2.1. Demographics

The lowest and highest number of respondents across the communities were 13 and 40, respectively. These were from the Ashanti and the Volta Regions, respectively, and constitute 7.3% and 22.5% of the total respondents. Fifty-two per cent of the respondents were 40 years of age and above compared to 47% and 1%, respectively, for age classes 20 – 40 years and below 20 years (Fig. 3.4). The educational background of respondents was distributed as follows; Primary or below 83% and High School and above, 17%.

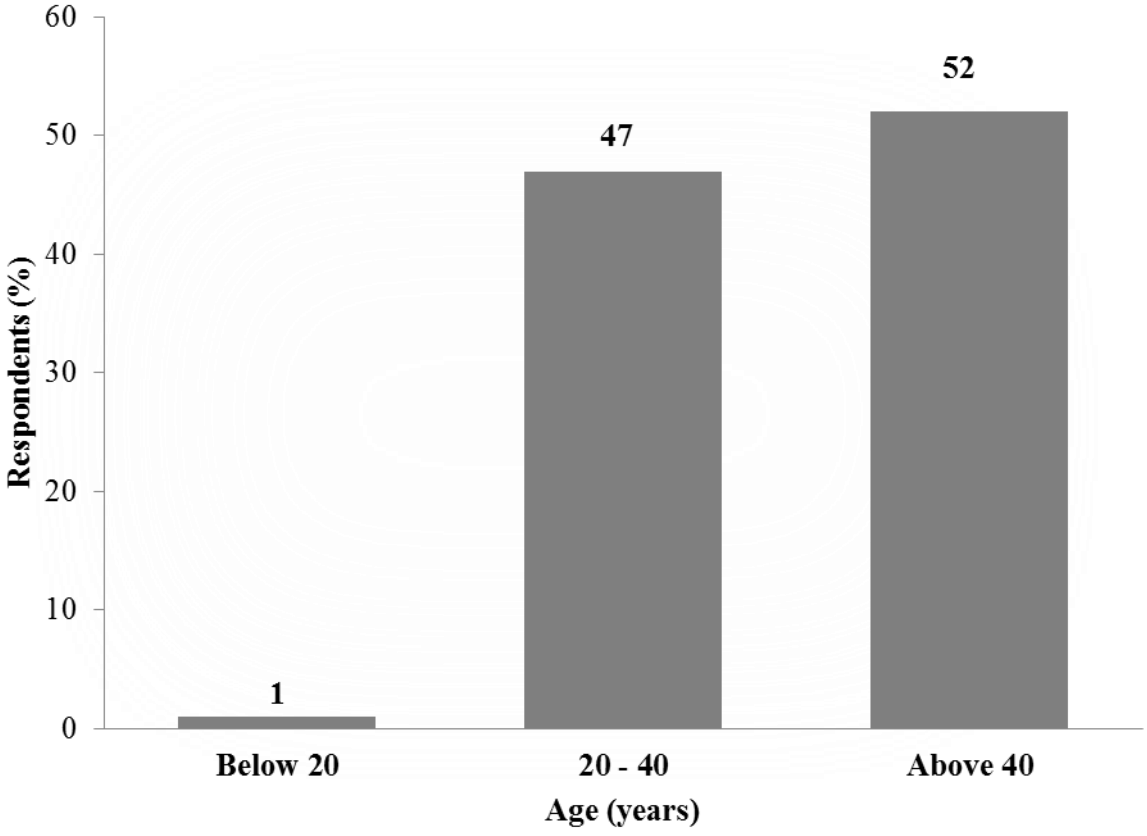

Figure 3.4 Age distribution of respondents

3.3.2.2. Farm level characteristics

Sweetpotato was ranked 1 - 10 among 24 crops cultivated and produced by the farmers. Out of the 123 farmers interviewed, 93.5% ranked sweetpotato between 1 and 5, whilst 39 farmers (31.7%) ranked sweetpotato as their first choice (Table 3.7). Majority of the farmers were engaged in sole cropping (92%) as against 8% for intercropping. The land area cultivated to sweetpotato ranged from 0.25 – 12.0 acres (Table 3.8). However, majority (91%) of the farmers had sweetpotato farm sizes of between 0.25 and 3.0 acres. Farmers cultivating one acre of land (25.2%) were in the majority followed by those cultivating 2 acres (20.3%).

Table 3.7 Relative ranking of sweetpotato among 24 cultivated crops by respondents

Rank	Number of farmers interviewed	Percent of farmers interviewed	Cumulative Percent of farmers interviewed
1	39	31.7	31.7
2	8	6.5	38.2
3	23	18.7	56.9
4	19	15.4	72.4
5	26	21.1	93.5
6	2	1.6	95.1
7	1	0.8	95.9
8	3	2.4	98.4
9	1	0.8	99.2
10	1	0.8	100
Total	123	100.0	

Table 3.8 Frequency distribution of sweetpotato cropping land area

Farm size (ac.)	Number of farmers interviewed	Percent of farmers interviewed	Cumulative Percent of farmers interviewed
0.25	21	17.1	17.1
0.5	22	17.9	35.0
0.75	1	0.8	35.8
1	31	25.2	61.0
1.25	1	0.8	61.8
1.5	6	4.9	66.7
2	25	20.3	87.0
2.5	1	0.8	87.8
3	5	4.1	91.9
4	3	2.4	94.3
5	2	1.6	95.9
6	2	1.6	97.6
7	1	0.8	98.4
10	1	0.8	99.2
12	1	0.8	100.0
Total	123	100.0	

3.3.2.3. Sweetpotato storage root utilization and quality preferences

Sweetpotato utilization pattern is presented in Figure 3.5. Thirty-eight percent (38.8%) of consumers ate sweetpotato two or three days per week whilst 27.5% consumed it at least six days per week with only 11.9% of the respondents consuming sweetpotato at most only once a week.

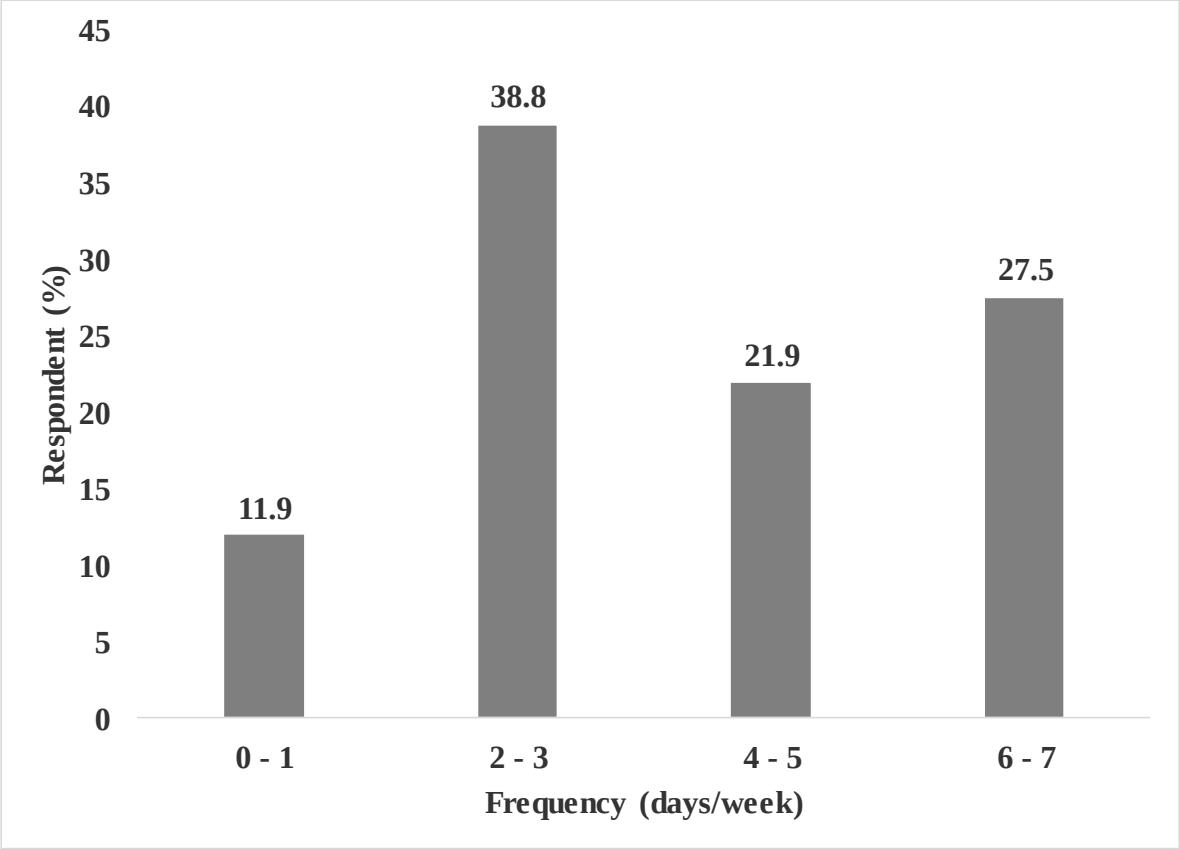

Figure 3.5 Sweetpotato consumption distribution

Varietal preferences distribution showed a response range of 7 – 138 respondents for the semantic differential scale (low, moderate, high, and any-type) for the storage root dry matter content (Fig 3.6). The lowest and the highest values represent preference for any sweetpotato type and sweetpotato with high storage root dry matter. Most respondents preferred high dry matter followed by moderate dry matter content whilst few preferred low dry matter or didn't care. Most respondents (88) preferred moderate beta carotene content (yellow-flesh) but 40 preferred low (white-flesh) and 33 preferred high beta carotene (Orange-flesh) whist 17 preferred any-type (Fig. 3.7). The results for the storage root taste (sweetness) are represented in Figure 3.8. The order of preference was less sweet- (87), sweet- (63), very sweet- (25), and

any-type (3), respectively. No significant interaction was observed between these storage root quality traits and age, educational background and sex of the respondents (Tables 3.9 – 3.12).

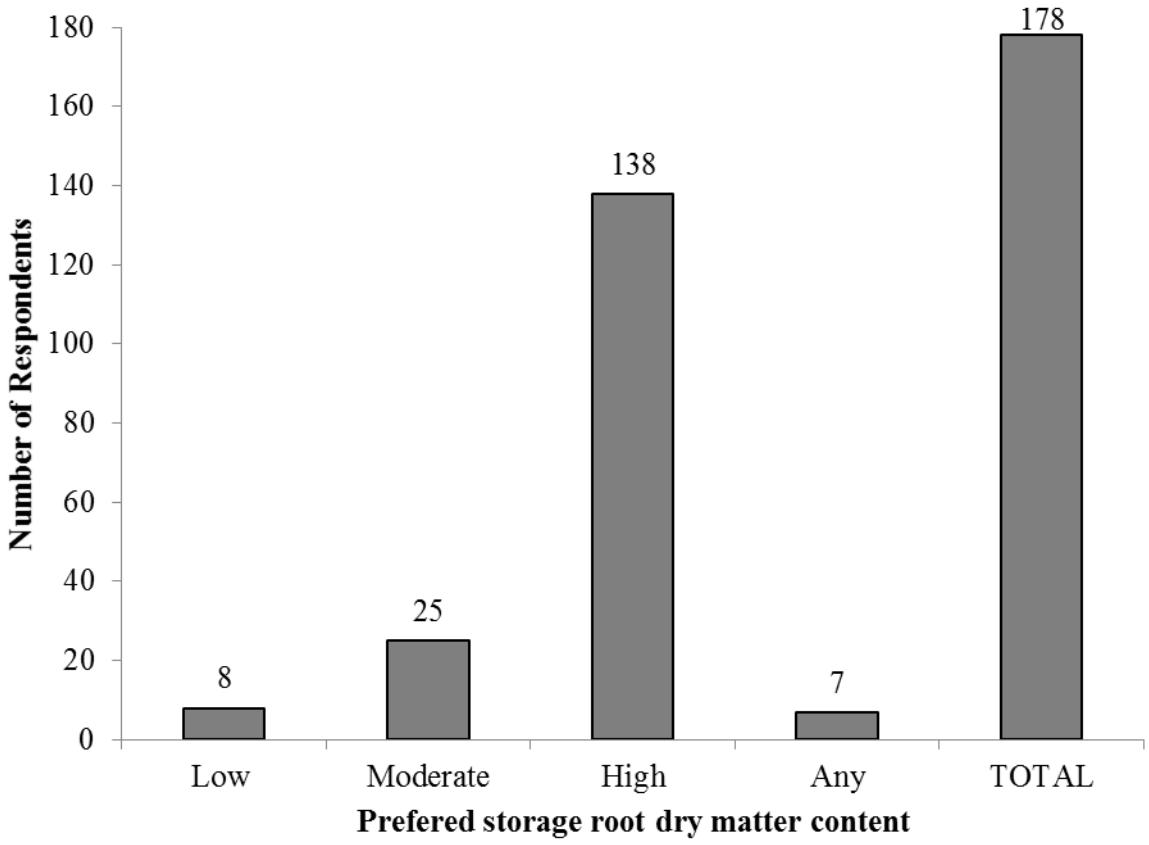

Figure 3.6 Preferred storage root dry matter content distribution

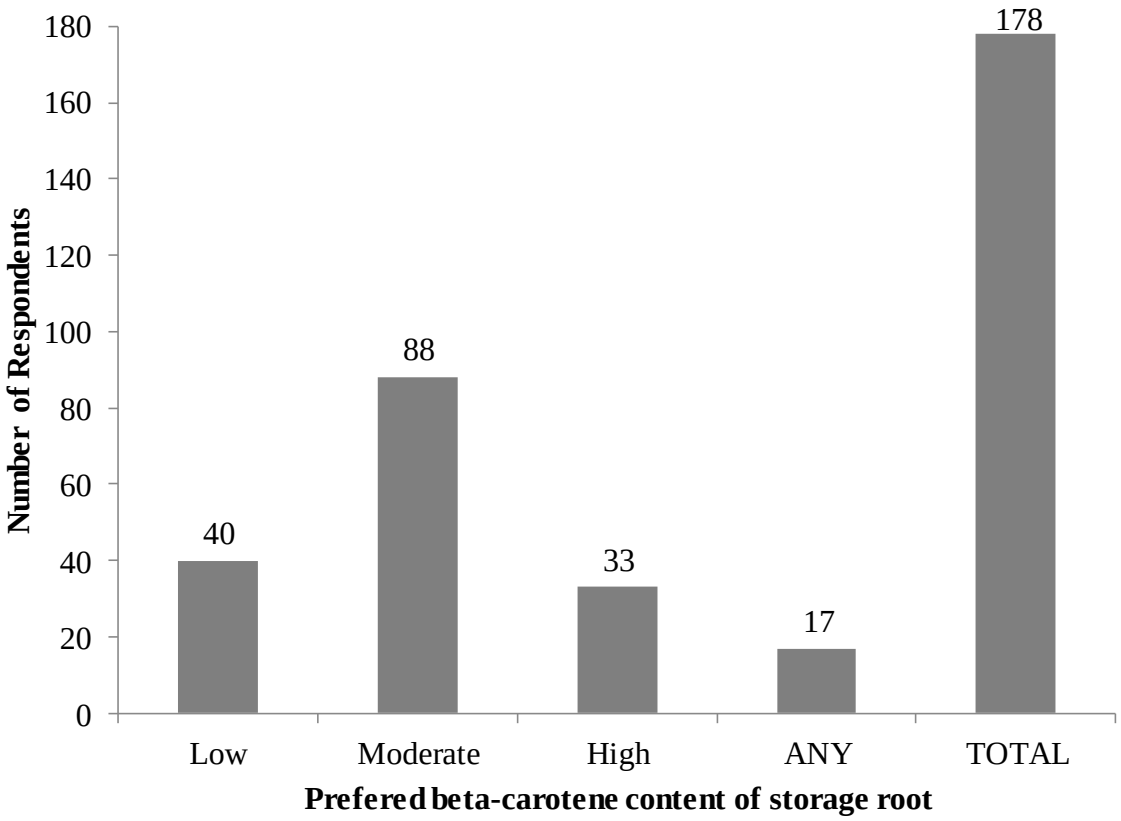

Figure 3.7 Distribution of preference for beta-carotene content of storage root

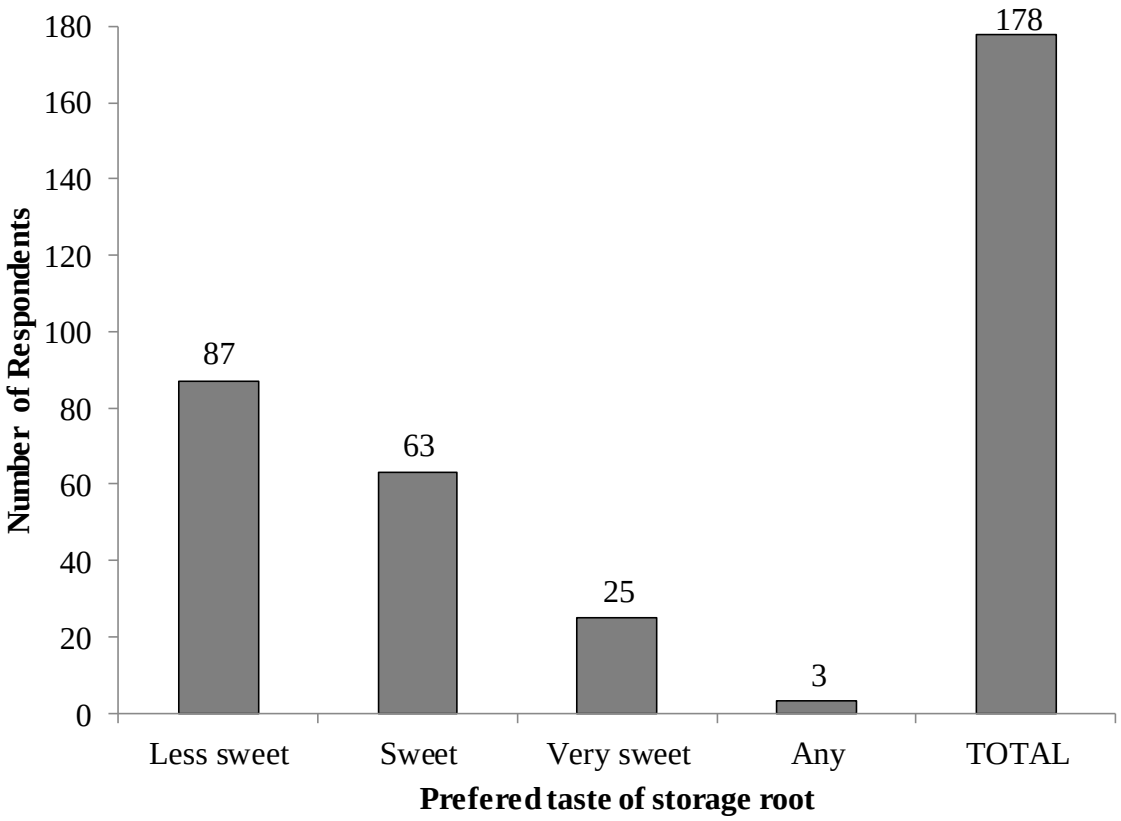

Figure 3.8 Storage root taste (sweetness) preference distribution

Table 3.9 Preference for beta-carotene and dry matter by different age groups

Trait	Age of Respondents	Preference				
		Low	Moderate	High	Any	Total
Beta-carotene						
	Below 20	0	0	0	2	2
	20 – 40	15	48	14	7	84
	Above 40	25	40	19	8	92
	Total	40	88	33	17	178
Dry matter						
	Below 20	0	0	2	0	2
	20 – 40	3	11	65	5	84
	Above 40	5	14	71	2	92
	Total	8	25	138	7	178

Table 3.10 Preference for beta-carotene and dry matter by different educational background

Trait	Respondents' Educational Background	Preference				
		Low	Moderate	High	Any	Total
Beta-carotene						
	Primary & below	35	63	33	17	148
	High School & above	5	25	0	0	30
	Total	40	88	33	17	178
Dry matter						
	Primary & below	6	20	117	5	148
	High School & above	2	5	21	2	30
	Total	8	25	138	7	178

Table 3.11 Beta-carotene and dry matter content preferences by sex

Trait	Sex of Respondents	Preference				
		Low	Moderate	High	Any	Total
Beta-carotene						
	Female	23	48	13	8	92
	Male	17	40	20	9	86
	Total	40	88	33	17	178
Dry matter						
	Female	5	10	70	7	92
	Male	3	15	68	0	86
	Total	8	25	138	7	178

Table 3.12 Taste (sweetness) preferences by different age groups, educational background and sex

Source	Preference				
	Less sweet	Sweet	Very sweet	Any	Total
AGE (years)					
Below 20	0	0	1	1	2
20 – 40	37	30	17	0	84
Above 40	50	33	7	2	92
Total	87	63	25	3	178
EDUCATION					
Primary & below	74	52	19	3	148
High school & above	13	11	6	0	30
Total	87	63	25	3	178
SEX					
Female	42	32	15	3	92
Male	45	31	10	0	86
Total	87	63	25	3	178

The results for the root quality traits – dry matter content, beta-carotene content, and sugar content (sweetness) as influenced by community are represented in Figures 3.9 – 3.11. The results show preference for high root dry matter content sweetpotatoes across all the communities (Fig. 3.9). Most communities also prefer moderate beta-carotene (yellow-flesh) sweetpotatoes (Fig. 3.10). However, the Upper East Region and the Greater Accra Region preferred low beta-carotene (white-flesh) and high beta-carotene (orange-flesh) sweetpotatoes, respectively. The results show that the highest number of respondents preferred less sweet sweetpotatoes across the communities, with the exception of the Upper East Region where sweet types were rated highest (Fig. 3.11). However, the proportion of respondents who preferred very sweet sweetpotato was quite substantial in the Volta Region.

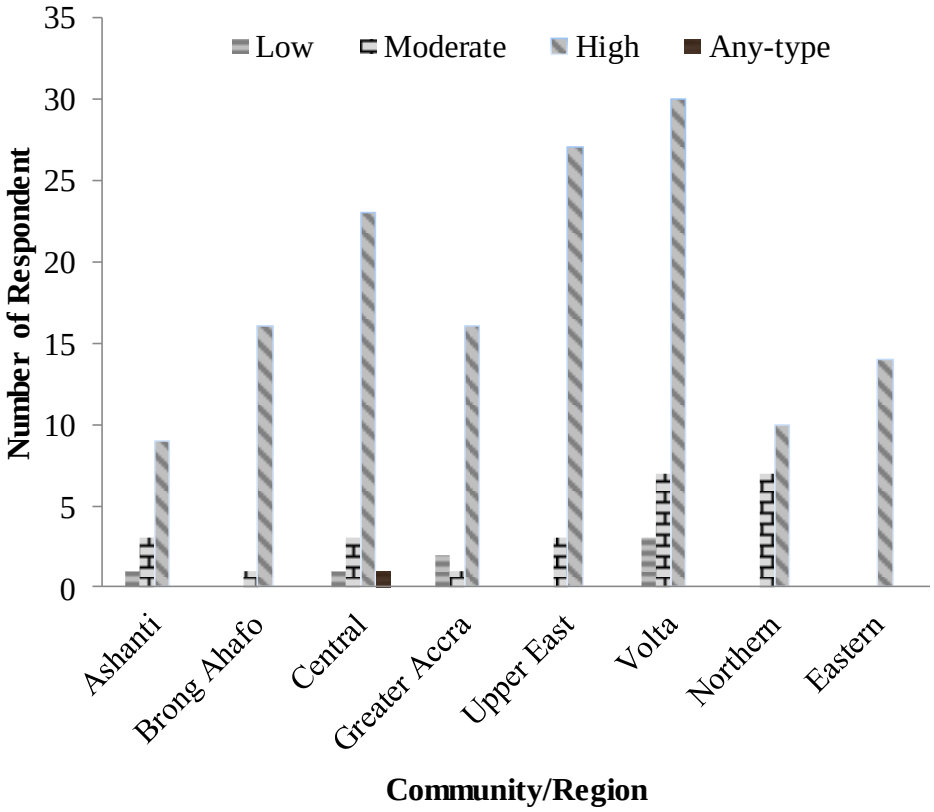

Figure 3.9 Preference for dry matter by different communities (Region)

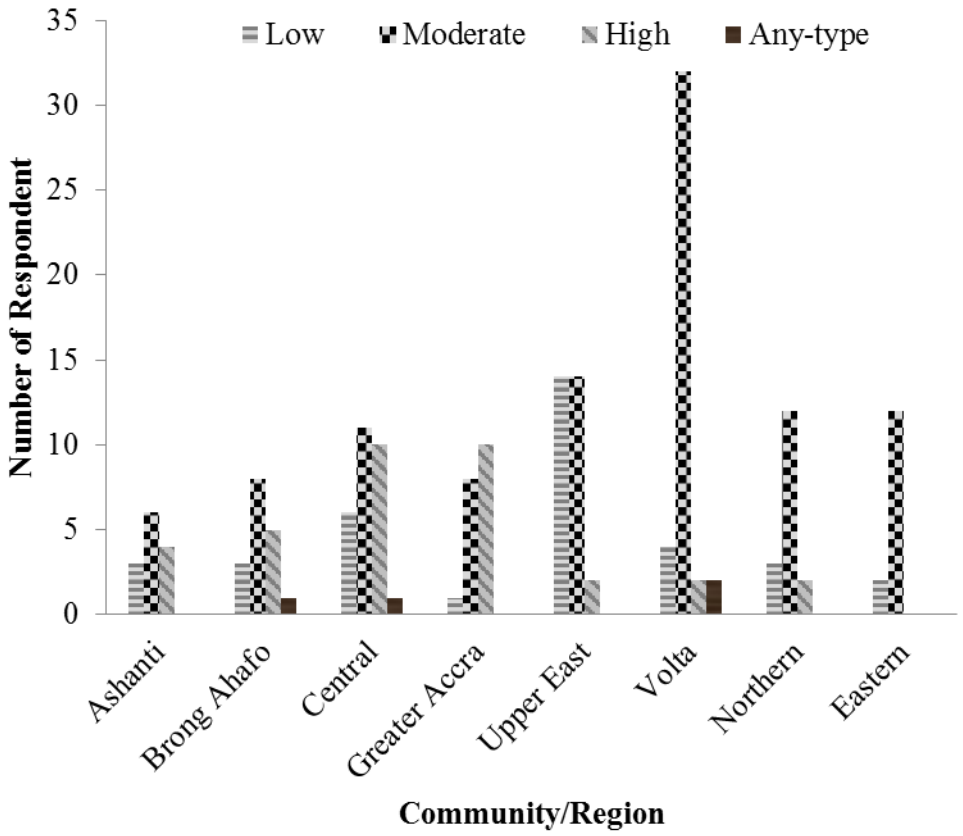

Figure 3.10 Preference for beta-carotene by different communities (Region)

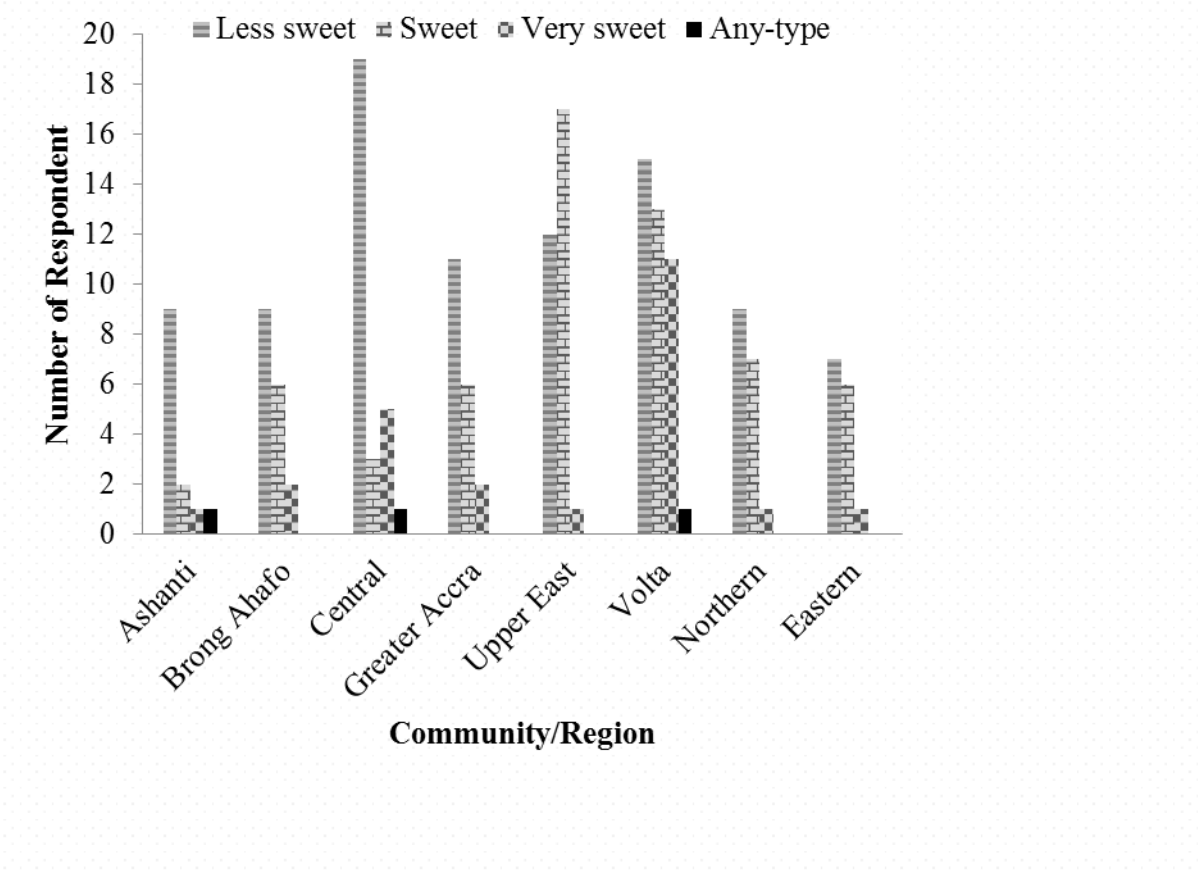

Figure 3.11 Preference for storage root taste (sweetness) by different communities (Region)

3.4. Discussion

The variation obtained in 13 out of the 15 variables (questions) used for the Focal Group Discussion (FGD) suggests presence of a high degree of varying perception, knowledge and opinion of sweetpotato in Ghana. The level of interest and participation of participants were very high, indicating that differences observed may be attributed to social background since discussions were held at different communities/regions. This is because, preference for sweetpotato varies with ethnic background and geographic location (Kays and Horvat, 1983). For most communities sweetpotato is mainly grown and produced in one season (major cropping season) per year. The reason is the availability of rainfall and elusion or avoidance of the sweetpotato weevil. The sweetpotato weevil is the major pest of the crop worldwide

especially in the drier agroecological zone (CIP, 1995; Ames *et al.*, 1996). Major season planting and harvesting are in March/April and August, respectively. Harvesting depends mainly on market availability and household demands. The decision on the crop grown was mainly based on food security and income generation. However, crop adaptability to the environment is also a critical factor in the Northern Region. The potential of sweetpotato as a food security and an income generation crop was confirmed by the current study. This is partly affirmed by the blend of stakeholders (farmers, consumers, processors, and marketers) identified to be associated with the crop. The relative ranking position of sweetpotato to the other crops grown in the study area also affirms the food security and income generating potential of the crop. The average land holding for sweetpotato is very small compared to the other staple crops. This is because in most developing countries, sweetpotato is a smallholder crop tolerant to a wide range of edaphic and climatic conditions and grown with limited inputs (Lebot, 2010). This may be the reason why it has not been captured in the National Agricultural Development Document among the key domestic staples demands in Ghana (METASIP, 2010). This may affirm the report that sweetpotato is still not very well integrated into the average Ghanaian diet (Adu-Kwarteng *et al.*, 2002).

Stakeholders prefer sweetpotatoes with high storage root dry matter content. These types suit their food preparation. This is because the method of cooking and the form of utilization have critical influence on taste and consumptive quality (Sugri *et al.*, 2012). Sweetpotatoes were mainly consumed by frying and boiling in the form of *ampesi*. Cooking leads to changes in physical, sensory and chemical characteristics of the final product (Vitrac *et al.*, 2000; Fontes *et al.*, 2011). The storage root flesh is mainly starch, which swells upon water absorption which hydrolyses the weak bonds making it more easily digestible. However, low dry matter types lose their cooking quality (mealiness) when cooked, affecting textural characteristics

preference. Frying enhances sensorial characteristics such as smell, flavour, colour, texture as well as overall palatability (Sugri *et al.*, 2012). Frying involves drying, cooking or fast dehydration in which the water is removed from the food by means of immersion into oil at temperatures of 120 – 180^{0}C (Vitrac *et al.*, 2000). The frying oil is incorporated into the food and occupies part of the space left by the evaporated water thereby increasing palatability, flavour, calorie supply and shelf-life (Vitrac *et al.*, 2000; Fontes *et al.*, 2011). For the reason that the oil occupies spaces left by water, low dry matter sweetpotatoes absorb more oil which is not economical to processors as well as healthy to the consumers. Other uses of sweetpotato were stew preparation from the leaves and as herb for jaundice (in the Eastern Region), and the use of the storage roots as a source of sugary flour for porridge in the Northern Region. One of the oldest uses was sweetening porridges and maize products, such as *Aboolo* (steamed or baked sweetened fermented maize dough) (Osei-Opare and Adjei-Poku, 1977). The latter two may be exploited for commercial medicinal and sugar flour production.

There were varied responses for constraints to sweetpotato consumption. With exception of Greater Accra Region that did not have any constraint, the other communities mentioned sweetness as the constraint that causes people to turn away from the crop as staple food. This affirms Missah and Kissiedu (1994) and Opare-Obisaw *et al.* (2000), report that locally available sweetpotatoes have very sweet taste, which limits their consumption as a staple food. It may also explain why it is uncommon to find sweetpotato served in Ghanaian restaurants, canteens, and schools unlike other roots and tubers which are widely consumed in a variety of preparations (Sam and Dapaah, 2009). This confirms the report that high levels of sweetness and strong flavour associated with many cultivars of sweetpotatoes may have reduced its popularity as a staple food (Woolfe, 1992). The findings also agree with the

observation that consumers in Ghana prefer sweetpotatoes with dry, mealy flesh and low sugar content (Sam and Dapaah, 2009). The sweetness was perceived to have negative effect on health and was believed to cause diabetes, malaria, piles, flatulence, allergies, and hernia. These may also be the reasons why it is still not an important component of the average Ghanaian diet. These justify and support the need to adjust sweetpotato breeding objectives to develop non-sweet sweetpotato cultivars in Ghana to raise its standard to a staple food status. This is because according Lebot (2010), although not thoroughly been investigated, the hundreds of cultivars found in Papua New Guinea and Island Melanesia, are low in sugars, allowing an important daily consumption. Sweetpotato varieties that suit staple consumption must therefore, according to Kays *et al.* (2005), be non-sweet with sugar content of less than 12%. Breeding such varieties is possible since a local variety of Vanuatu which suits staple purpose has a total sugar content as low as 1.49% of dry matter (Lebot *et al.*, 2009).

In spite of these perceived hazards, good health attributes that were mentioned include better vision for children, and being good food for pregnant women. This suggests that the respondents have some knowledge of the benefit of beta-carotene found in the orange-flesh cultivars. Sweetpotatoes are used in a number of African countries to combat the widespread Vitamin A deficiency that results in blindness and/or death of 250,000 - 500,000 African children a year (CGIAR, 2005). However, preference for beta-carotene is skewed towards low- and moderate beta-carotene sweetpotatoes. Orange-flesh sweetpotato is not popular in Ghana even though it has been shown that even small amounts of these varieties as a regular part of the diet will eliminate vitamin A deficiency in adults and children. According to Thottappilly (2009), African countries have traditionally grown white-flesh sweetpotatoes which are low in vitamin A. The orange-flesh cultivars are low in root dry matter content and

high root dry matter is preferred by most Ghanaians and this may be the reason for consumers' lack of preference for the orange–flesh types. However, considering the health benefits of the beta-carotene in the orange-fleshed types, it is important to incorporate high dry matter into the high beta-carotene genetic backgrounds. For a genetically complex crop like sweetpotato (a hexaploid) and negatively correlated traits like beta-carotene and dry matter content, crossing and recurrent selection should be used. Crossing and recombination among superior, yet complementary parents, and selection among segregating progenies for improved performance is needed to develop superior new varieties. Recurrent selection increase the frequencies of favourable alleles at multiple loci in breeding populations through inter-mating of selected individuals (Moose and Mumm, 2008). Recurrent selection could be used for the development of sweetpotatoes that have high dry matter content, high beta-carotene content and low sugar content (bland taste). There is also the need to educate consumers on their health concerns to ease their fears. This is because even though the galactoside oligosaccharides, verbascose, starchyose and raffinose in legumes have been correlated with their gas formation (flatulence) (Padmaja, 2009), there is no concrete evidence to that in sweetpotato (Truong *et al.*, 1986). Again, despite its name sweetpotatoes may be a good food for diabetics as they help to stabilize blood sugar levels and provide lower insulin resistance (Kusano and Abe, 2000; Ray and Tomlins, 2010). They also need to be aware that sweetpotato consumption does not cause malaria. High incidence of malaria is due to the widespread unclean environment which serves as the breeding grounds for the mosquitoes.

Food preference may vary among individuals, age groups, gender and sometimes cultures as well as geographic locations (Sugri *et al.*, 2012). Even though technology adoption is

influenced by socio-economic factors such as age, sex, and educational background, no significant interaction was established between these and the preferences identified in this study. Preference for non-sweet sweetpotato cultivars with high storage root dry matter and low or moderate beta-carotene content was consistent across the entire respondents. All of the communities preferred high dry matter content. However, there were differences among communities for preference for storage root beta-carotene, and taste (sweetness). The breeding objectives for developing and releasing sweetpotato in Ghana could be community specific. This is because preferences for the sweetpotato vary with ethnic background and geographic location (Kays and Horvat, 1983). Even though less sweet types were preferred in all the communities, consumers in the Upper East region preferred moderately sweet types as well. The Ashanti, Brong Ahafo, Central, Volta, Northern, and the Eastern Regions preferred moderate beta-carotene (yellow-flesh) types. On the other hand, Greater Accra Region preferred high beta-carotene (orange-flesh) varieties more than moderate beta-carotene (yellow-flesh) types whilst Upper East Region also preferred both low beta-carotene (white-flesh) and moderate (yellow-flesh) sweetpotatoes.

3.5. Conclusion

The survey established the potential of sweetpotato as an income generating and food security crop in Ghana. It also revealed that consumers in Ghana desire non-sweet sweetpotatoes with high storage root dry matter content and low or moderate beta-carotene content. There is therefore, a justification to adjust sweetpotato breeding objectives to develop high dry matter non-sweet sweetpotato types in Ghana. Sweetpotato breeding programmes should be adjusted to accommodate specific community needs as well.

CHAPTER FOUR

4.0 GENETIC DIVERSITY OF SWEETPOTATO GENOTYPES AND THEIR UTILIZATION IN GHANA

4.1. Introduction

A prerequisite for genetic improvement of sweetpotato is knowledge of the extent of genetic variation present within genotypes or between cultivars. Information on genetic diversity guides selection of divergent parents to broaden genetic base of a breeding population and produce progenies with heterosis (Manosh *et al.*, 2008). There are very few studies on the genetic diversity and breeding potential of sweetpotato populations. It is, therefore, useful to assess the genetic diversity of sweetpotato accessions assembled for end-user preferred traits improvement. Genetic markers are commonly used to assess genetic diversity among populations and accessions (Turyagyenda *et al.*, 2012). Selectable markers (agro-morphological traits) respond to selection pressure and change after several years of natural and/or artificial selection (Yong-Jin *et al.*, 2009). On the contrary, neutral genetic markers are least subjected to selection pressure and can accurately detect genetic diversity among populations and accessions (Chakravarthi and Naravaneni, 2006; Raji *et al.*, 2009). Application of both markers to determine the genetic variation in a breeding population of a highly heterozygous crop like the sweetpotato is the best.

In spite of the availability of many genetic markers, simple sequence repeats (SSR) markers are currently the genetic markers of choice for diversity studies in sweetpotato (Buteler *et al.*, 1999; Diaz and Gruneberg, 2008; Tumwegamire *et al.*, 2011). SSR markers are competitive because they are multi-allelic, highly polymorphic, highly reproducible, co-dominant and provide rich genetic information with good genome coverage (Kawuki *et al.*, 2009; Sree *et*

al., 2010). They are also affordable and amenable to most breeding procedures and, thus, applicable in public breeding programmes which may not be able to afford expensive diversity assessment techniques (Turyagyenda *et al.*, 2012).

The objectives of this study were to:

a) Characterize sweetpotato accessions in Ghana using agro-morphological and physico-chemical descriptors.
b) Determine the genetic variation among and within the accessions using SSR markers to guide the selection of divergent parents for the genetic improvement of storage root dry matter content, beta-carotene content, and sugar content.
c) Assess the breeding potential of the sweetpotato accessions in Ghana for the improvement of these desired traits.

4.2. Materials and Methods

Three activities were carried out as follows: agro-morphological and physico-chemical characterization, molecular characterization using SSR markers, and the estimation of genetic parameters useful for determining genetic potential.

4.2.1. Agro-morphological and Physico-chemical Characterization

4.2.1.1. Germplasm collection and evaluation

Germplasm were collected from the major sweetpotato growing areas in Ghana in 2010. These were the Northern, Upper East, Upper West, Volta, Eastern, Central and the Brong Ahafo Regions. Collections from the CSIR-Crops Research Institute, Kumasi and the CSIR-Plant Genetic Resource Institute, Bunsu, were also included. In addition, accessions were

collected from the Crop Science Department, University of Ghana and the International Potato Centre (CIP) gene bank in Accra and Kumasi, respectively. A total of 115 sweetpotato accessions (Table 4.1) were collected. These represent four groups, namely local accessions (32), local improved accessions (13), exotic and local accessions in National Agricultural Research Systems (NARS) or programmes (43), and exotic accessions from CIP, Kumasi germplasm (27). Evaluation of the sweetpotato germplasm was carried out under rain-fed conditions using Randomised Complete Block Design (RCBD) with three replications at CSIR-Crops Research Institute research fields at Fumesua (forest ecozone of Ghana) in 2011, after planting material multiplication in 2010. Planting distance was 1 m between ridges and 30 cm (0.30 m) within row of ridge length 3.6 m.

4.2.1.2. Data collection

Data collection was done based on the sweetpotato descriptor for field phenotyping (CIP/AVRDC/IBPGR, 1991) as well as storage root quality traits as shown in Table 4.2. Data on foliage were taken at about 90 days after planting. Harvesting was done at three and half months after planting. At harvest, data were taken on storage root yield and its components and a random sample of storage roots (one small, one medium and one large) were taken for physicochemical analysis. Storage roots considered for the yield data were those approximately over 3 cm in diameter and without cracks, insect damage or rotten parts (Ekanayake *et al.*, 1990). With the exception of the dry matter content, all the storage root quality traits were determined using the near-infrared reflectance spectroscopy (NIRS). Fifty grams fresh sample was used. It was freeze-dried for 72 hours using a freeze dryer. Dry matter content was calculated as ratio of dry weight to fresh weight of sample expressed as a percentage. These were determined at CIP Laboratories in Kumasi, Ghana and Lima, Peru.

Table 4.1 List of the 115 accessions collected and their source

Local accessions	Local improved accessions	NARS Accessions		CIP accessions
CRIWAC 01-10	SANTOMPONA*	TAG 03-019*	B-REGARD*	CIP 442903
CRIWAC 02-10	FARAA*	NS 001*	FIASO RED*	CIP 442291*
CRIWAC 03-10	TEKSANTOM	OK 03-015	TAG 03-030*	CIP 440069
CRIWAC 04-10	OGYEFO*	DOS 03-021	GWERI	CIP 440390*
CRIWAC 05-10*	OKUMKOM*	CARROT C	BD 96-029*	CIP 442462*
CRIWAC 06-10*	OTOO*	HUMBERCHERO*	FREMA*	CIP 442776
CRIWAC 07-10*	HISTARCH*	B/FASO 002*	DOS O3-006*	CIP 440062*
CRIWAC 08-10*	SAUTI*	FA 10-026*	NS 003	CIP 442589*
CRIWAC 09-10	APOMUDEN*	RESISTO*	AAT 03-004	CIP 442145
CRIWAC 10-10*	LIGRI*	NASPOT 1*	OK 03-021	CIP 442147*
CRIWAC 11-10*	BOHYE*	AAT 03-017	BOT 03-030*	CIP 440095*
CRIWAC 12-10*	PATRON*	OK 03-014	OK 03-017	CIP 441771
CRIWAC 13-10*	DADANUIE*	JONATHAN*	KAYIA WHITE	CIP 442901*
CRIWAC 14-10		H-ASIATOR*	UKEREWE*	CIP 443016*
CRIWAC 15-10*		TANZANIA	OK 03-018	CIP 440071*
CRIWAC 16-10		NINGSHU 1*		CIP 442896*
CRIWAC 17-10*		BOT 03-021		CIP 442162*
CRIWAC 18-10		KEMB 37		CIP 442775
CRIWAC 19-10*		BOT 03-028*		CIP 443027*
CRIWAC 20-10		BOT 03-020*		CIP 443129*
CRIWAC 21-10		J-ORANGE*		CIP 442264*
CRIWAC 22-10		BOT 03-027*		CIP 442654
CRIWAC 23-10*		ADA 001		CIP 443035*
CRIWAC 24-10*		DOS O3-017*		CIP 442913*
CRIWAC 25-10*		NAV 001		CIP 442237*
CRIWAC 26-10		AAT 03-025*		CIP 443019
CRIWAC 27-10*		B/FASO 001*		CIP 442850*
CRIWAC 28-10*		ZAMBEZI*		
CRIWAC 29-10*				
CRIWAC 30-10				
CRIWAC 31-10*				
CRIWAC 32-10*				

*** List of the 76 sweetpotato accessions used for the molecular characterization**

Table 4.2 List of agro-morphological descriptors and root quality traits

Foliage descriptors	Agronomic descriptors and storage root morphology	Storage root quality descriptors
Vine inter-node length	Storage root shape (1 - 9)	dry matter
Vine inter-node Diameter	Variability of storage root shape (3 - 7)	fructose
	Storage root surface defects (0 - 8)	glucose
Vine colour (1 - 9)	Storage root cortex thickness (1 - 9)	sucrose
Vine tip pubescence (0 - 7)	Storage root skin colour (1- 9)	maltose
Mature leaf size	Storage root flesh colour (1 - 9)	total sugars
Petiole length	Storage root formation (1 - 7)	beta-carotene
Petiole pigmentation (1 - 9)	Storage root stalk (0 - 9)	starch
Vine weight	Number of storage roots/plant	Protein
General outline of leaf (1 - 7)	Number of storage root (marketable)	Calcium
	Number of storage root (unmarketable)	Magnesium
	Weight of storage root	Iron
	Weight of storage root (Marketable)	Zinc
	Weight of storage root (Unmarketable)	
	Variability of storage root size	
	Harvest index	
	Latex production in storage roots (3 - 7)	
	Oxidation in storage roots (3 - 7)	

Values in parenthesis indicate scale of measurement

4.2.1.3. Data analysis

The data were subjected to Principal Component Analysis (PCA) and Cluster Analysis using Genstat version 9.2.0.152 (Genstat, 2007). The PCA was done based on the correlation

matrix. Data for beta-carotene, dry matter and total sugar contents were subjected to an Analysis of Variance (ANOVA) using Genstat version 9.2.0.152 (Genstat, 2007). Based on their mean performance, the top 10 and the bottom 10 accessions were selected to construct the dendrogram and a GGE Biplot. This was done using the most important traits for the first two principal components which accounted for the most variation in the sweetpotato accessions studied. The dendrogram was constructed based on the hierarchical, single link method using Euclidean test. The biplot was constructed to depict the phenotypic relationships among the accessions, their correlation with the traits significant for PC1 and PC2, as well as the association among the traits. The biplot was constructed using GGE Biplot software (Yan and Kang, 2003).

4.2.2. Molecular Characterization using SSR Markers

The work was carried out at the Molecular Biology Laboratories of the Crops Research Institute of the Council for Scientific and Industrial Research (CSIR-CRI), Fumesua, Ghana, and the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India, in 2012.

4.2.2.1. Planting material

A total of 76 sweetpotato accessions were used for the study (Table 4.1). These represented four groups, namely collections from International Potato Centre (CIP) gene bank in Kumasi, Ghana (19), local collection from farmers' field (19), local improved varieties (12), and local and exotic collections sourced from the National Agricultural Research Systems (NARS) or programmes (26). These were planted at the CSIR-Crops Research Institute research fields at Fumesua.

4.2.2.2. DNA extraction

This was done at the Molecular Laboratory of the CSIR-Crops Research Institute, Fumesua using the method of Egnin *et al.* (1998). Two hundred milligram (200 mg) of young tender leaf tissue was weighed into 2 ml Eppendorf tube and was ground to powder after freeze drying with liquid nitrogen. Eight hundred microliter (800 µl) of buffer A (lysis powder) was added and incubated at 90ºC for 10 minutes, and vortexed every 5 minutes. The suspension was cooled at room temperature for 2 minutes after which 400 µl of 5 M potassium acetate was added and then gently mixed by inversion 5 – 6 times. The suspension was then incubated on ice for 30 minutes with continuous shaking, followed by centrifuging at 13,000 rpm for 10 minutes. The upper phase was transferred to a new Eppendorf tube. One volume of cold isopropanol and $1/10^{th}$ of 3 M sodium acetate was added and mixed 10X by inverting the tube. This was followed by incubation at -20^0C for 1hr, and centrifuging at 13,000 rpm for 10 minutes. The supernatant was poured off, the pellets were washed with 800 µl, 80% ethanol, and centrifuged at 14,000 rpm for 5 minutes. The alcohol was then discarded and the pellets were dried. Five hundred microliter (500 µl) of 1X TE buffer was used to dissolve the pellets, followed by the addition of 4 µl RNase A, and incubation at 37^0C for 30 minutes. This was followed by addition of 250 µl of 7.5M ammonium acetate. The suspension was incubated on ice for 3 minutes, and centrifuged at 13,000 rpm for five minutes, and then transferred into a new 1.5 ml tube. Seven hundred microliters (700 µl) of isopropanol was added, mixed by inversion (ice inversion), and centrifuged at 13,000 rpm for 15 minutes. The supernatant was discarded and the pellets were washed with 1ml 80% ethanol by centrifuging at 14,000 rpm for five minutes. Again the supernatant was discarded, followed by drying of the pellets at room temperature. The DNA pellets were then dissolved in 200 µl 1X TE buffer, and its quality was checked on 0.8% agarose gel.

4.2.2.3. Genotyping with simple sequence repeats (SSR) markers

The genotyping was carried out at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India. A 3 ng sample of total genomic DNA from each of the samples was used for the polymerase chain reactions (PCRs). Twenty-five pairs of SSR markers confirmed for sweetpotato DNA amplification (Buteler *et al.*, 1999; Diaz and Gruneberg, 2008; Tumwegamire *et al.*, 2011) were used (Table 4.3). A final volume of the reaction mixture of 10 µL, which contains 25 mM MgCl2, 10x buffer, 10 mM deoxyribonucleotide triphosphate (dNTPS), 1 µM M13 FORWARD 700/800, 1 µM forward primer, 1 µM reverse primer, 5 U µL–1 *Taq* polymerase, 10 ng µL–1 DNA, and a double distilled water were used for the PCR. The amplification conditions were set up at 94°C for four minutes and denaturation at 94°C for one minute; annealing at between 56.0 - 62.0°C (depending on the annealing temperature of the primer); and polymerization at 72°C for one minute. Step 2 annealing was 56.0 - 62.0°C (depending on the annealing temperature of the primer) and was repeated 30 times, and a final extension at 72°C for 7 minutes.

Table 4.3 List and description of the 25 SSR markers used to characterize the sweetpotato accessions

Marker	Repeat	Primer F	Primer R	Size	Temperature (^{0}C)	Reference
Ib3/24	Not determined	TTTGGCATGGGCCTGTATT	GTTCTTCTGCACTGCCTGATTC	-	56	Tseng_et_al,_2002
Ib-316	(CT)3C(CT)8	CAAACGCACAACGCTGTC	CGCGTCCCGCTTATTTAAC	150	58	Buteler_et_al,_1999
Ib-242	(CT)3CA(CT)11	GCGGAACGGACGAGAAAA	ATGGCAGAGTGAAAATGGAACA	135	58	Buteler_et_al,_1999
Ib-297	(CT)13	GCAATTTCACACACAAACACG	CCCTTCTTCCACCACTTTCA	134	58	Buteler_et_al,_1999
IBCIP-1	(ACC)7	CCCACCCTTCATTCCATTACT	GAACAACAACAAAAGGTAGAGCAG	140-153	63	Yañez,_2002
IBCIP-2	(ACC)2+6	GTAACCTGTCAGCCATCTGT	CCTAGTGGGTATTTGCAGAG	268-290		Yañez,_2002
IbC12	(TTC)6	TCTGAGCTTCTCAAACATGAAA	TGAGAATTCCTGGCAACCAT	94-108	55	Solis_et_al,_2009
IbS01	(AGA)10	TCCTCCACCAGCTCTGATTC	CCATTGCAGAGCCATACTTG	210 – 228	56	Benavides_et_al,_2005
IbR03	(GCG)5	GTAGAGTTGAAGAGCGAGCA	CCATAGACCCATTGATGAAG	245-263	56	Benavides_et_al,_2005
IbS07	(TGTC)7	GCTTGCTTGTGGTTCGAT	CAAGTGAAGTGATGGCGTTT	177-194	55	Benavides_et_al,_2005
IbS10	(CT)12	CTACGATCTCTCGGTGACG	CAGCTTCTCCACTCCCTAC	253-298	60	Benavides_et_al,_2005
IbS11	(TTC)10	CCCTGCGAAATCGAAATCT	GGACTTCCTCTGCCTTGTTG	217 -242	60	Benavides_et_al,_2005
IbS17	(GGA)4	CAGAAGAGTACGTTGCTCAG	GCACAGTTCTCCATCCTT	158 – 198	58	Benavides_et_al,_2005
IbS18	(TAGC)4	CTGAACCCGACAGCACAAG	GGGAAGTGACCGGACAAGA	232-242	58	Benavides_et_al,_2005
IbR12	(CAG)5A	GATCGAGGAGAAGCTCCACA	GCCGGCAAATTAAGTCCATC	331-393	60	Benavides_et_al,_2005
IbR13	(TTC)6	GTACCGAGCCAGACAGGATG	CCTTTGGGATTGGAACACAC	205-258	60	Benavides_et_al,_2005
IbR14	(CCT)6	CCTATGGCAATTCGGTCACT	GGAACATTGCCTACACTCTG	216 -222	58	Benavides_et_al,_2005
IbR16	(GATA)4	GACTTCCTTGGTGTAGTTGC	AGGGTTAAGCGGGAGACT	196-215	60	Benavides_et_al,_2005
IbR19	(CAG)5b	GGCTAGTGGAGAAGGTCAA	AGAAGTAGAACTCCGTCACC	192-213	60	Benavides_et_al,_2005
IbR21	(GAC)5	GACAGTCTCCTTCTCCCATA	CTGAAGCTCGTCGTCAAC	169-186	58	Benavides_et_al,_2005
IbR20	(GGC)5	CTTCACTCTGCTCGCCATTA	GTACTTGGACGGGAGGATGA	194 – 212	48	Benavides_et_al,_2005
J175	(AATC)4	ATCTATGAAATCCATCACTCTCG	ACTCAATTGTAAGCCAACCCTC	-	58	Solis_et_al,_2009
J10A	(AAG)6	TCAACCACTTTCATTCACTCC	GTAATTCCACCTTGCGAAGC	-	58	Solis_et_al,_2010
J67	(GAA)5	CACCCATTTGATCATCTCAACC	GGCTCTGAGCTTCCATTGTTAG	-	58	Solis_et_al,_2011
J116A	(CCT)6	TCTTTTGCATCAAAGAAATCCA	CCTCAGCTTCTGGGAAACAG	-	58	Solis_et_al,_2012

4.2.2.4. Simple sequence repeats data scoring and analysis

Accessions amplified were noted and used to estimate percent accessions amplified. The number of alleles for each marker was noted and recorded. Markers that showed variation in at least 25% of the accessions were noted and their alleles were recorded as unique alleles. Percent unique alleles were computed as the ratio of number of unique alleles to the total number of alleles. Genotypes were scored for the presence (1) or absence (0) of each fragment. NTSYSpc software version 2.1 (Rohlf, 1993; Rohlf, 2002) was used to run the binary data. Jacard's coefficients (Jaccard, 1908) were used to construct a similarity matrices from the binary data by using SIMQUAL algorithm. This was followed by construction of a dendrogram using the unweighted paired group method average (UPGMA) applying the SHUAN algorithm. Principal Coordinate Analysis (PCoA) was performed from Jacard's coefficients using Genstat (Genstat, 2007). The polymorphic information content (PIC) was determined based on the approach and method of Weir (1996) as presented below;

$$PIC = 1 - \Sigma P_i^2 \text{ ; Where, Pi is the frequency of the ith allele.}$$

Analysis of Molecular Variance (AMOVA) was also performed using Arlequin 3.1 version computer software (Excoffier *et al.*, 2006), to quantify the genetic variation and relationship existing between and among the sweetpotato clones and the four population groups studied.

4.2.3. Estimation of Genetic Parameters

4.2.3.1. Field and laboratory work

This was carried out at Fumesua (Forest ecozone) and Pokuase (Coastal Savanna ecozone) in the major and minor cropping seasons from May to December, 2011. The sweetpotato accessions used were same as presented in Table 4.1. The planting arrangement was one row

per ridge with a distance of 1 m between ridges from their centers. The length of a ridge was 3.6 m and within row planting space was 30 cm making a total of 12 plants per ridge. The laboratory work was carried out in the Laboratories of the International Potato Centre in the CSIR-Crops Research Institute, Fumesua, Ghana and Lima, Peru, respectively.

4.2.3.2. Data collection

Harvesting was done at three and half months after planting. The 10 central plants were harvested and one large, one medium, and one small storage roots were randomly selected for physicochemical analysis after yield data were recorded. Storage roots considered for the yield data were those approximately over 3 cm in diameter and without cracks, insect damage or rotten parts (Ekanayake *et al.*, 1990). The yield data taken were total root yield and marketable root yield. In addition, harvest index was recorded as the ratio of the total root yield to the total biomass. The physico-chemical traits determined were beta-carotene content, dry matter content, fructose, glucose, sucrose, total sugars, starch content, protein content, iron content and zinc content. The physico-chemical traits were determined using the Workflow for Sample Preparation and near-infrared reflectance spectroscopy (NIRS) analysis of sweetpotato developed by the Quality and Nutrition Laboratory of the International Potato Centre (CIP), Lima, Peru. With exception of dry matter content, all the storage root quality traits were determined using the NIRS after milling. Fifty grams (50g) fresh sample was used. The sample was freeze-dried using freeze dryer for 72 hours. Dry matter content was calculated as the ratio of the dry sample expressed as a percentage of the weight of the wet sample.

4.2.3.3. Data analysis

Only data for 102 out of the 115 accessions were analysed due to missing information. The analysis also excluded minor cropping season data for Pokuase because the experiment failed due to erratic rainfall. The data were subjected to Analysis of Variance (ANOVA) using Genstat statistical package (Genstat, 2007). The relative efficiency (RE) of an alpha lattice design over randomized complete block design (RCBD) was not significant. The RE was determined as shown below;

$$RE = \frac{S.E_{RCBD}}{S.E_{\alpha\text{-lattice}}} \quad \text{OR} \quad RE = \frac{MSe_{RCBD}}{MSe_{\alpha\text{-lattice}}}$$

Where; S.E = standard error; MSe = Error means square; RE is significant if the ratio is >1 and vice versa. Hence, RCBD with two replications was used to analyse the data employing the method of Steel and Torrie (1980) as shown in Table 4.4.

Table 4.4 Format of Analysis of Variance for the study

Source	MS	Expected of Mean Square (EMS)
Loc. (L)		
Rep R (L)		
L X R (L)		
Genotype (G)	MS_G	$\sigma^2_E + r\sigma^2_{GL} + rl\sigma^2_G$
G X L	MS_{GL}	$\sigma^2_E + r\sigma^2_{GL}$
Pooled error	MS_E	σ^2_E

Note: MS = Means Square for a particular source of variation; σ^2_G = Genotypic variance; σ^2_{GL} = Genotype by location interaction variance; σ^2_E = error variance; r = number of replications/location, and l = number of location or environment

The variance components were used to determine the genotypic variance (GV) and phenotypic variance (PV) as per Prasad *et al.* (1981) as follows:

$$\text{Genotype x Location interaction variance } (\sigma^2_{GL}) = \frac{MS_{GL} - MS_E}{r}$$

$$\text{Genotypic variance } (\sigma^2_G) = \frac{MS_G - MS_{GL}}{rl} = \frac{\sigma^2_E + r\,\sigma^2_{GL} + rl\,\sigma^2_G - \sigma^2_E + r\,\sigma^2_{GL}}{rl}$$

$$\text{Phenotypic variance } (\sigma^2_P) = \frac{\sigma^2_G + \sigma^2_{GL}}{l} + \frac{\sigma^2_E}{rl} = \frac{\sigma^2_G + (MS_{GL} - MS_E)/r}{l} + \frac{\sigma^2_E}{rl}$$

$$\text{Error Variance } (\sigma^2_E) = MS_E$$

Furthermore, the variance components were used to compute broad sense heritability (H_b^2), Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV) and Genetic Advance (GA) as reported (Burton, 1952; Johnson *et al.*, 1955; Kumar *et al.*, 1985). These are presented below.

$$\text{Heritability in broad – sense } (H^2_b) = \frac{\sigma^2_G}{\sigma^2_P} = \frac{\sigma^2_G}{\sigma^2_G + \sigma^2_{GL}/l + \sigma^2_E/rl}$$

$$\text{Genotypic Coefficient of Variation} = \frac{\sigma_G}{X} \times 100$$

$$\text{Phenotypic Coefficient of Variation} = \frac{\sigma_P}{X} \times 100$$

Where; X is the grand mean of a trait.

$$\text{Genetic Advance } (R) = H_b^2 \,.\, k \,.\, \sigma_p$$

Where; k (selection differential expressed in phenotypic standard deviation at 5%) = 2.06.

The genetic advance from selection expressed as percent of grand mean was obtained as shown below.

$$\text{Genetic Advance } (R_{(X)}) = H_b \,.\, k \,.\, GCV$$

This expression shows that the expected genetic advance from selection when expressed as a percent of the mean is the product of the selection differential measured in terms of the phenotypic standard deviation, the genetic coefficient of variation, and the square root of the heritability ratio (Johnson *et al.*, 1955).

Estimates of genotypic correlation coefficient was also computed according to Miller *et al.* (1958) and (IRRI, 2006) as shown below.

The product-moment correlation for two variables 1 and 2 is given by

$$r = \frac{\sigma_{1.2}}{(\sigma^2_1\ \sigma^2_2)}$$

The variance sum of traits 1 and 2 if Y = 1+2 is given by

$$\sigma^2_Y = \sigma^2_1 + \sigma^2_2 + 2\,\sigma^2_{1.2}$$

Therefore, the covariance of traits 1 and 2 is given by

$$\sigma^2_{1.2} = \frac{\sigma^2_Y - (\sigma^2_1 + \sigma^2_2)}{2}$$

$$\text{Genotypic correlation Coefficient } r_{G_{(1.2)}} = \frac{\sigma_{1.2}}{\sqrt{(\sigma^2_{G1})(\sigma^2_{G2})}}$$

Where $\sigma_{G\,(1.2)}$ is the genetic covariance between two traits, σ^2_{G1} is the genetic variance of the first trait and σ^2_{G2} is the genetic variance of the second trait.

4.3. Results

4.3.1. Agro-morphological and Physico-chemical Characterization

4.3.1.1. Principal component analysis

In all 40 agro-morphological and physicochemical traits were studied (Table 4.2). The first six principal components (PCs) with Eigen values greater than 1.0 jointly explained 54.86% of the total variation in the accessions (Table 4.5). The traits of importance for the first component involved root traits of commercial interest. Beta-carotene, dry matter and total sugar contents were of importance for PC 2.

Table 4.5 Principal Component Analysis of the agro-morphological and physico-chemical traits

Trait	PC1	PC2	PC3	PC4	PC5	PC6
Root weight	**-0.371**	-0.091	-0.133	0.005	-0.028	-0.033
Marketable root wgt.	**-0.362**	-0.082	-0.139	0.021	-0.003	-0.008
Unmarketable yield.	**-0.370**	-0.094	-0.128	-0.002	-0.038	-0.043
β-carotene	0.168	**-0.310**	-0.128	-0.050	-0.030	0.024
Calcium	0.035	**-0.300**	0.205	0.155	-0.143	-0.063
Dry matter	0.168	**-0.310**	-0.128	-0.050	-0.030	0.024
Iron	0.172	-0.035	**-0.416**	0.063	-0.126	-0.099
Fructose	0.041	-0.259	-0.056	-0.257	**0.343**	0.173
Glucose	0.023	**-0.316**	0.020	-0.212	**0.307**	0.143
Maltose	-0.046	-0.284	**0.310**	0.119	-0.197	0.009
Magnesium	0.086	**-0.308**	-0.140	0.043	-0.049	-0.086
Rt. Oxidation	-0.064	0.020	-0.111	0.069	-0.032	**0.414**
Protein	0.114	0.071	**-0.401**	0.107	-0.178	-0.125
Starch	-0.141	0.144	**0.361**	0.201	-0.133	-0.018
Sucrose	0.018	-0.235	0.145	0.191	**-0.336**	-0.143
Total sugar	0.029	**-0.404**	0.133	0.030	-0.012	-0.025

Table 4.5 Cont'd. Principal Component Analysis of the agro-morphological and physico-chemical traits

Trait	PC1	PC2	PC3	PC4	PC5	PC6
Zinc	0.157	-0.021	**-0.364**	0.147	-0.249	-0.140
Outline of leaf	0.087	0.017	0.091	0.106	-0.052	0.090
Harvest index	-0.245	0.016	-0.012	**-0.323**	-0.165	-0.165
Latex in roots	-0.001	0.037	-0.015	-0.005	-0.153	0.128
Mature leaf size	-0.165	-0.031	-0.010	**0.301**	0.125	0.037
Storage root no.	**-0.371**	-0.091	-0.133	0.005	-0.028	-0.033
Marketable roots no.	**-0.325**	-0.043	-0.097	-0.087	-0.089	-0.26
Unmarketable rt. no.	-0.144	-0.101	-0.087	0.164	0.102	0.094
Petiole length	-0.119	0.079	-0.085	0.184	0.226	-0.156
Petiole pigmentation	-0.021	0.115	-0.001	-0.185	-0.153	0.260
Cortex thickness	-0.007	0.122	-0.051	0.104	-0.006	0.014
Flesh colour	0.118	0.124	0.061	0.023	0.040	**-0.335**
Root formation	0.070	0.014	-0.022	-0.025	-0.150	0.039
Root shape	-0.038	0.034	0.062	0.045	0.056	**-0.310**
Root skin colour	-0.011	-0.013	-0.114	0.008	-0.239	**0.346**
Root stalk	0.113	0.075	-0.029	0.129	0.146	0.144
Root surface defects	-0.056	-0.066	-0.131	-0.020	0.113	-0.083
Root shape	0.057	0.070	0.011	0.038	0.047	-0.148
Root size variability	-0.079	0.038	0.053	0.116	-0.201	0.168
Vine colour	-0.032	0.164	-0.009	-0.116	-0.261	0.254
Inter-node diameter	-0.105	-0.012	-0.051	-0.116	0.194	0.015
Inter-node length	-0.037	-0.067	-0.075	0.200	0.011	0.185
Vine tip pubescence	0.013	-0.017	-0.026	**0.300**	0.129	0.096
Vine weight	0.023	0.001	-0.039	**0.441**	0.156	0.137
Latent roots (Eigen vectors)	6.304	4.501	3.688	2.817	2.419	2.215
Variability (%)	15.76	11.25	9.22	7.04	6.05	5.54
Cumulative (%)	15.76	27.01	36.23	43.27	49.32	54.86

***Values in bold indicate the most relevant characters (>0.3) that contributed most to the variation of the particular component**

4.3.1.2. Mean performance of the top- and bottom 10 accessions

The mean performance of the top 10 and the bottom 10 selected accessions for beta-carotene, dry matter and sugar contents are presented in Table 4.6. Significant differences were observed between the accessions for all the traits. The range of values obtained for the beta-carotene, dry matter, and total sugar content were 9.83 – 30.34 (mg/100g)DW, 27 – 50%, and 9.83 – 30.34%, respectively. The lowest and the highest values for beta-carotene content were obtained by BOT -03-020 and Apomuden. Apomuden had the lowest dry matter content whilst FA-10-026 had the highest dry matter content. Similarly, CRIWAC 19-10 and CIP 442850 were the accessions that gave the lowest and highest total sugar content, respectively.

4.3.1.3. Bi-plot analysis for the top- and bottom 10 accessions

The distribution of PC1 and PC2 among the correlated traits, the selected accessions as well as between the selected accessions and the correlated traits are shown in Figure 4.1. Three groups were observed for the correlated traits. Beta-carotene content, fructose, total sugars, calcium (Ca), and magnesium (Mg) were bunch together in quadrant 1. Similarly, the storage root yield traits were group in quadrant 2, whilst only dry matter content was found in quadrant 3. Four groups were detected for the accessions. Beauregard and Apomuden were the most distantly related accessions in quadrant 1, whilst CIP 440032 and CIP 442264 were the most distantly related accessions in quadrant 2. The most distant related accessions in the third and fourth quadrants were Histarch and Ogyefo, and CIP 442850 and TAG 03-030, respectively.

Table 4.6 Performance of the top 10 and bottom 10 selected parents for beta-carotene, dry matter and sugar content

ACCESSION	Total Sugars (%)	ACCESSION	Beta-Carotene (mg/100g)DW	Dry matter (%)
Top 10 accessions			**Top 10 accessions**	**Bottom 10 accessions**
CIP 442850	30.34	APOMUDEN	33.67	27
APOMUDEN	28.97	RESISTO	27.53	38
B/FASO 002	24.04	B-REGARD	24.31	32
CIP 440062	23.30	CRIWAC 03-10	23.32	32
B-REGARD	22.90	CIP 442850	20.21	27
CRIWAC 12-10	22.84	CIP 443035	19.75	36
B/FASO 001	22.69	CRIWAC 05-10	19.00	39
TAG 03-030	21.92	BOT 03-028	17.83	38
CIP 440071	21.84	ZAMBEZI	17.58	40
UKEREWE	21.10	BOT 03-020	17.35	39
Bottom 10 accessions			**Bottom 10 accessions**	**Top 10 accessions**
CRIWAC 25-10	12.54	FA 10-026	16.75	50
CRIWAC 30-10	12.45	HISTARCH	9.85	45
DOS O3-006	12.35	CIP 442264	7.74	45
AAT 03-025	12.26	ABAIDOO 01	7.00	44
CRIWAC 11-10	12.26	BD 96-029	12.97	43
CIP 440095	12.06	OGYEFO	6.83	42
OGYEFO	11.67	FARAA	12.27	42
CIP 442264	11.06	CRIWAC 31-10	9.74	41
HISTARCH	10.43	CIP 442896	11.27	40
CRIWAC 19-10	9.83	BOT 03-030	17.35	39
SED (P<0.05)	**2.62**	**SED (P<0.05)**	**1.52**	**3.00**

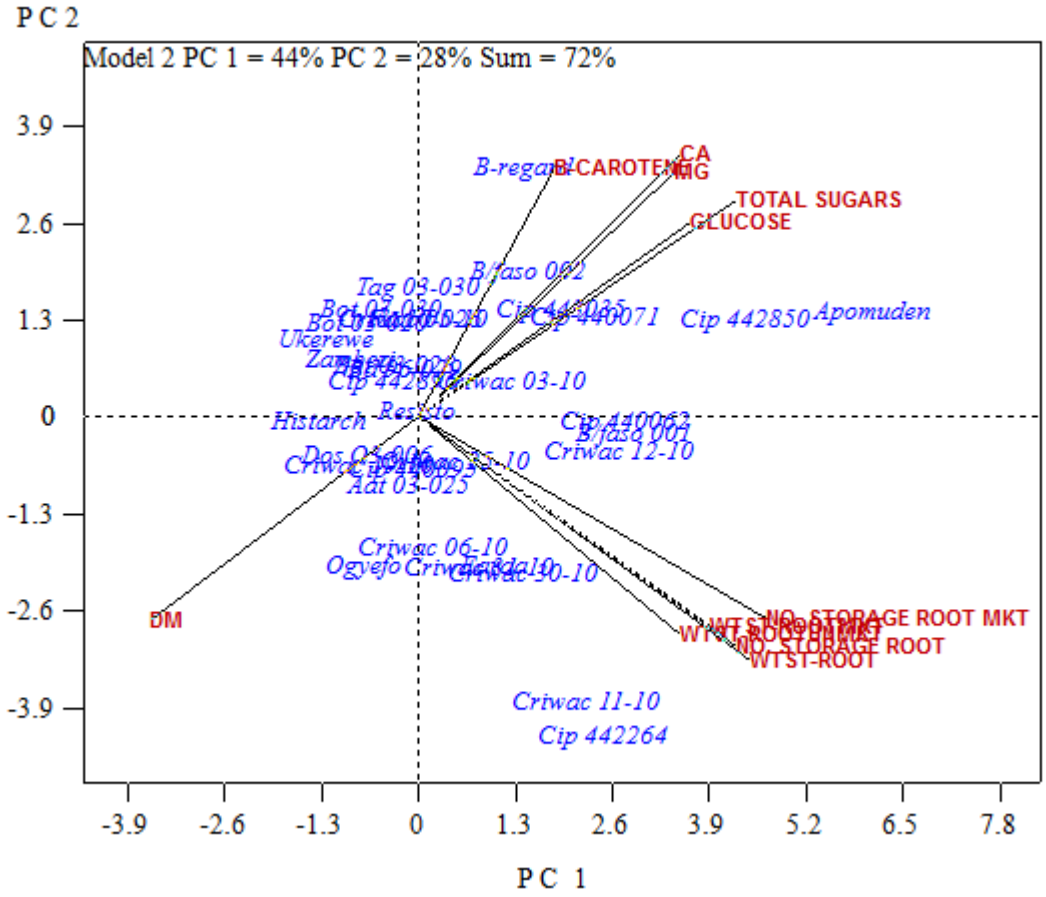

Figure 4.1 Relationship between correlated traits and selected accessions

4.3.1.4. Dendrogram for the top- and bottom 10 accessions

The dendrogram separated the 34 selected accessions with a Euclidean similarity distance ranging from 1.00 to 0.93 (Fig. 4.2). At 1.00 level of similarity, all the accessions were distinct from each other except BOT 03- 030 and CIP 442896. Conversely, at about 0.93 levels of significance, two clusters were identified with all the accessions being similar except for CRIWAC 12-10. Five main clusters A, B, C, D, and E at 94.5% (0.945) level of significance were identified. The first four clusters contained 1 – 5 accessions per cluster whilst the fifth cluster (E) had 26 accession.

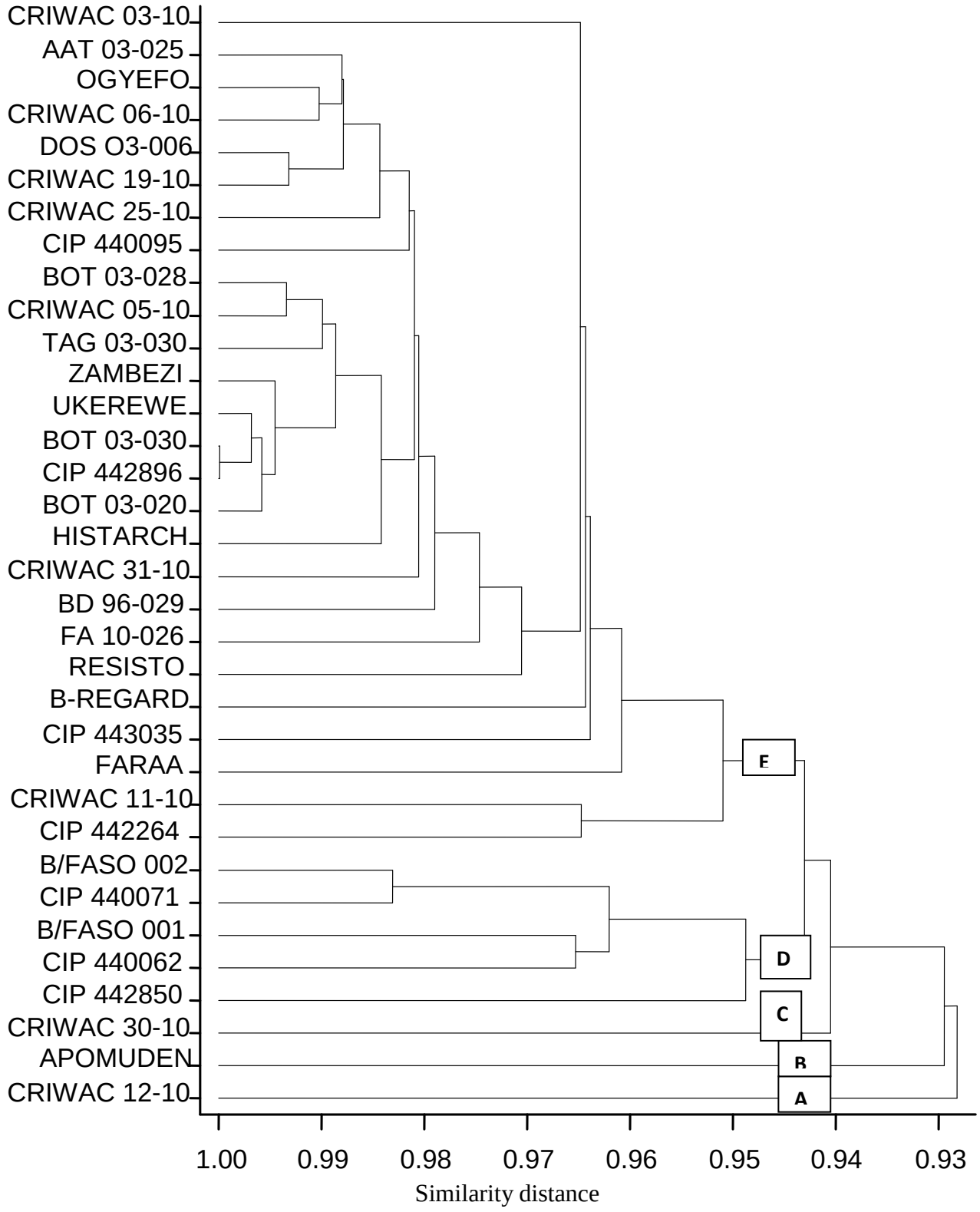

Figure 4.2 Dendrogram constructed based on the selected accessions and correlated traits for PC1 and PC2

4.3.2. Molecular Characterization using SSR Markers

4.3.2.1. Polymorphism, PIC and base range of the 20 SSR markers

Out of the 25 SSR markers used to assess the genetic diversity of the sweetpotato accessions, only 20 produced amplifications. The five markers that did not produce amplification were IbS01, IbS07, IbS10, IbCIP2 and IbR20. A total of 87 polymorphic alleles were observed across the accessions and loci. These ranged from two to six with mean of 4.25. Markers IbS18 and IbR21 recorded the lowest number of alleles whilst Ib3/24, Ib316, Ib-297, IbC12, IbS11, J10A and J116A recorded the highest number of alleles (Table 4.7). Out of the 87 alleles revealed by the 20 SSR markers across accessions and loci, 40 (45.98%) were unique alleles and the average number of unique alleles was two. IBCIP-1, IbC12 and J67 produced no unique alleles whilst Ib3/24 recorded the highest number (5) of unique alleles followed by Ib-297 and J10A with 4 unique alleles. However, Ib3/24 obtained the highest percent polymorphism (83.33%), followed by IbR14 (75.00%). The range and the average percent polymorphism were 0 – 83.33% and 45.50%, respectively. The PIC values were high and ranged between 0.62 for J67 and 0.96 for IbR16 and IbR19, with a mean of 0.84. The highest amplification was recorded by IbR14 (90.91%) followed by IbR316 and J67 with value of 77.92%. However, IbR16 recorded the lowest amplification. Base range for the markers was highest and lowest for IbR03 (262-277) and J175 (133-147). IbS11 recorded the highest number of loci (1- 6) across accessions followed by IbC12 (2 - 6). The lowest number of loci (1-2) across accessions was produced by Ib3-24, IbS18, IbR14 and IBR21.

Table 4.7 Polymorphism and base range of the 20 SSR markers

Marker	Accessions Amplified	Accessions Amplified (%)	No. of Alleles	Loci across Accessions	No. of unique Alleles	Percent Polymorphism	PIC	Base Range
Ib3/24	47	61.04	6	1 - 2	5	83.33	0.87	136 – 150
Ib-316	60	77.92	6	1 - 4	2	33.33	0.66	152 – 168
Ib-242	39	50.65	4	1 - 4	2	50.00	0.90	135 – 155
Ib-297	40	51.95	6	1 – 4	4	66.67	0.86	151 – 183
IBCIP-1	38	49.35	4	1 – 4	0	0.00	0.89	154 – 166
IbC12	54	70.13	6	2 – 6	0	0.00	0.72	108 – 123
IbR03	43	55.84	4	1 – 4	1	25.00	0.86	262 – 277
IbS11	47	61.04	6	1 – 6	2	33.33	0.88	241 – 256
IbS17	51	66.23	5	1 – 3	3	60.00	0.84	181 – 202
IbS18	40	51.95	2	1 – 2	1	50.00	0.87	249 – 253
IbR12	57	74.03	4	1 – 3	2	50.00	0.73	336 – 357
IbR13	32	41.56	4	1 – 4	2	50.00	0.91	222 – 231
IbR14	70	90.91	4	1 – 2	3	75.00	0.75	179 – 188
IbR16	30	38.96	3	1 – 3	2	66.67	0.96	220 – 230
IbR19	31	40.26	3	1 – 3	1	33.33	0.96	212 – 223
IbR21	42	54.55	2	1 – 2	1	50.00	0.84	182 – 203
J175	46	59.74	3	1 – 3	2	66.67	0.93	133 – 147
J10A	38	49.35	6	1 – 4	4	66.67	0.91	192 – 220
J67	60	77.92	3	1 – 3	0	0.00	0.62	191 – 212
J116A	50	64.94	6	1 – 5	3	50.00	0.84	206 – 229
Mean	45.75	59.42	4.35	1.1-3.4	2	45.50	0.84	192.1-208.7

4.3.2.2. Principal coordinates analysis for the 76 accessions

Principal coordinate analysis (PCoA) which was determined from the similarity coefficients are graphically presented in Figure 4.3 (showing diversity in sweetpotato accessions), and Figure 4.4 (showing diversity in the group structure of the sweetpotato accessions). The two axes explained 45.21% of the total similarity (54.79% of total variation) with the first axis (PCoA1) accounting for 28.08% and the second (PCoA2) accounting for 17.13%. The 76 sweetpotato accessions investigated by PCoA did not form clear groups according to the group structure both within and between.

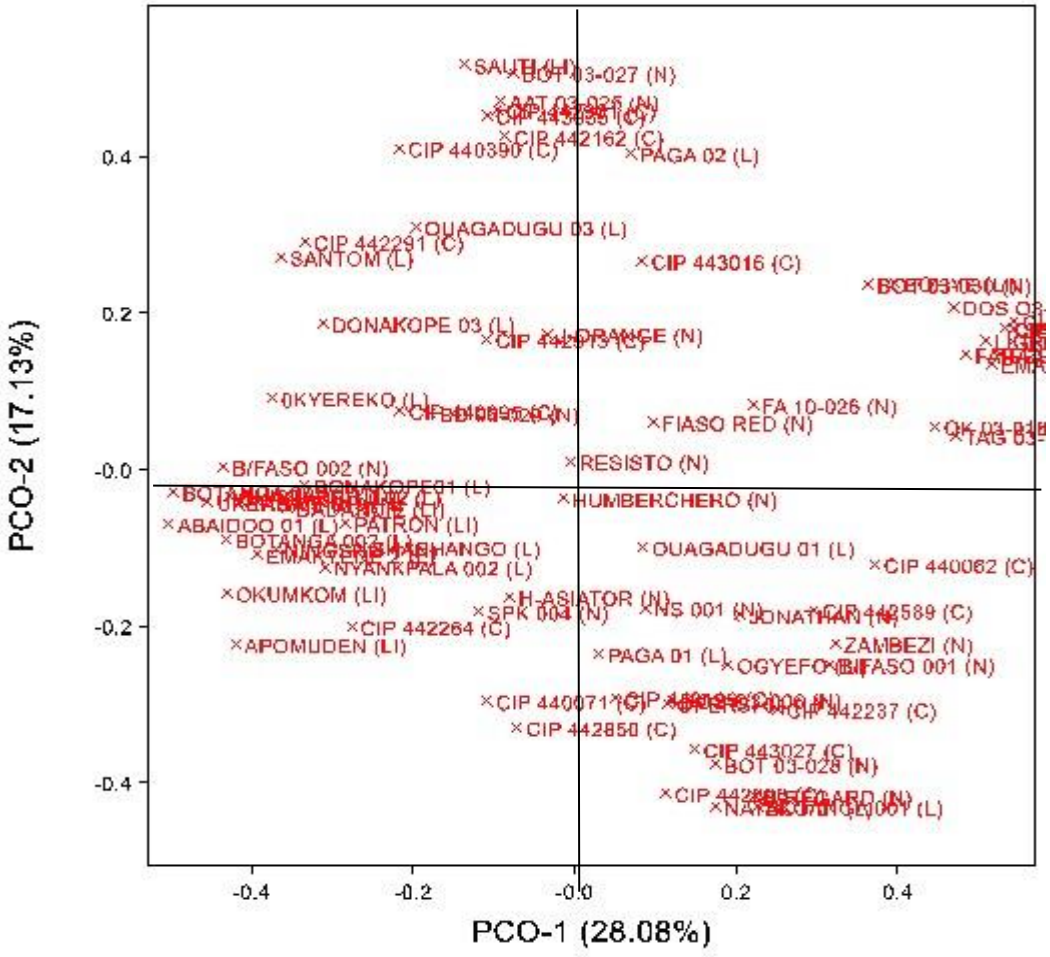

Figure 4.3 Principal coordinates analysis from similarity coefficients of 76 sweetpotato accessions

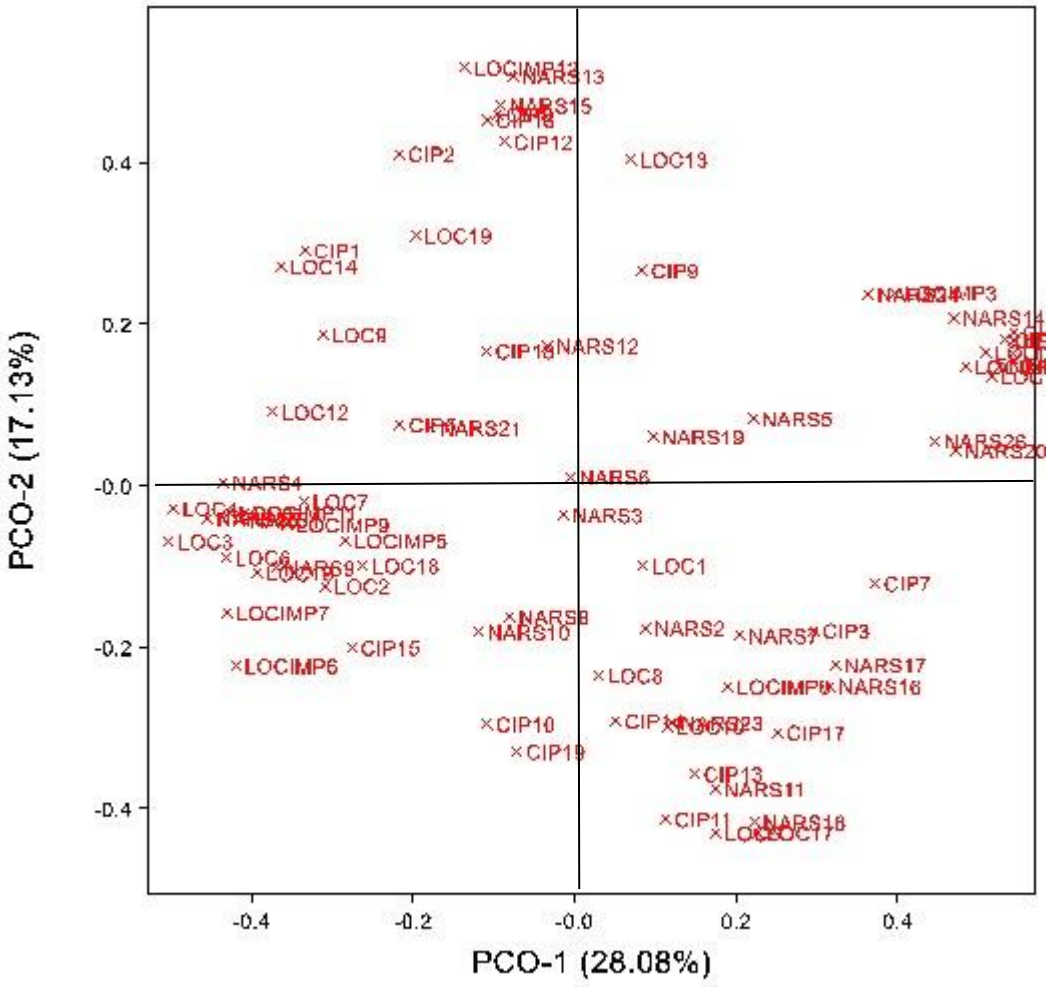

Figure 4.4 Principal coordinates analysis from similarity coefficients of 76 sweetpotato accessions showing the diversity in the group structure

4.3.2.3. Dendrogram for the 76 accessions

The dendrogram constructed separated the 76 sweetpotato accessions into major clusters at different similarity levels ranging from 0.00 to 1.00 (Fig. 4.5). At slightly greater than 0.00 similarity level, two major clusters were observed. CIP 6 (CIP 442462) constitutes the first cluster whist the second cluster consisted of the other 75 accessions. At 0.25 similarity level, seven major clusters were observed whilst 17 were found at 0.50 similarity level. The markers fully discriminated against the 76 sweetpotato clones by the 1.00 level of similarity

except for two improved cultivars LOCIMP2 (Santompona) and LOCIMP10 (Otoo). The primers, however, did not fully discriminate the accessions into the different group structures.

4.3.2.4. Analysis of Molecular Variance (AMOVA) for the 76 accession

Significant differences were observed between the sweetpotato accession within the populations (P<0.01) as well as between the groups (P<0.05) as shown in Table 4.8. The differences observed within the groups however accounted for the greater percentage (97.12%) of variation observed than that found between the groups (2.88%).

Table 4.8 Analysis of molecular variance (AMOVA) for the 76 sweetpotato accession

Source of variation	Df	Sum of squares	Variance components	Percentage of Variation
Among groups	3	55.894	0.35619*	2.88
Within groups	72	865.198	12.01664**	97.12
Total	75	921.092	12.37284	

***Significant at 0.05 **Significant at 0.01**

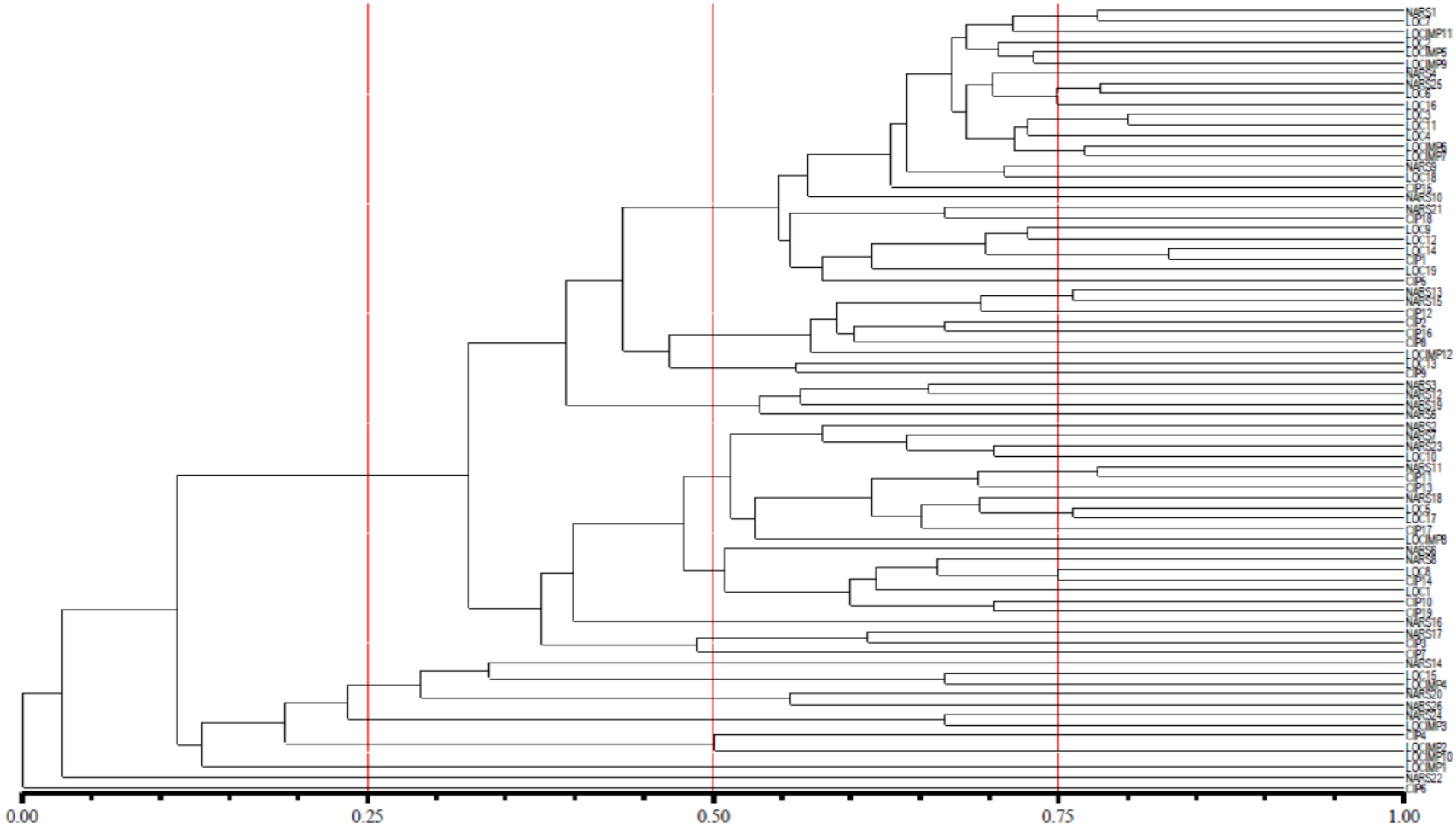

Figure 4.5 Dendrogram showing genetic relationships among 76 sweetpotato accessions

4.3.3. Estimation of Useful Genetic Parameters

4.3.3.1. Mean Squares for the 102 sweetpotato accessions

The mean square values obtained from the ANOVA showed highly significant ($p < 0.01$) genotype by environment interaction for all the traits except storage root dry matter content, starch content, sucrose content and total sugars. The analysis of variance also indicated highly significant differences ($P<0.01$) among the accessions for all the traits except sucrose content which was significant at $p<0.05$ (Tables 4.9a and 4.9b).

Table 4.9a Mean squares for the agronomic traits of the 102 sweetpotato accessions

Source of var.	Df	Dry matter	Starch	Harv. Index	Root weight	Marketable root weight
Block	1	0.032	296.97	0.054	2.41	3.08
Gen.	101	0.008**	64.52**	0.146**	12.14**	9.13**
Loc.	2	0.067**	1356.31**	1.358**	74.82**	76.62**
GXE	202	0.003^{ns}	17.80^{ns}	0.021**	2.11**	1.65**
Error	299	0.003	14.79	0.013	1.12	0.95

**** Significant at 0.01; ^{ns} not significant.**

Table 4.9b Mean squares for the physicochemical traits of the 102 sweetpotato accessions

Source of var.	Df	Beta-carotene	Fructose	Glucose	Sucrose	Total sugars	Protein	Iron	Zinc
Block	1	0.83	62.55	116.60	352.64	0.84	2.71	0.64	0.01
Gen.	101	140.93**	8.78**	15.04**	29.35*	75.75**	2.91**	0.18**	0.06**
Loc.	2	721.91**	6.53**	7.36*	66.88*	119.73**	46.32**	2.83**	0.51**
GXE	202	13.52**	1.32*	2.16*	20.48^{ns}	23.02^{ns}	1.06*	0.07**	0.02**
Error	299	7.12	1.06	1.64	20.32	21.38	0.83	0.05	0.01

***Significant at p<0.05; ** Significant at 0.01; ^{ns} not significant.**

4.3.3.2. Descriptive statistics for the 12 physicochemical and the three agronomic traits

The range of values obtained for the individual traits, their grand mean, coefficient of variation (CV), and standard error of mean (SE) are represented in Table 4.14. Their grand mean ranged from 0.40 for harvest index to 68.56% for starch. The ranges for the CV and the SE were 5.6 - 48.3% and 0.11 - 5.00.

Table 4.10 Descriptive statistics for the agronomic and physicochemical traits of the 102 sweetpotato accessions

Trait	Range	Grand Mean	CV (%)	SE
Dry matter	27.00 – 50.00	38.00	14.1	5.00
Beta-carotene	3.72 – 33.67	11.44	23.3	2.67
Fructose	0.63 – 8.05	2.01	51.2	1.03
Glucose	1.74 – 11.66	3.97	32.3	1.28
Sucrose	6.77 – 17.15	10.19	44.2	4.51
Total sugars	9.83 – 30.34	16.46	28.1	4.62
Starch	54.72 – 75.64	68.56	5.6	3.85
Protein	2.68 -6.62	4.47	20.4	0.91
Iron	1.53 -2.42	1.99	11.1	0.22
Zinc	0.76 -1.28	1.01	11.9	0.12
Harvest index	0.08 – 0.68	0.40	28.0	0.11
Root weight	0.34 – 6.43	2.58	41.0	1.06
Marketable Root weight	0.10 – 4.45	2.02	48.3	0.98

4.3.3.3. Genotypic and phenotypic variance for the traits studied

The phenotypic variance was slightly higher than the genotypic variance except for dry matter content and iron content (Table 4.10). A similar trend was observed for their respective ratios. The lowest and the highest values for the genotypic variance were obtained from the dry matter (0.001) and beta-carotene (21.235). A similar trend was found for the phenotypic variance with values of dry matter and beta-carotene as 0.001 and 23.488.

Table 4.11 Estimate of genotypic and phenotypic variance for the agronomic and physico-chemical traits of the 102 sweetpotato accessions

Trait	Genotypic Variation	Phenotypic Variation	Ratio $\sigma^2_G : \sigma^2_P$
Dry matter	0.001	0.001	1: 1.0
Beta-carotene	21.235	23.488	1 : 1.1
Fructose	1.243	1.463	1: 1.2
Glucose	2.147	2.507	1 : 1.2
Sucrose	1.478	4.892	1: 3.3
Total sugars	8.788	12.625	1 :1.4
Starch	7.787	10.753	1 : 1.4
Protein	0.308	0.485	1 : 1.6
Iron	1.243	0.030	1 : 0.02
Zinc	0.007	0.010	1 : 1.5
Harvest index	0.022	0.025	1 : 1.1
Root weight	1.672	2.023	1 : 1.2
Marketable Root weight	1.247	1.522	1 : 1.2

4.3.3.4. Components of variation of the traits

The genotype x environment interaction variance ranged from 0.0 to 3.20, whilst that of the error variance ranged from 0.003 to 21.380 (Table 4.11). The dry matter had the lowest values whilst the highest values were recorded for beta-carotene and total sugars, respectively. Generally, the values for the genotype x environment interactions were lower than those of the genotypic variance and the error variance. However, the values for the genotypic variance were lower than those for the error variance for all the traits except beta-carotene, fructose, glucose, iron, harvest index, root weight and marketable root weight.

Table 4.12 Components of variance for agronomic and physicochemical traits of the 102 accession

Trait	σ^2_G	σ^2_{GxL}	σ^2_E	Ratio σ^2_G: σ^2_{GxE}: σ^2_E
Dry matter	0.001	0.00	0.003	1 : 0 .0 : 3.6
Beta-carotene	21.235	3.20	7.120	1 : 0.15 : 0.34
Fructose	1.243	0.13	1.060	1 : 0.10 : 0.85
Glucose	2.147	0.26	1.640	1 : 0.12 : 0.76
Sucrose	1.478	0.08	20.320	1 : 0.05 :13.75
Total sugars	8.788	0.82	21.380	1 : 0.09 : 2.43
Starch	7.787	1.51	14.790	1 : 0.19 : 1.90
Protein	0.308	0.12	0.830	1 : 0.37 : 2.69
Iron	1.243	0.01	0.050	1 : 0.55 : 0.04
Zinc	0.007	0.01	0.010	1 : 0.75 : 1.43
Harvest index	0.022	0.01	0.010	1 : 0.23 : 0.46
Root weight	1.672	0.50	1.120	1 : 0.30 : 0.67
Marketable Root weight	1.247	0.35	0.950	1 : 0.28 : 0.76

4.3.3.5. Variability, heritability and expected genetic advance for the traits

The phenotypic coefficient of variation (PCV) values were generally higher than the genotypic coefficient of variation (GCV) values. The PCV values ranged from 9.61% for dry matter content to 61.07% for marketable root weight. A similar trend was observed for the GCV which ranged from 7.60% for dry matter content to 61.07% for marketable root weight. The broad sense heritability ranged from 0.30 for sucrose to 0.90 for beta-carotene. The lowest and the highest values obtained for the expected gain from selection and genetic advance (as percent of grand mean) were 0.05% (dry matter) and 9.03 mg/100gDW (beta-carotene), and 7.13% (starch) and 105.34% (fructose) (Table 4.12).

Table 4.13 Genotypic and phenotypic coefficient of variation, heritability and expected genetic advance for the traits

Trait	Genotypic coefficient of variation	Phenotypic coefficient of variation	Heritability (H^2_b)	Expected Selection Gain (R)	Expected Selection Gain (R % of mean)
Dry matter	7.60	9.61	0.63	0.05	12.37
Beta-carotene	40.28	42.36	0.90	9.03	78.90
Fructose	55.48	60.18	0.85	2.12	105.34
Glucose	36.91	39.88	0.86	2.79	70.35
Sucrose	11.93	21.70	0.30	1.38	13.51
Total sugars	18.01	21.59	0.70	5.10	30.95
Starch	4.78	4.78	0.72	4.89	7.13
Protein	15.58	15.58	0.64	0.91	20.40
Iron	6.80	8.70	0.61	0.22	10.96
Zinc	8.08	9.90	0.67	0.14	13.60
Harvest index	36.80	39.53	0.87	0.28	70.57
Root weight	55.13	55.13	0.83	2.42	93.83
Marketable Root weight	61.07	61.07	0.82	2.08	103.06

4.3.3.6. Genotypic correlation coefficient for the traits

Whilst dry matter showed positive and strong association with starch (0.71), its relationship with beta-carotene (-1.20), fructose (-0.76), glucose (-0.78), total sugars (-0.77), and harvest index (-0.69) was strong but negative (Table 4.13). On the other hand, with the exception of starch (-0.61) that was strong but negatively correlated with beta-carotene, glucose (0.62), sucrose (0.74), total sugars (0.56), iron (0.74), and zinc (0.58) showed strong and positive correlation with beta-carotene. In addition, whilst a very strong and positive relationship was observed between fructose and glucose (0.98), these traits had strong and negative correlation with starch and positive and strong correlation with total sugars. Similarly, negative but very strong relationship was observed between total sugars and starch (-0.99). Harvest index was strong and positively related to root weight (0.56) and marketable root weight (0.57). Furthermore, the latter two traits had a very strong and positive association.

Table 4.14 Genotypic correlation coefficient for the12 physicochemical and the three agronomical traits of 102 sweetpotato accessions

Trait	DM	BC	F	G	S	TS	ST	P	Fe	Zn	HI	RWT	MKTRWT
DM		**-1.20**	**-0.76**	**-0.78**	-0.23	**-0.77**	**0.71**	0.08	-0.11	0.18	**-0.69**	-0.12	-0.06
BC			0.30	**0.62**	**0.74**	**0.56**	**-0.61**	0.15	**0.74**	**0.58**	-0.41	-0.41	-0.41
F				**0.98**	0.04	**0.85**	**-0.61**	-0.24	0.02	-0.22	0.30	0.06	0.01
G					0.05	**0.91**	**-0.78**	-0.19	0.11	-0.10	0.30	0.06	0.01
S						**1.09**	**-0.71**	**0.75**	**1.07**	**1.15**	-0.14	-0.42	-0.41
TS							**-0.99**	0.15	**0.60**	0.39	0.22	-0.12	-0.17
ST								0.21	**0.71**	0.39	**0.57**	-0.19	0.49
P									**0.75**	**0.75**	0.27	-0.48	-0.46
Fe										**0.90**	-0.08	**-0.54**	**-0.62**
Zn											0.00	**-0.51**	**-0.50**
HI												**0.56**	**0.57**
RWT													**1.00**

DM: Dry matter, BC: Beta-carotene, F: Fructose, G: Glucose, S: Sucrose, TS: Total sugars, ST: Starch, P: Protein, Fe: Iron, Zn: Zinc, HI: Harvest index, RWT: Root weight, MKTRWT: Marketable root weight

4.3.3.7. Beta-carotene, dry matter and sugar content for the top- and bottom 10 accessions

Apomuden and CIP 440095 had the highest and the lowest beta-carotene content of 33.67 mg/100g DW and 3.72 mg/100gDW, respectively (Table 4.15). FA 10-026 (50%) had the highest dry matter whilst the lowest dry matter content of 27% was given by Apomuden and CIP 442850. On the other hand, the lowest and the highest values for the total sugar content were obtained by Ouagadougou 02 and CIP 442850, respectively.

Table 4.15 Storage root dry matter, beta-carotene, and sugar contents for the top 10 and bottom 10 accessions evaluated across three locations

Rank	ACCESSION	Root dry matter (%)	ACCESSION	Beta-carotene (mg/100g) DW	ACCESSION	Total sugars (%)
1	FA 10-026	50	APOMUDEN	33.67	CIP 442850	30.34
2	HISTARCH	45	RESISTO	27.53	APOMUDEN	28.97
3	CIP 442264	45	B-REGARD	24.31	B/FASO 002	24.04
4	ABAIDOO 01	44	DONAKOPE04	23.32	CIP 440062	23.30
5	BD 96-029	43	CIP 442850	20.21	B-REGARD	22.90
6	AAT 03-017	42	CIP 443035	19.75	PAGA 01	22.84
7	FIASO RED	42	KROBO 01	19.00	B/FASO 001	22.69
8	OGYEFO	42	BOT 03-028	17.83	TAG 03-030	21.92
9	FARAA	42	ZAMBEZI	17.58	CIP 440071	21.84
10	OPERSI 02	42	BOT 03-020	17.35	UKEREWE	21.10
“	“	“	“	“	“	“
“	“	“	“	“	“	“
93	B/FASO 001	33	NS 001	6.70	EMAKYENE 1	12.54
94	0KYEREKO	33	ABAIDOO 03	6.42	OPERSI 02	12.45
95	CIP 440071	33	CIP 442147	6.38	DOS O3-006	12.35
96	B-REGARD	32	H-ASIATOR	6.38	AAT 03-025	12.26
97	DONAKOPE04	32	DONAKOPE 05	6.01	DONAKOPE01	12.26
98	CIP 442462	32	BOT 03-027	5.96	CIP 440095	12.06
99	PAGA 01	31	SANTOMPONA	5.30	OGYEFO	11.67
100	B/FASO 002	30	CIP 442237	5.04	CIP 442264	11.06
101	APOMUDEN	27	CIP 442162	4.39	HISTARCH	10.43
102	CIP 442850	27	CIP 440095	3.72	OUAGADOUGOU 02	9.83
	SED (P<0.05)	**3.00**	**SED (P<0.05)**	**1.52**	**SED (P<0.05)**	**2.63**

4.4. Discussion

Variability was observed in all the physicochemical traits and 20 out of the 27 agro-morphological traits. This shows existence of a high degree of agro-morphological and physicochemical polymorphism among the accessions. Diversity in flesh colour (beta-carotene content) in sweetpotato cultivars has been reported (Waramboi *et al.*, 2011). Sugar content in sweetpotato is also reported to be cultivar-dependent (Ravindran *et al.*, 1995; Aina *et al.*, 2009), and showed high levels of polymorphism with SSR markers. This confirms the discriminatory capacity of the SSR markers on sweetpotato (Gichuru *et al.*, 2006; Tumwegamire *et al.*, 2011). High level of polymorphism was observed in this study with an allele range of two to six alleles per SSR marker and this is in agreement with Yada *et al.* (2010a). Buteler *et al.* (1999) obtained high polymorphism with an allele range of 3 - 10. Somé *et al.* (2014), also reported 1 to 8 alleles. An range of 2 – 11 alleles was reported by Tumwegamire *et al.* (2011). A lower level of polymorphism, ranging between one and four alleles per SSR locus has also been reported (Hwang *et al.*, 2002). Differences observed may be attributed to the use of different SSR primers, sweetpotato genotypes and annealing temperatures. Varying number of SSR primers used in diversity studies may also account for the differences in observations. Hwang *et al.* (2002), attributed high level of polymorphism to large genome size and heterozygosity of sweetpotato. It should also be noted that genetic diversity due to heterozygosity in sweetpotato is driven by both the mating system (outcrossing in combination with self-incompatibility) and the high ploidy level of the crop (autohexaploid) (Tumwegamire *et al.*, 2011). The AMOVA and ANOVA results also indicated significant differences within and between the different sweetpotato groups studied. All of these results demonstrate significant genetic diversity and indicates that meaningful selection and improvement of these traits is possible (Mohammed *et al.*, 2012; Nwangburuka and Denton, 2012). Furthermore, these demonstrate the existence of diversity at the

individual genotype level that can be exploited to obtain trait combinations in specific varieties. In addition, the divergences indicate that it is possible to select contrasting parents from these populations for improvement of beta-carotene, sugar and dry matter contents in sweetpotato. This result agrees with results of other authors (Zhang *et al.*, 2000; Zhang *et al.*, 2001; Gichuki *et al.*, 2003; Gichuru *et al.*, 2006; Abdelhameed *et al.*, 2007; Grüneberg *et al.*, 2009; Tumwegamire *et al.*, 2011).

PIC is a measure of the discriminatory capacity of a marker (Jia *et al.*, 2009). According to Heng-Sheng *et al.* (2012), a PIC value greater than 0.5 is high, and any marker with such value may be effectively in genetic diversity study. In this study, the PIC value for all the markers that showed amplification were greater than 0.5. This implies that the values which ranged from 0.62 to 0.96 with mean of 0.84 were very high indicating a high discriminating power of the SSR markers used. These values are greater than range and mean of 0 – 0.88, and 0.72 as reported by Somé *et al.* (2014). Based on the number of unique alleles and the PIC values, all the SSR markers that showed amplification were very effective in discriminating among the sweetpotato accessions. In spite of this, the markers did not discriminate between cultivars LOCIMP2 (Santompona) and LOCIMP10 (Otoo) at 1.00 level of similarity even though these cultivars are morphologically distinct. It is probable that no repeats were found that could differentiate the two cultivars and therefore, more SSR markers need to be used in the future to have a full diversity study.

G x E interaction is important in evaluating genotype adaptation, selection of parents and developing genotypes with improved end-product quality (Ames *et al.*, 1999). The significant G x E interaction observed may complicate selection for such traits. The existence of G x E indicates that selection should be carried out in a range of environments (Falconer and

Mackay, 1996). This is because progress from selection is realized only when genotypic effects can be separated from environmental effects (Miller *et al.*, 1958). However, beta-carotene may be an exception because of the orange-flesh colour associated with it, and it may be controlled by relatively few genes. The differences in the genotypic and phenotypic variance may be attributed to environmental effects. It is essential, therefore, that germplasm testing procedures are designed to maximize the genetic effects relative to the environmental and interaction effects (Miller *et al.*, 1958). Information on the relative magnitudes of the different sources of variance observed in the sweetpotato clones provides a guide towards this objective. The magnitude of the G x E interaction variances were smaller relative to the error variances. This means that the accessions were tested in adequate sample environments. However, a large number of replicates may be required for traits with lower genetic variance than the error variance (root dry matter content, sucrose content, total sugars, starch content, protein content and zinc content) to enhance the optimization of their genetic effects.

The trend of the PVC and the GVC values were in agreement with results reported for *Solanum anguivi* (Denton and Nwangburuka, 2011), *Corchorus olitorius* (Nwangburuka and Denton, 2012), *Triticale* (Kumar *et al.*, 1985) and oat (Prasad *et al.*, 1981). The observed trend between PVC and GVC could be attributed to environmental effects (Denton and Nwangburuka, 2011). High PCV and GCV values which were detected for marketable root weight, root weight, fructose, beta-carotene, glucose, harvest index, and total sugars suggest that these traits accounted for the highest variation observed in the sweetpotato accessions. This means that there may be useful genetic variation in the gene pool to provide for substantial amount of improvement through breeding for these traits.

GCV provides a measure to compare the genetic variability present in various quantitative traits. However, it is not possible to estimate heritable variation with the help of the GCV alone (Prasad *et al.*, 1981). The GCV together with heritability estimates would give the best picture of the amount of advance to be expected from selection (Burton, 1952). Heritability indicates the effectiveness with which selection of genotypes can be based on phenotypic performance (Johnson *et al.*, 1955). In this study, broad-sense heritability estimates varied from medium to high with the exception of sucrose content which had low heritability. Traits with medium to high heritability are influenced by additive gene effects (Denton and Nwangburuka, 2011). This suggests that selection based on phenotype will be effective. However, the heritability value in itself does not provide an indication of the amount of genetic progress that would result from selecting the best individuals (Johnson *et al.*, 1955). The utility of estimates of heritability is increased when they are used in conjunction with the selection differential (the amount that the mean of the selected lines exceeds the mean of the entire population), since genetic advance is commonly predicted as the product of the heritability and the selection differential.

Prediction of the response of an individual to selection are more reliable when GCV, broad-sense heritability and genetic advance are combined (Ghandi *et al.*, 1964; Ibrahim and Hussein, 2006). Thus, high GCV and high heritability does not necessary mean high genetic gain. If the GCV is high and heritability is mainly due to non-additive gene effects (i.e. dominance and epistasis), genetic gain will be low, but a high genetic advance may be expected if GCV is high and heritability is predominantly due to additive gene effects. The predicted improvement over the means for this population is above 10% up to 105% for all the traits except starch content (7.13%), and this is good. Miller *et al.* (1958), observed 13 –

15% for lint yield of upland cotton and reported that it was particularly encouraging. This suggests that sufficient useful genetic variation is present in these populations which could be used to provide substantial improvement through the selection of superior genotypes. The type of gene action operating is also critical since the expected amount of superiority will be realized in subsequent generations only if all of the genetic effects are additive (Miller *et al.*, 1958). Conversely, non-additive effects (epistasis, dominance, and interactions) may decrease the amount of genotypic superiority passed on. It is therefore, important to seek out additional information concerning the nature of gene action in order to buttress this point in sweetpotato.

Genetic relationships between traits may result from pleiotropic gene effects, linkage of two genes, linkage disequilibrium and epistatic effects of different genes or environmental influences (Falconer and Mackay, 1996). Except for the very higher (>1) values observed for dry matter and beta-carotene (-1.2), sucrose and total sugars (1.09), sucrose and iron (1.07), and sucrose and zinc (1.15), the values for the genetic correlation coefficient were all generally in agreement with those reported by Grüneberg *et al.* (2009). Denton and Nwangburuka (2011) also reported genotypic correlation coefficient greater than one in a study on *Solanum anguivi.* A similar observation was also made by Nwangburuka and Denton (2012) for character association on leaf *Corchorous olitorius*. The correlations observed are thus population specific. This is because the interrelationships might be quite different in populations in which different gene associations exist in the parental lines of the segregating population (Miller *et al.*, 1958). It could also be that the mean values of the characters under study are at levels different from those observed in the other studies. The strong positive association observed between dry matter and starch, and the strong negative

relationship found for sugars and dry matter and starch indicates that it is possible to develop non-sweet high dry matter sweetpotatoes. A similar observation was made by Gruneberg *et al*., (2009), who also reported that development of non-sweet sweetpotatoes should not be too difficult. However, developing non-sweet high dry matter and high beta-carotene sweetpotatoes could be challenging due to the strong negative association between dry matter and beta-carotene and the positive association existing between beta-carotene and the sugars. Breeding for such cultivars may require many cycles of selection and hybridization to break genetic linkages associated with the traits. However, beta-carotene seems to be controlled by a limited number of genes and should be easy to manipulate. The results also showed that dry matter, sugar content and most of the physicochemical traits (except protein) may indirectly be selected using beta-carotene content (the orange-fleshed colour).

Based on their descriptive statistics and the mean separation, the top- and bottom 10 accessions for beta-carotene content, dry matter content and total sugar content were selected for full diallel mating. The aim of the selection was to establish a crossing block for studies into the inheritance of the above mentioned traits.

4.5. Conclusion

This study provides estimate on the level of genetic variation among sweetpotato clones in Ghana. Significant genetic diversity was found between the clones for dry matter, beta-carotene and total sugars. This information can be used in sweetpotato germplasm management and improvement in Ghana. The study also affirmed the discriminatory capacity of the SSR markers and agro-morphological markers for sweetpotato characterization especially for breeding programmes with limited resources. The relative magnitude of the G x E variance to the other variance indicates that a high potential progress from selection is

possible since the superior genotypes in the population can be readily identified. Sufficient useful genetic variation is present in the materials studied which may be exploited to provide for substantial amount of improvement through selection of superior genotypes. High heritability coupled with the high expected genetic advance as per cent of mean may indicate high breeding value and mostly additive genetic effects. This suggests that selection can be effective for these traits. The strong negative association between dry matter and total sugars indicates that it is feasible to develop non-sweet high dry matter sweetpotato cultivars. However, developing non-sweet, high dry matter and high beta-carotene sweetpotato types may require many cycles of selection.

CHAPTER FIVE

5.0 ASSESSMENT OF COMPATIBILITY STATUS OF SWEETPOTATO GENOTYPES

5.1. Introduction

The major barriers to genetic improvement of sweetpotato are its polyploidy, high level of heterozygosity, self- and cross-incompatibility and large chromosome number (Cervantes-Flores, 2006; Chang *et al.*, 2009). Variation in flowering prolificacy among different genotypes also impedes and limits the genetic progress of sweetpotato. The limitations to improvement of sweetpotato through breeding include poor flowering in temperate environments, limited seed set in all environments, and genetic incompatibility (Martin, 1967; Martin and Cabanillas, 1968). While the problem of poor flowering can be reduced by applying various flower induction techniques, incompatibility remains a barrier for the genetic improvement and conservation of the crop (Fekadu *et al.*, 2013). Most sweetpotato genotypes used in one study were self- and cross-incompatible and were not able to produce viable seeds either through both self- or cross-pollinations (Vimala and Hariprakash, 2011). Self- and cross-incompatibility in sweetpotato inhibits breeding progress because parents with desirable traits may belong to the same incompatibility group (Wang, 1964; Charles *et al.*, 1973; Vimala, 1989). This limits the scope of understanding the genetics and improvement of the crop, therefore, slowing down progress in genetic advances. Understanding the compatibility status of a breeding population of sweetpotato helps to make vital decisions such as the level of selection intensity to adopt. It is, therefore, critical to ascertain the compatibility status and its effect on a sweetpotato breeding population. This will facilitate efficient management and conservation of genetic resources in the breeding programme especially at the beginning of a hybridization programme.

This chapter evaluates the cross compatibility of the sweetpotato clones and its effect on the breeding progress. In addition, it seeks to identify incompatibility testers for the sweetpotato breeding programme at the CSIR-Crops Research Institute and beyond.

5.2. Materials and Methods

5.2.1. Establishment of Hybridization blocks

Hybridization blocks were established at the research fields of the CSIR-Crops Research Institute (CSIR-CRI), Fumesua in 2012. The list of parents used is shown in Tables 5.1 and 5.2. Two crossing blocks were established. One block for the study of dry matter content and beta-carotene content whilst the other was for the study of sugar content. They were established first in the screen house with all the parents except those marked (*) as the entries in the major season of 2012. These entries were selected from the five top and bottom five performing accessions of the base population. The hybridization blocks were re-established in the field with the 10 top and bottom 10 performing accessions from the base population during the minor season of 2012 at planting distance of 0.3 x 1m due to lack of or poor flowering of most genotypes when they were even grafted onto *I setosa*.

5.2.2. Mating design used and management of the hybridization blocks

The full diallel mating design was used. The hybridization blocks in the screen house were 10 x 10 full diallel whilst the field ones were 12 x 12, and 15 x 15, for the dry matter/beta-carotene and the sugar content, respectively. Flowers ready for pollination the next morning, were tied the previous afternoon using a piece of drinking straw to prevent out-crossing by insects. At the time of pollination, the corolla was carefully opened, pollinated and carefully tied again afterwards to avoid insect contamination after pollination. Although self-

fertilization occurs only rarely in sweetpotato (Poole, 1955), emasculation was done on the female parents to eliminate such a possibility.

Table 5.1 List of sweetpotato genotypes selected as parents for the establishment of the dry matter/beta-carotene crossing block

Crossing block ID	Genotype	Dry matter content (%)	Beta-carotene content (mg/100g)DW
BC87	Histarch	45	9.85
BC64	CIP 442264	45	7.74
BC27*	Faara	42	12.27
BC61*	Ogyefo	42	6.83
BC115	Ouagadougou 03	41	9.74
BC53	CIP 442896	40	11.27
BC108	BOT 03-020	39	17.35
BC79	CIP 443035	36	19.75
BC109	CIP 442850	27	20.21
BC82	Beauregard	32	24.31
BC21	Resisto	38	27.53
BC50	Apomuden	27	33.67
	Range	**27 – 45**	**6.83 - 33.67**
	SED	**3.00**	**1.52**

***Genotypes not included in the crossing block set-up in the screen house**

Table 5.2 List of sweetpotato parents for the establishment of the sugars crossing block

Crossing block ID	Genotype	Sugar content (%)
S109	CIP 442850	30.34
S50	Apomuden	28.97
S15	B/Faso 002	24.04
S82	Beauregard	22.90
S75	B/Faso 001	22.69
S97*	Ehiamankyene 01	12.54
S72	AAT 03-025	12.26
S31	CIP 440095	12.06
S61*	Ogyefo	11.67
S64	CIP 442264	11.06
S87	Histarch	10.43
S74	Ouagadougou 02	9.83
S113*	Ukerewe	21.10
S48*	CIP 440071	21.84
S43*	Paga 01	22.84
	Range	**9.83 - 30.34**
	SED	**2.63**

***Genotypes not included in the crossing block set-up in the screen house**

5.2.3. Seeds harvesting, sowing and transplanting

Seeds obtained from the crosses were harvested at maturity (when capsule turns brown) and placed in Petri dishes, sun dried and stored in labelled envelopes. All seeds obtained from crosses among the low sugars parents and among the high beta-carotene parents were sown to generate progenies for the development of the low sugar and the high beta-carotene populations. In addition, seeds from crosses among two parents with low sugar, high dry matter and low beta-carotene contents and two other parents with high sugar, low dry matter and high beta-carotene contents obtained from a 4 x 4 full diallel mating design were also sown to study the genetic control of these traits. The seeds were germinated on moist filter paper in a Petri dish after sand paper scarification. Germinated seeds were then transplanted to prepared nursery pots in the screen house for the establishment of seedling nursery.

5.2.4. Data collection and analysis

Observations were made on parents that produced flowers and those that did not. The number of crosses made and seeds obtained were noted and recorded. The following data were also taken on crosses for the development of the high beta-carotene and low sugar populations, and the gene action study. The number of capsules and seeds harvested per cross were recorded. Success rate of the crosses were calculated as the ratio of number of capsules harvested to the total number of crosses made and expressed as a percentage. In addition, number of seeds per capsule was also determined as the ratio of number of seeds harvested to number of capsule harvested. Data were also taken on the number of seeds sown and those germinated. Germination rate was computed as the ratio of number of seeds sown to the number of seeds germinated expressed as percentage. Meteorological data of the study site during the period of the work were sourced from the CSIR-CRI weather station. The data

included minimum temperature, maximum temperature, mean temperature, total rainfall, relative humidity and solar radiation.

5.3. Results

5.3.1. Crosses made and seeds harvested

A total of 6388 crosses were made to generate the F_1 seeds. These were 4575 crosses from the beta-carotene/dry matter hybridization block and 1813 from the sugars hybridization block. The overall seeds harvested were 3214, and was composed of 2356 seeds from the beta-carotene/dry matter content hybridization block and 858 seeds for the sugar content hybridization block. In general, more crosses and seeds were generated from the crossing blocks established in the field than those established in the screen house as shown in Tables 5.3 – 5.10.

5.3.1.1. Crosses and seeds obtained from the screen house

For the beta-carotene/dry matter hybridization block, four out of the 10 parents (BOT-020, CIP 442850, CIP 442264 and CIP 442896) did not produce flowers at all (Table 5.3). For the other six clones that produced flowers, only Histarch produced enough flowers to generate cross combinations with the other five clones and selfs. Histarch x CIP 443035 gave the highest number of crosses (31). Histarch x Apomuden produced the highest number of seeds (78) (Table 5.4). Selfing (pollen from the same flower of the two parents) produced the lowest number of seeds. Only four parents (CIP 442264, Histarch, Beauregard, and Apomuden) produced flowers in the sugar content crossing block (Table 5.5). Only the latter three were prolific in generating substantial quantities of flowers for cross combinations to produce seeds (Table 5.6). The most prolific parent was Histarch. The highest number of

crosses (40) was made between Histarch and Apomuden (Table 5.5). The number of seeds per cross ranged from 2 (Histarch x CIP 442264) to 100 (Histarch x Apomuden) (Table 5.6).

Table 5.3 Number of crosses made in the screen house for the Beta-carotene/Dry matter content

Parents	BC87	BC108	BC50$	BC109$	BC64	BC115	BC82$	BC53	BC21$	BC79$
BC87	s=17 87x87=10		24			4	22		2	31
BC108		*								
BC50$	9		S=1 50x50=2			4				4
BC109$				*						
BC64					*					
BC115	4		7			*				
BC82$	9						*			1
BC53								*		
BC21$									*	1
BC79$	22		3				3		1	3

$High beta-carotene parents. * Selfing (S=cross between flowers on the same plant); BC87 (Histarch), BC108 (BOT 03-020), BC50 (Apomuden), BC109 (CIP 442850), BC64 (CIP 442264), BC115 (Ouagadougou 03), BC82 (Beauregard), BC53 (CIP 442896), BC21 (Resisto), BC79 (CIP 443035)

Table 5.4 Number of F_1 seeds obtained for the Beta-carotene/Dry matter crossing block in the screen house

Parents	BC87	BC108	BC50$	BC109$	BC64	BC115	BC82$	BC53	BC21$	BC79$
BC87	*S=1; 87x87=0		78			10	21		1	25
BC108		*								
BC50$	17		*s=1 *50x50=0			2	4			
BC109$				*						
BC64					*					
BC115	1		5			*				
BC82$	12		1				*			4
BC53								*		
BC21$									*	
BC79$	31		11				8			*

$High beta-carotene parents. * Selfing (S=cross between flowers on the same plant); BC87 (Histarch), BC108 (BOT 03-020), BC50 (Apomuden), BC109 (CIP 442850), BC64 (CIP 442264), BC115 (Ouagadougou 03), BC82 (Beauregard), BC53 (CIP 442896), BC21 (Resisto), BC79 (CIP 443035)

Table 5.5 Number of crosses made in the screen house for the generation of F_1 seeds (sugar content)

	S64$^{\$}$	S87$^{\$}$	S50	S31$^{\$}$	S74$^{\$}$	S75	S82	S15	S109	S72$^{\$}$
S64$^{\$}$	*	5								
S87$^{\$}$	5	*	40				22		3	
S50		9	*				2			
S31$^{\$}$				*						
S74$^{\$}$					*					
S75						*				
S82		9	1				*			
S15								*		
S109									*	
S72$^{\$}$										*

$^{\$}$Low sugar content parents. * Selfing; S64 (CIP 442264), S87 (Histarch), S50 (Apomuden), S31 (CIP 440095), S74 (Ouagadougou 02), S75 (B/Faso 001), S82 (Beauregard), S15 (B/Faso 002), S109 (CIP 442850), S72 (AAT 03-025)

Table 5.6 Number of seeds obtained from the screen house to generate F_1 population (sugar content)

	S64$^{\$}$	S87$^{\$}$	S50	S31$^{\$}$	S74$^{\$}$	S75	S82	S15	S109	S72$^{\$}$
S64$^{\$}$	*	4								
S87$^{\$}$	2	*	100				21			
S50			*				4			
S31$^{\$}$				*						
S74$^{\$}$					*					
S75						*				
S82		12	21				*			
S15								*		
S109									*	
S72$^{\$}$										*

$^{\$}$Low sugar content parents. * Selfing; S64 (CIP 442264), S87 (Histarch), S50 (Apomuden), S31 (CIP 440095), S74 (Ouagadougou 02), S75 (B/Faso 001), S82 (Beauregard), S15 (B/Faso 002), S109 (CIP 442850), S72 (AAT 03-025)

5.3.1.2. Number of crosses and seeds obtained in the field to generate F_1 population

For the beta-carotene/dry matter crossing block, the clones varied for number of flowers and crosses in the field. CIP 442264 produced no flowers (Table 5.7). The highest number of flowers and crosses were produced by Histarch, Apomuden, Faara and Beauregard. CIP 442896 and Resisto produced the lowest number of flowers. Crosses between Faara, Histarch and Apomuden were the most successful whilst crosses involving CIP 442896, Resisto, and CIP 442850 were not very successful. A similar trend was observed for the seeds harvested (Table 5.8).

Table 5.7 Number of crosses made in the field for the generation of F_1 population for the beta-carotene/dry matter content

Parents	BC27	BC 108	BC 115	BC 53	BC 61	BC 64	BC 87	BC 50#	BC 109#	BC 79#	BC 21#	BC 82#
BC27	*11	33	54		26		443	224	94	21	19	55
BC108	34	*			4			39	12	19		10
BC115	8	6	*					20	8	3	4	3
BC53	7			*			3	6				2
BC61	24				*		27	29	13			25
BC64						*						
BC87	443	50	34	84	137		*	157	37	67	74	145
BC50#	533	227	118	91	112		143	*	81	31	22	102
BC109#	1	1	23	4	6		22	20	*	1		6
BC79#	38	10	4	3	17		19	10	1	*	21	2
BC21#	35	1		13	6		8	12	4	5	*	3
BC82#	98	14	1	9	20		42	35	13	11	9	*

#High beta-carotene parents. White quadrant = crosses among high dry matter parents; Light green=low BC/high Dm X High BC/low Dm crosses, dark green= reciprocal crosses; Pink=crosses among high beta-carotene clones. BC27 (Faara), BC108 (BOT 03-020), BC115 (Ouagadougou 03), BC53 (CIP 442896), BC61 (Ogyefo), BC64 (CIP 442264), BC87 (Histarch), BC50 (Apomuden), BC109 (CIP 442850), BC79 (CIP 443035), BC21 (Resisto), BC82 (Beauregard)

Table 5.8 Seeds harvested from the field to generate the F_1 population for the beta-carotene/dry matter content

Parents	BC 27	BC 108	BC 115	BC 53	BC 61	BC 64	BC 87	BC 50#	BC 109#	BC 79#	BC 21#	BC 82#
BC27		34	21		14		45	404	78	10	3	12
BC108	11	*						36	7	5		1
BC115	2		*					1	1			
BC53				*								
BC61	17				*		26	53				14
BC64						*						
BC87	285	33	15	19	139		*	186	11	7	3	31
BC50#	384	76	45	9	63		18	*	16	4	4	13
BC109#	3	2	13		4		5	3	*			4
BC79#	12	17					3	15	3	*	2	4
BC21#	6	2		1	2			3	1		*	
BC82#	35	8			5		15	31	1			*

#High beta-carotene parents. White quadrant = crosses among high dry matter parents; Light green=low BC/high Dm X High BC/low Dm crosses, dark green= reciprocal crosses; Pink=crosses among high beta-carotene clones. BC27 (Faara), BC108 (BOT 03-020), BC115 (Ouagadougou 03), BC53 (CIP 442896), BC61 (Ogyefo), BC64 (CIP 442264), BC87 (Histarch), BC50 (Apomuden), BC109 (CIP 442850), BC79 (CIP 443035), BC21 (Resisto), BC82 (Beauregard)

In the sugars crossing block, only Ouagadougou 02 did not produce flowers. However, the other clones produced variable number of flowers. More crosses were made between Histarch and Apomuden, and Ogyefo and Paga 01 than the other parents (Table 5.9). These parents also produced the highest number of flowers. The least number of flowers (Table 5.9) and quantity of seeds (Table 5.10) were produced by Ehiamankyene 01.

Table 5.9. Number of crosses conducted in the field to generate F_1 population (sugar content)

Parents	S50	S48	S43	S113	S82	S15	S109	S75	S61#	S87#	S97#	S31#	S64#	S72#	S74#
S50	*				102	4	81		112	143	1	53	3	74	
S48		*								4					
S43			*						35	423		6		13	
S113				*					13	4		1		7	
S82	35				*		13		20	42		2			
S15						*			57	145		72		37	
S109	20				6		*		6	22					
S75								*	54	37		38		1	
S61#	29		3		25	27	14	8	*	29					
S87#		6	203	24	142	315	37	31	137	*				12	
S97#											*				
S31#	6			4		5	3	10	3	3		*			
S64#													*		
S72#	19						1	4	1					*	
S74#															*

#Low sugar parent. Light green quadrant = crosses between low and high sugar parent; dark green= reciprocal crosses; Pink=crosses among low sugar clones. S50 (Apomuden), S48 (CIP 440071), S43 (Paga 01), S113 (Ukerewe), S82 (Beauregard), S15 (B/Faso 002), S109 (CIP 442850),), S75 (B/Faso 001), S61 (Ogyefo), S87 (Histarch), S97 (Ehiamankyene 01), S31 (CIP 440095), S64 (CIP 442264), S72 (AAT 03-025), S74 (Ouagadougou 02)

Table 5.10 Number of seeds harvested from field for the generation of F_1 population (Sugar content)

Parents	S50	S48	S43	S113	S82	S15	S109	S75	S61#	S87#	S97#	S31#	S64#	S72#	S74#
S50	*								63	17		3		27	
S48		*													
S43			*						30	25				6	
S113				*					5						
S82	13				*		1		5	3					
S15						*			56					48	
S109	3				4		*		4	5					
S75								*	39	1					
S61#	53		2		14	25	11	7	*	26					
S87#	180		2		13			1	139	*				6	
S97#											*				
S31#	7						1					*			
S64#													*		
S72#	8					2	1	2						*	
S74#															*

#Low sugar parent. Light green quadrant = crosses between low and high sugar parent; dark green= reciprocal crosses; Pink=crosses among low sugar clones. S50 (Apomuden), S48 (CIP 440071), S43 (Paga 01), S113 (Ukerewe), S82 (Beauregard), S15 (B/Faso 002), S109 (CIP 442850),), S75 (B/Faso 001), S61 (Ogyefo), S87 (Histarch), S97 (Ehiamankyene 01), S31 (CIP 440095), S64 (CIP 442264), S72 (AAT 03-025), S74 (Ouagadougou 02)

5.3.2. Success rate and seedling vigour of selected crosses

For the hybrids used for the F_1 evaluation, the number of crosses carried out ranged from 1 for CIP 443035 x CIP 442850 to 157 for Histarch x Apomuden. The number of capsules also ranged from 1 to 79 for the same crosses. The grand mean for the number of crosses and the number of capsules were 45.41 and 22.7, respectively. The success rate of the crosses ranged from 50% to 100%, with a mean of 54.1%. Only 18% of the crosses had a success rate above the mean. The number of seeds produced by the crosses also varied from 1 for Beauregard x CIP 442850 to 186 for Histarch x Apomuden with a mean of 24.74. The mean number of seeds per capsule was 1.21 and it ranged from 0.14 for Beauregard x CIP 442850 to 4 for CIP 443035 x Beauregard. The mean number of seeds sown was 14.74 and that of seeds geminated was 13.85. Their ranges were 1 – 89 and 1 – 80, respectively. The germination rate ranged from 80% to 100% with a mean of 96.3%. The cross Apomuden x Resisto gave the lowest germination rate whilst a number of crosses gave 100% germination rate (Table 5.11).

Table 5.11 Success rate and germination percentage of the crosses

Cross	Number of crosses	Number of capsule	Success rate (%)	number of Seeds harvested	Seeds per capsule	Seeds sown	Seeds germinated	Percent germination (%)
[+]61 x 87	27	14	51.9	26	1.86	21	20	95.2
[$]61 x 50	29	15	51.7	53	3.53	25	22	88.0
[$]61 x 82	25	13	52.0	14	1.08	6	6	100.0
[+]64 x 87	5	3	60.0	4	1.33	4	4	100.0
[+]87 x 61	137	69	50.4	139	2.01	89	80	89.9
[+]87 x 64	5	3	60.0	2	0.67	2	2	100.0
[$]87 x 50	157	79	50.3	186	2.35	40	38	95.0
[$]87 x 82	145	73	50.3	31	0.42	23	22	95.7
[+]87 x 72	12	6	50.0	5	0.83	5	5	100.0
[$]50 x 61	112	56	50.0	63	1.13	36	35	97.2
[$]50 x 87	143	72	50.4	18	0.25	15	13	86.7
***50 x 109**	81	41	50.6	16	0.39	14	13	92.9
***50 x 79**	31	16	51.6	4	0.25	4	4	100.0
***50 x 21**	22	11	50.0	4	0.36	5	4	80.0
***50 x 82**	102	51	50.0	13	0.25	14	13	92.9
***109 x 50**	20	10	50.0	3	0.30	2	2	100.0
***109 x 82**	6	3	50.0	4	1.33	4	4	100.0
***79 x 50**	10	5	50.0	15	3.00	16	16	100.0
***79 x 109**	1	1	100.0	3	3.00	3	3	100.0
***79 x 21**	21	11	52.4	2	0.18	2	2	100.0
***79 x 82**	2	1	50.0	4	4.00	11	10	90.9
***21 x 50**	12	6	50.0	3	0.50	3	3	100.0
[$]82 x 61	20	10	50.0	5	0.50	4	4	100.0
[$]82 x 87	42	21	50.0	15	0.71	13	13	100.0
***82 x 50**	35	18	72.0	31	1.72	32	31	96.9
***82 x 109**	13	7	53.9	1	0.14	1	1	100.0
***82 x 79**	11	6	54.5	4	0.67	4	4	100.0
Mean	45.41	22.7	54.1	24.74	1.21	14.74	13.85	96.3

[+]Crosses involving low sugar parents; [*]Crosses involving high beta-carotene parents; [$] crosses involving two contrasting parents. [87=Histarch; 61=Ogyefo; 50=Apomuden; 82=Beauregard; 64=CIP 442264; 72=AAT 03-025; 79=CIP 443035; 109=CIP 442850; 21=Resisto;]

5.3.3. Climatic data for the hybridization block environments

5.3.3.1. Climatic data for the hybridization block established in the screen house

The minimum values for all the weather data were obtained in August 2012 except for relative humidity which was in April 2012. The maximum values for all the data were recorded in April 2012 except for total rainfall and average relative humidity that recorded peak values in June 2012. The total rainfall and the average relative humidity (RH) ranged from 4.60 mm to 204.0 mm and 83.24% to 89.52%, respectively. Similarly, solar radiation ranged from 195.37 w/m^2 to 351.14 w/m^2. The ranges of values for the minimum and maximum temperatures were 21.28 – 22.47^{o}C, and 28.42 – 32.63^{o}C, whilst that of the mean temperature ranged from 24.93^{o}C to 27.51^{o}C as shown in Table 5.12.

Table 5.12 Climatic condition over the period of the crossing block in the screen house

MONTHLY	April 2012	May 2012	June 2012	July 2012	August 2012
Total Rainfall (mm)	152.60	170.40	204.00	43.60	4.60
Relative Humidity (%)	83.24	85.29	89.52	89.12	86.74
Solar Radiation w/m^2	351.14	315.14	263.60	233.90	195.37
Temperature (Min) °C	22.47	22.16	21.96	21.67	21.28
Temperature (Max) °C	32.63	31.57	29.65	28.44	28.42
Mean Temperature °C	27.51	26.83	25.80	25.04	24.93

5.3.3.2. Climatic data recorded for the hybridization block established in the field

The total rainfall and the average relative humidity (RH) during the hybridization period in the field ranged from 0.00 mm (February 2013) to 215.20 mm (October, 2012), and 56.63% in January 2013 to 88.42% in October 2012. Similarly, solar radiation ranged from 307.25 w/m^2 in October 2012 to 321.45 w/m^2 in December 2013. The ranges for the minimum and maximum temperatures were 15.68^{o}C (January 2013) to 20.51^{o}C (November, 2012), and 33.65^{o}C (October 2012) to 37.34^{o}C (January 2013), respectively. Mean temperature ranged from 23.34^{0}C to 28.18^{0}C. These values were obtained in October 2012 and February 2013 (Table 5.13).

Table 5.13 Climatic condition over the period of the crossing block in the field

MONTHLY	October 2012	November 2012	December 2012	January 2013	February 2013
Total Rainfall (mm)	215.20	41.40	40.80	3.00	0.00
Relative Humidity (%)	88.42	85.17	80.10	56.63	61.26
Solar Radiation w/m^2	307.25	318.45	321.45	313.95	309.12
Temperature (Min) °C	20.13	20.51	16.30	15.68	18.27
Temperature (Max) °C	33.65	34.39	34.57	37.34	37.02
Temperature Mean °C	23.34	26.17	25.90	26.51	28.18

5.4 Discussion

Lack of flowering in sweetpotato breeding is a severe impediment to understanding its genetics and make gains in selection. The use of a genotype selected as parent for hybridization may be impeded by poor flowering. This makes it prudent to verify flowering ability at the start of a hybridization programme. In this work, 70% of the sweetpotato parents

did not flower when the hybridization blocks were first established in the screen house, and those that did (30%) produced only a few flowers. For this reason, the sweetpotato parents were grafted onto a flower inducing rootstock *I. setosa*, and flowering was improved. However, this technique failed just after hybridization due to wilting and death of the root stock since the *I. setosa* could not tolerate virus particles in the apparently clean scion. This indicates that flower promotion using *I. setosa* in sweetpotato will be successful only if laboratory certified virus-free scion (sweetpotato) are used. This necessitated the re-establishment of the crossing blocks in the field. In spite of this, the parents still varied in flowering prolificacy and the differences may be attributed to varietal differences. According to Fekadu *et al.* (2013), flowering prolificacy in sweetpotato is variety dependent. Whilst some varieties do not flower at all, others produce very few flowers. In addition, many sweetpotato clones rarely flower under normal conditions as a result of differential response to seasonal variation. Most sweetpotato genotypes are day length sensitive. Thus whilst some genotypes flower readily any season, flowering in others occurs only during short day length (Martin, 1988b).

Seasonal observations in north-western Argentina showed that sweetpotatoes flower best with daily maximum temperatures of 23 – 24^{0}C and minimum temperatures between 13 – 19^{0}C (Folquer, 1974). Night temperatures of 16 – 17^{0}C and day temperatures of 24 – 30^{0}C appeared to be optimum (Edmond and Martin, 1946). The best season for pollination in Taiwan, in the northern hemisphere, is from the beginning of November to the middle of December, when the average daily temperature is between 20^{0}C and 25^{0}C with maximum seed set occurring at mean daily temperature of 23.9^{0}C (Wang, 1982). In this study, whilst the daily minimum temperature range observed for the hybridization blocks established in the field (15.68 – 20.51^{0}C) is in agreement with what is reported to favour flowering, that of the

screen house (21.28 – 22.47^{0}C) was higher. The maximum daily temperatures of 28.42 – 32.63^{0}C observed for the screen house, and 33.65 – 37.34^{0}C for the field in this study were higher than the values reported elsewhere. This suggests that minimum temperatures may be important in promoting flowering in sweetpotato in addition to day length. This is because greenhouse crosses are best done at days of 12 hours and temperatures not excessively high (Jones, 1980), and 24^{0}C is the optimum temperature (Montelaro and Miller, 1951). Similar observation was made in Puerto Rico (Campbell *et al.*, 1963), where flowering in the greenhouse did not occur above 27^{0}C. In this study, the hybridization blocks were established in the screen house when day lengths were generally longer and temperatures were generally higher than the optimum temperatures of about 20^{0}C for night and around 25^{0}C for day for flower promotion. The reverse was observed for the hybridization blocks established in the field. This may have resulted in the variable flowering prolificacy between the hybridization blocks established in the screen house and the field. The hybridization blocks in the screen house were established in the major cropping season when day lengths are longer whilst that established in the field was in the minor cropping season when day lengths are shorter. Establishing sweetpotato crossing blocks in the minor cropping season in the forest ecozone of Ghana where this work was done is better than in the major season. Furthermore, sweetpotato seed matures in about a month, a little earlier under hot, summer temperatures and later in cool, fall temperature (Jones, 1980). This also gives minor cropping season crosses an advantage since capsules mature earlier saving money and time. However, seed abortion may be higher due to dry spells, but this can be managed through supplementary irrigation as was done in this study.

The improvement of sweetpotato through conventional breeding is hindered by two factors, poor flowering and incompatibility (Martin, 1967; Martin and Cabanillas, 1968). Whilst

incompatibility is largely attributed to genetics, poor flowering can be overcome by applying various flower induction techniques which include physiological shocks such as grafting, girdling, and chemical treatment to induce flowering (Miller, 1937; Edmond and Martin, 1946). Special efforts are necessary to promote flowering if sweetpotatoes are to be hybridized. In this study, genotypes like CIP 442264 and Ouagadougou 02, which were difficult to use as parents for hybrid development as a result of their inability to produce flowers, should be subjected to treatments in future work to improve their chances of success.

While the problem of poor flowering can be reduced by applying various flower induction techniques, incompatibility remains a global barrier for the genetic improvement and conservation of sweetpotato (Fekadu *et al.*, 2013). Both self- and cross-incompatibility were observed in this study. Among the selfings done, only selfing involving Apomuden produced one seed, which was sterile and failed to germinate. Self-fertilization in sweetpotato is rare (Jill *et al.*, 1989). However, although sweetpotato is almost always self-incompatible (Martin, 1967), self-compatible clones may be observed (Tumana and Kesavan, 1987). Some of the crosses also did not produce seeds. Most sweetpotato used in a previous study were self- and cross-incompatible, and therefore were not able to produce viable seeds through self- and cross-pollination (Vimala and Hariprakash, 2011).

Self-incompatibility is genetically controlled by a single multi-allelic locus, the S-locus. The S-locus has been shown to encode at least two distinct genes, the pollen and pistil determinant genes, which are responsible for the self-incompatible reaction (Takayam and Isogali, 2005; Mcclure and Franklin-Tong, 2006). There are two types of self-incompatibilities in plants and these are heteromorphic and homomorphic (Acquaah, 2011). The self-incompatibility observed in this work was homomorphic because there was no

difference between the relative heights of the stamen and the style. However, further work is needed to determine whether homomorphic self-incompatibility observed is gametophytic or sporopytic.

Cross-incompatibility is presumed to result from pollination between parents with the same self-incompatibility phenotype (Kowyama *et al.*, 2008). If cross-pollination takes place, and the cross is compatible, then pollen germination occurs on the stigma in about 10-20 minutes after pollination (Kowyama *et al.*, 2000). Therefore, out-crosses that failed to produce viable seeds such as crosses between Beauregard and CIP 442850, CIP 443035 and Resisto, indicate the existence of cross-incompatibilities among the sweetpotato genotypes studied. As a result, there was difficulty in using most of the cross combinations for genetic studies. According to Charles *et al.* (1973) and Vimala (1989), cross-incompatibility among different varieties hinders targeted breeding especially when the parents with desirable traits of interest belong to the same incompatibility group. Fekadu *et al.* (2013), identified three types of cross compatibilities which are distinguished by the success of fertility (i.e. germinability of the pollen and differences with respect to stimulation of pollen itself and by the style). These are reciprocal fertility (fertility occurs in both directions), reciprocal incompatibility (incompatibility in both directions) and unilateral incompatibility (fertility occurs only when the genotype is used as female and not when used as male or vice versa). All of these types were observed in this study. For example, crosses Histarch x Apomuden, Histarch x Ogyefo, Ogyefo x Apomuden, Faara x Histarch, and Faara x Apomuden exhibited reciprocal fertility whilst crosses CIP442896 x Beauregard, Ouagadougou 03 x CIP 443035, Ouagadougou 03 x Resisto, and Ouagadougou 03 x Beauregard showed evidence of reciprocal incompatibility. Unilateral incompatibility was also observed for the crosses Histarch x CIP 442850 and Ogyefo x CIP 442850.

Two methods of determining incompatibility in sweetpotato have been suggested (Williams and Cope, 1967). These are the number of seeds set per capsule after self- or cross-fertilization, and *in vivo* tests of pollen germination on stigma and pollen tube penetration into the style at intervals ranging from 3 to 24 hours after pollination. This study sort to understand the genetic incompatibilities based on the number of seeds set per capsule after self- or cross-fertilization. According to Martin (1967), to obtain full knowledge of the genetic control of incompatibility by the use of the first method, it is necessary to make several crosses among selected cross-fertile individuals, test the compatibilities of parents and offspring, undertake further back-crosses and second generation crosses, and finally draw up an explanatory model of gene number and gene action based on seed set. This makes the findings of this study inconclusive. Further study should therefore be done. Similarly, to understand the physiological control, it is essential also to study the pollen behaviour during the process of germination, pollen tube growth, fertilization, and the processes of ovule and embryo development. This can be done by employing the methods of Reynoso *et al.* (1999), which employs aceto-carmine glycerol solution (2%) to stain pollen grains to estimate male fertility microscopically. Since Terao (1934), first observed cross-incompatibility in some cultivars of sweetpotato, a large number of local varieties and lines have been classified into several incompatibility groups (Kowyama *et al.*, 2008). The groups are defined by their ability to achieve successful cross-pollination which is usually assessed by pollen-tube growth on the stigma and/or by seeds set following reciprocal pollinations with tester lines. Since the findings of this work may not be conclusive, identification of testers for the classification of the sweetpotato genotypes into incompatibility groups could not be done until the issue of incompatibility is confirmed.

In spite of this, a higher success rate was attained in this study because the 54% mean success rate observed exceeds the 1 – 48% reported. The success rate in the same crossing block normally varies from 1% to 47% for different female parents and an average success of 35% should be considered good (Jones, 1980). Jill *et al.* (1989), reported that in the Tongan programme, about 48% of the flowers pollinated developed into capsules with an average of two seeds in each capsule. The high success rate observed in this study indicates that failure of seed development for some crosses may not be due to seed abortion alone but possibly to incompatibilities as well. The mean number of seeds per capsule found in this study (1.21) is in the range of 1.1 – 1.7 as reported by Jones (1980), but lower than that reported by Jill *et al.* (1989). The differences, according to Jill *et al.* (1989), may be attributed to the weather, health of plant, parents used and skill of pollinating staff. Sterilities, incompatibilities and environmental conditions all affect capsule set percentages (Martin and Cabanillas, 1966; Jones *et al.*, 1977). The higher germination rates of the seeds and the seedling vigour observed may suggest either the absence of sterility or low sterility among the parents used for this study.

5.5. Conclusion

Breeding progress in sweetpotato is affected by many genetic and physiological factors. The major ones are flowering prolificacy, polyploidy and the large chromosome number, coupled with self- and cross-incompatibilities among different genotypes. These slow down the breeding progress of the crop. In addition to polyploidy and large chromosome number, this study suggested that flowering and self- or cross-incompatibility are major constraints to sweetpotato breeding in Ghana. In spite of this, the results of cross combination between four genotypes Histarch, Apomuden, Beauregard, and Ogyefo were good and they may be used to

exploit the gene action influencing beta-carotene content, dry matter content and sugar content of sweetpotatoes. The work also revealed that the best period to establish hybridization block in the forest ecozone is the minor cropping season.

CHAPTER SIX

6.0 GENE ACTION CONTROLLING THE END-USER TRAITS OF SWEETPOTATO

6.1. Introduction

Sweetpotato breeding until recently was exclusively based on heritability of the traits concerned. Heritability estimate measures the correspondence between phenotypic values and breeding values (Shumbusha *et al.*, 2014). High estimate of heritability does not explain how good materials are, only that superior parents tend to give the best progeny (Rex, 2002). The expected amount of superiority will be realized in subsequent generations only if all of the genetic effects are additive (Miller *et al.*, 1958). Conversely, non-additive effects (epistasis, dominance, and interactions) may decrease the amount of genotypic superiority. Knowledge on the type of gene action operating in a breeding population is therefore, critical for making genetic progress.

Mating designs are important tool in plant breeding programmes to obtain information on genetic parameters such as general combining ability (GCA) and specific combining ability (SCA) of quantitative traits (Hayman, 1954a; Griffing, 1956; Fry, 2004). Even though other mating schemes like the North Carolina II (NCII) have been used for trait inheritance study in sweetpotato (Oduro, 2013), the diallel mating scheme may provide more genetic information on a complex crop like the sweetpotato than the other mating designs. This is because the diallel mating design in addition to estimating GCA and SCA variance components from a set of randomly chosen parental lines (random effects), is also generally used to obtain estimates of genetic effects for a fixed set of parental lines (fixed effects) from multiple-environment experiments (Yudong and Manjit, 1997). The diallel cross is also used as a mating system for determining cumulative gene effects of breeding populations (Hayman, 1954a; Hayman,

1954b; Griffing, 1956; Hayman, 1957; Hayman, 1958). Furthermore, diallel mating scheme provides information on heterosis effects. Heterosis effects provide a basis for the formation of genetic pools (Gardner, 1982). Elisa *et al.* (2000), employed diallel mating scheme for studies on the inheritance of sweetpotato feathery mottle virus (SFMV) resistance. Similarly, Shumbusha *et al.* (2014)**,** also used half diallel for sweetpotato storage root dry matter inheritance study. But, because every seed of sweetpotato is genetically different and has the potential as a cultivar, full diallel mating scheme may provide more genetic information than half diallel.

Griffing (1956), diallel methods have extensively been used for crop plants that are not clonally or vegetatively propagated. Even though Shumbusha *et al.* (2014) and Elisa *et al.* (2000) used Griffing (1956) Model I, Method 4 (only one set of F_1's; with parents, reciprocals excluded) for inheritance studies on sweetpotatoes, Gardner and Eberhart (1966) had proposed alternative analyses of data from diallel crosses produced from heterogeneous parents/populations ("varieties"). They proposed three methods namely Gardner and Eberhart (1966) Analysis I (GEAN I), Analysis II (GEAN II) and Analysis III (GEAN III). GEAN I is resource-intensive, involving the evaluation of n parents, n(n -1)/2 F_1 crosses, and an inbred progeny of parents and crosses, but gives information on additive and dominance gene action, heterosis, and inbreeding depression (Gardner and Eberhart, 1966; Murray *et al.*, 2003). The GEAN II is useful in evaluating *n* populations (varieties) and their n(n – 1)/2 F_1 crosses. Variation among entries (varieties) in GEAN II is partitioned into entries and mid-parent heterosis (Gardner and Eberhart, 1966; Hallauer and Miranda Fo, 1988; Murray *et al.*, 2003). Heterosis is further partitioned into variety, average, and specific heterosis, but additive and dominance parameters cannot be determined since they are confounded with the source of variation entry (variety) (Murray *et al.*, 2003). According to Murray *et al.* (2003), GEAN III

involves parents, parents vs. F_1 crosses, and F_1 crosses as sources of variation to provide estimates of variety and GCA effects (Yudong *et al.*, 2005). Estimates of GCA is similar to Griffing's Method 4, respectively (Murray *et al.*, 2003). GEAN II has successfully been used for studying heterosis and estimating GCA and SCA in variety diallels (Crossa *et al.*, 1987; Ali *et al.*, 2001; Harold *et al.*, 2001; Lee *et al.*, 2003). The objective of the study was to determine the inheritance of storage root beta-carotene content, dry matter content, sugar content, starch content as well as iron and zinc contents of sweetpotato to facilitate the crop's improvement in Ghana and beyond.

6.2. Materials and Methods

6.2.1. Experimental sites

The hybridization block was established at the research station of the Crops Research Institute of the Council for Scientific and Industrial Research, Ghana (CSIR-CRI), at Fumesua in the minor cropping season in 2012. The F_1 progenies were evaluated at three locations which span across three agroecological zones of Ghana. These were the CSIR-CRI research station at Fumesua (forest ecozone), the National Agricultural Research Stations at Wenchi (transition ecozone) and Pokuase (coastal savanna ecozone).

6.2.2. Genetic materials used

The sweetpotato genotypes used as parents in this study were three released varieties (Apomuden, Histarch and Ogyefo), and one breeding line (Beauregard). These were among the superior genotypes selected from the base population which was developed from the sweetpotato germplasm collected and evaluated as presented in Chapter Four of this thesis. Their selection as parents for this study was based on their beta-carotene, dry matter and

sugar contents and amenability to produce viable seeds in both direct and reciprocal crosses as has been shown in Chapters Four and Five of this thesis. Their attributes are presented in Table 6.1.

Table 6.1 Genetic materials used in the study and their desirable characteristics

Parents	Dry matter content (%)	β-carotene content (mg/100g)DW	Sugar content (%)	Other agronomic qualities	Description
Apomuden	27.0	33.67	28.97	Extra early, high yielding, susceptible to sweetpotato weevil.	Very sweet (high sugar content), high beta-carotene content, low dry matter content.
Histarch	45.0	9.85	10.43	Early, high yielding, tolerant to sweetpotato weevil.	Less sweet (low sugar content), low beta-carotene content, high dry matter content.
Ogyefo	42.0	6.83	11.67	Early, high yielding, tolerant to sweetpotato weevil	Less sweet (low sugar content), low beta-carotene content, high dry matter content
Beauregard	32.0	24.31	22.90	Medium maturing, high yielding, tolerant to sweetpotato weevil	Very sweet (high sugar content), high beta-carotene content, low dry matter content.

6.2.3. Experimental layout

The four parents were crossed using the full diallel mating scheme. The number of progenies per cross that were obtained from the hybridization are shown in Table 6.2. In all, 234 F_1 hybrids were obtained, but due to poor vigour of some genotypes 196 of them were evaluated alongside their parents at the three locations using an alpha lattice design with two replications in the minor cropping season of 2013. All entries were planted in single row on ridges at five stands per genotype at planting distance of 0.3 m within row and 1m between rows. Four node vines from the middle portion to the tip were used for planting. Genotypes within family were randomised to adjacent plots.

Table 6.2 Full diallel mating scheme used (number of F_1 highlighted)

*Parents	Histarch	Ogyefo	Apomuden	Beauregard
Histarch	P87	**30**	**30**	**22**
Ogyefo	**20**	P61	**22**	**6**
Apomuden	**13**	**30**	P50	**13**
Beauregard	**13**	**4**	**31**	P82

***[P87 (Histarch), P61 (Ogyefo) = low sugar, low beta-carotene, high dry matter];**
[P50 (Apomuden), P82 (Beauregard) = high sugar, high beta-carotene, low dry matter]

6.2.4. Data collection

Harvesting was done at three and half months after planting. The three middle plants for each genotype were harvested, and one large, one medium, and one small, storage roots were randomly selected for physicochemical analysis after yield data were taken. Storage roots considered for the yield data were those approximately over 3 cm in diameter and without cracks, insect damage or rotten parts (Ekanayake *et al.*, 1990). The yield data recorded were

mean root weight and root yield. The physico-chemical traits determined were beta-carotene content, dry matter content, total sugar (fructose, glucose and sucrose) content, starch content, and iron and zinc contents. This was done at the Quality and Nutrition Laboratory of CIP-Ghana at CSIR-CRI, Fumesua. The physico-chemical traits except dry matter content were determined using the Workflow for Sample Preparation and NIRS analysis of sweetpotato developed by the Quality and Nutrition Laboratory of the International Potato Centre (CIP), Lima, Peru. Fifty grams of fresh sample was freeze-dried for 72 hours using a freeze dryer. Dry matter content was calculated as the ratio of the dry sample expressed as a percentage of the weight of the wet sample.

6.2.5. Data analysis

F_1 hybrids with missing data were eliminated from the analysis. Data for 156 F_1 hybrids from a total of 196 and their four parents were therefore, used for the analyses. The data were analysed by employing Gardner and Eberhart (1966) Analysis II. According to Harold *et al.* (2001), this analysis summarizes the performance of varieties (entries) as parents on the basis of the deviations in performance of the crosses from that of the parents, where parents and crosses assumed to be fixed effects and environments random effects. The approach is based on fitting parents and parent cross means, Xij to the linear model represented below;

$$Xij = \mu_v + \tfrac{1}{2}(Vi + Vj) + \sigma hij$$

Where;

μ_v = mean effects of parents.

Vi and V_j = estimates of variety effects for the ith and the jth parents, respectively.

h = estimate of heterosis effects when parent i is crossed to parent j.

$\sigma = 0$ when $i = j$, and 1 when $i \neq j$.

Heterosis effects only present in crosses is further partitioned as $Hij = h + hi + hj + sij$

Where;

h = estimate of average heterosis.

hi and hj = estimates of variety heterosis (expressed as deviation from h) and indicates GCA.

Sij = estimate of specific heterosis from crossing parents i and j.

The analysis was carried out using SAS 9.2 computer software (SAS, 2002), based on the macros in DIALLEL-SAS05 (Yudong *et al.*, 2005). General Analysis of Variance (ANOVA) was also performed on the four parents and their 156 F_1 derived individuals using Genstat version 9.2.0.152 (Genstat, 2007), to ascertain the performance among the F_1s and between the F_1s and their parents. The ANOVA was carried out in a 10 x 16 alpha lattice design.

6.3. Results

6.3.1. GEAN II (Gardner and Eberhart, 1966) for the four parents and their 156 F_1 hybrids across three environments

Results for the crosses and their reciprocals are presented in Table 6.3a and 6.3b, respectively. The mean square values obtained for the crosses for all the traits did not show significant difference ($P>0.05$) for genotype (entry) by environment interaction (G x E) except for zinc ($P<0.01$) (Table 6.3a). However, G x E was only significant ($P<0.01$) for sugar content, ($P<0.05$) beta-carotene, iron and zinc contents for the reciprocals (Table 6.3b). The analysis showed highly significant differences ($P<0.01$) between the genotypes for all the traits. Whilst there was no significant ($P>0.05$) effect of environment on beta-carotene and dry matter for the crosses (Table 6.3a), only dry matter did not show significant ($P>0.05$) variation across the environments for the reciprocals (Table 6.3b). Overall heterosis was significant ($P<0.05$) for all the traits (Table 6.3a and 6.3b) except zinc content for the crosses (Table 6.3a). Similarly, average heterosis was also significant ($P<0.05$) for all the traits except dry matter content and sugar content for the crosses (Table 6.3a) and dry matter content for the reciprocals (Table 3b). Variety heterosis on the other hand was significant ($P<0.05$) for all the traits except iron and zinc contents for the crosses. Specific combining ability (SCA) was also significant ($P<0.01$) for only beta-carotene content for the crosses and beta-carotene content, sugar content and starch content for the reciprocals. The R-square values for the analysis ranged from 0.65 to 0.98. Coefficient of variation (CV) ranged from 3.42% to 23.22% whilst the root error mean square (Root MSE) ranged from 0.03 to 3.36. The grand means also ranged from 34% to 64.57% for dry matter content and starch content (Table 6.3a and 6.3b).

Table 6.3a Mean squares and other statistics for GEAN II (Gardner and Eberhart, 1966) for the four parents and their crosses across three environments

Source of variation	Df	Beta-carotene (mg/100g)DW	Dry matter (%)	Sugars (%)	Starch (%)	Iron (mg/100g)DW	Zinc (mg/100g)DW
Environment (Env.)	**2**	**23.974^{ns}**	**0.0005^{ns}**	**51.77****	**37.50***	**1.18****	**0.73****
Rep. (Env.)	**3**	**4.696^{ns}**	**0.0002^{ns}**	**8.20^{ns}**	**2.19^{ns}**	**0.05^{ns}**	**0.02^{ns}**
Entry	**9**	**801.825****	**0.0193****	**294.76****	**408.02****	**0.64****	**0.21****
Env. x Entry	**18**	**13.436^{ns}**	**0.8000^{ns}**	**8.61^{ns}**	**5.81^{ns}**	**0.05^{ns}**	**0.02****
R-Square		0.97	0.89	0.96	0.94	0.90	0.89
CV (%)		21.44	8.61	10.46	4.68	10.73	12.32
Root MSE (SE)		3.10	0.03	2.26	3.00	0.19	0.13
Overall heterosis (h_{ij})	**5**	**305.932****	**0.0017***	**74.38****	**107.11****	**0.360****	**0.1056^{ns}**
Average heterosis (h)	**1**	**533.216****	**0.0014^{ns}**	**5.48^{ns}**	**41.85***	**1.141****	**0.2310***
Variety heterosis (h_j)	**3**	**264.286****	**0.0032****	**132.78****	**107.70****	**0.233^{ns}**	**0.1992^{ns}**
SCA	**2**	**104.175****	**0.0014^{ns}**	**13.453^{ns}**	**17.40^{ns}**	**0.001^{ns}**	**0.0003^{ns}**
R-Square		0.93	0.82	0.86	0.90	0.87	0.83
CV (%)		23.22	7.99	13.44	4.57	16.51	20.78
Root MSE (SE)		3.36	0.03	2.90	2.93	0.30	0.22
Mean (μ)		14.46	0.34	21.57	64.22	1.79	1.05

***Significant at P< 0.05; **Significant at P<0.01; ^{ns} Not significant.**

Table 6.3b Mean squares and other statistics for GEAN II (Gardner and Eberhart, 1966) for the four parents and their reciprocals across three environments

Source of variation	Df	Beta-carotene (mg/100g)DW	Dry matter (%)	Sugars (%)	Starch (%)	Iron (mg/100g)DW	Zinc (mg/100g)DW
Environment (Env.)	**2**	**26.08***	**0.0019^{ns}**	**29.21****	**43.69****	**1.43****	**0.90****
Rep. (Env.)	**3**	**2.87^{ns}**	**0.0005^{ns}**	**10.10****	**3.37^{ns}**	**0.03^{ns}**	**0.02^{ns}**
Entry	**9**	**719.56****	**0.0214****	**288.60****	**426.35****	**0.72****	**0.23****
Env. x Entry	**18**	**11.24***	**0.0005^{ns}**	**6.40****	**4.48^{ns}**	**0.05***	**0.02***
R-Square		0.98	0.92	0.98	0.97	0.94	0.94
CV (%)		16.42	7.25	6.21	3.42	8.82	9.26
Root MSE (SE)		2.29	0.03	1.30	2.21	0.16	0.10
Overall heterosis (h_{ij})	**5**	**213.01****	**0.0036****	**88.99****	**158.11****	**0.36****	**0.129***
Average heterosis (h)	**1**	**686.72****	**0.0001^{ns}**	**37.64****	**75.05****	**1.03****	**0.210***
Variety heterosis (h_j)	**3**	**90.03****	**0.0049****	**113.12****	**206.65****	**0.30***	**0.145***
SCA	**2**	**80.17****	**0.0015^{ns}**	**34.01****	**47.88****	**0.02^{ns}**	**0.003^{ns}**
R-Square		0.94	0.86	0.91	0.93	0.70	0.65
CV (%)		20.38	7.23	10.65	3.85	16.83	21.25
Root MSE (SE)		2.85	0.03	2.23	2.49	0.30	0.23
Mean		13.97	0.35	20.97	64.57	1.80	1.06

***Significant at P<0.05; **Significant at P<0.01; ^{ns} Not significant.**

6.3.2. Performance of the four parents and their 156 F_1's hybrids over three environments for beta-carotene, dry matter and sugar content

With reference to beta-carotene content, Apomuden performed best as parent (37.19mg/100gDW) and the second best in the overall cross performance (14.66 mg/100gDW). Histarch performed poorly as parent for the beta-carotene content, whilst Ogyefo was the poorest in the overall crosses.

In terms of dry matter content, Histarch performed well as parent (43%) and second best in the overall crosses (38%). The poorest performing parent was Apomuden with mean of 26%, but it was the best performer in the overall crosses with mean of 39%. Ogyefo was the second best performing parent (40%) and the third in the overall cross performance with a mean of 36%.

In the case of sugar content, Ogyefo obtained the lowest value among the parents (14.36%) followed by Histarch (15.17%), but Histarch performed better than Ogyefo in the overall crosses with respective means of 18.51% and 18.73% which were not significantly different ($P>0.05$). Apomuden produced the highest sugar content (36.71%) followed by Beauregard (21.52%) among the parents, but the reverse occurred for the overall crosses with respective means of 22.67% and 24.41%. These results are presented in Table 6.4.

Table 6.4 Beta-carotene, dry natter and total sugars means of the four parents and their 12 F_1's from all crosses over three environments

Parents	F_1 means				Mean Performance			
	Apomuden	**Ogyefo**	**Beauregard**	**Histarch**	**Crosses**	**Reciprocals**	**Overall crosses**	**Parents**
				Beta-carotene content (mg/100g)DW				
Apomuden		7.90	23.84	13.29	15.01	14.31	14.66	37.19
Ogyefo	8.79		3.98	4.04	5.31	8.32	6.82	5.95
Beauregard	22.56	11.55		19.10	15.64	14.08	14.86	25.64
Histarch	11.59	4.62	8.13		12.14	8.11	10.13	3.67
Lsd (5%)					**6.20**	**4.58**	**5.39**	**5.39**
				Dry matter content (%)				
Apomuden		33.0	28	36	32	33	39	26
Ogyefo	33		33	41	36	35	36	40
Beauregard	28	31		32	31	33	32	31
Histarch	38	40	40		36	39	38	43
Lsd (5%)					**6**	**5**	**6**	**6**
				Sugar content (%)				
Apomuden		19.33	28.91	20.89	23.04	22.29	22.67	36.71
Ogyefo	20.40		19.32	14.80	17.82	19.63	18.73	14.36
Beauregard	28.02	22.86		24.70	24.31	24.50	24.41	21.52
Histarch	18.44	15.62	16.61		20.13	16.89	18.51	15.17
Lsd (5%)					**4.52**	**2.60**	**3.56**	**3.56**

$^{S}F_1$ means for crosses above diagonal; F_1 means for reciprocals below diagonal

6.3.3. Performance of the four parents and their 156 F_1's over three environments for starch, iron and zinc content

Histarch was the best performing parent (72.70%) and in the overall crosses (68.28%) for starch content. Apomuden was the poorest parent for starch content with mean of 45.44%, whilst Beauregard was the poorest performing parent in the overall crosses with mean of 62.17%.

Ogyefo and Histarch had the lowest iron content among the parents with means of 1.68 mg/100gDW and 1.49 mg/100gDW. Their means in the overall crosses were 1.64 mg/100gDW and 1.56 mg/100gDW, respectively. The iron content for Apomuden (2.56 mg/100gDW) was the highest followed by Beauregard (2.12 mg/100gDW). The reverse was true for their overall cross performance with means of 1.73 mg/110DW and 1.79 mg/100gDW.

The performance of the parents for zinc content was of the same trend as the iron content with Apomuden (1.53 mg/100gDW) having the highest value followed by Beauregard (1.12 mg/100gDW). Ogyefo which gave the third highest zinc content (1.01 mg/100gDW) produced the highest zinc content in the overall crosses (1.05 mg/100gDW). Histarch was the poorest performer for zinc content both as parent (0.86 mg/100gDW) and in the overall crosses (0.39 mg/100gDW). These results are presented in Table 6.5.

Table 6.5 Starch, iron and zinc means of the four parents and their 12 F_1's from all crosses over three environments

Parents	F_1 means				Mean Performance			
	Apomuden	**Ogyefo**	**Beauregard**	**Histarch**	**Crosses**	**Reciprocals**	**Overall crosses**	**Parents**
				Starch content (%)				
Apomuden		66.22	56.67	65.99	62.96	63.78	63.37	45.44
Ogyefo	65.38		66.58	72.01	68.27	65.62	66.95	71.37
Beauregard	57.02	60.74		61.95	61.73	62.61	62.17	63.27
Histarch	68.93	70.75	70.06		66.65	69.91	68.28	72.70
Lsd (5%)					**6.02**	**4.42**	**5.22**	**5.22**
				Iron content (mg/100g)DW				
Apomuden		1.65	1.88	1.61	1.71	1.74	1.73	2.56
Ogyefo	1.78		1.77	1.47	1.63	1.75	1.64	1.68
Beauregard	1.91	1.96		1.72	1.79	1.79	1.79	2.12
Histarch	1.52	1.51	1.51		1.60	1.51	1.56	1.49
Lsd (5%)					**0.38**	**0.32**	**0.35**	**0.35**
				Zinc content (mg/100g) DW				
Apomuden		1.05	1.09	0.94	1.03	1.03	1.03	1.53
Ogyefo	1.10		1.08	0.92	1.02	1.07	1.05	1.01
Beauregard	1.08	1.16		0.96	1.04	1.04	1.04	1.12
Histarch	0.90	0.94	0.89		0.94	0.91	0.93	0.86
Lsd (5%)					**0.26**	**0.20**	**0.23**	**0.23**

[$]$F_1$ means for crosses above diagonal; F_1 means for reciprocals below diagonal

6.3.4. Estimates of variety effects and heterosis for beta-carotene, dry matter and sugar contents

Variety effect (v_j) was significant for beta-carotene, dry matter and sugar contents of the four parents both for the crosses and the reciprocal crosses (Table 6.6). Variety effect (v_j) for beta-carotene ranged from -14.44 mg/100gDW (Histarch) to 19.08 mg/100gDW (Apomuden). Dry matter content ranged from -0.09% (Apomuden) to 0.09% (Histarch). Values for sugar content ranged from -7.58% to 14.77% for Ogyefo and Apomuden. All four parents had significant ($P<0.01$) variety effects for all the traits except Beauregard which did not show significant ($P>0.05$) variety effect for sugar content.

Variety heterosis (h_j) was also significant for beta-carotene, dry matter and sugar content (Table 6.6). Unlike the variety effect (v_j), variety heterosis (h_j) effects for the parents varied significantly for the traits between the crosses and the reciprocals. For example, Ogyefo and Histarch had variety heterosis (h_j) effects which were not significant ($P>0.05$) for dry matter content for the crosses, whilst Beauregard had non-significant variety heterosis effect for the reciprocals. In addition, Beauregard did not show significant ($P>0.05$) variety heterosis (h_j) effect for beta-carotene content in either the crosses or the reciprocals. Similarly, Ogyefo and Histarch did not have significant ($P>0.05$) variety heterosis (h_j) effect for sugar content for the crosses, but their effects were significant for the reciprocals. Values for beta-carotene ranged from -5.06 to 7.40 and these were given by Apomuden and Histarch. Those of dry matter content ranged from -0.03 (Ogyefo) to 0.03 (Apomuden). The range of values for sugar content was from -4.81 to 4.69 for Apomuden and Beauregard. Average heterosis was higher for the crosses than the reciprocals for beta-carotene and sugar contents. The reverse was observed for dry matter content (Table 6.6).

Table 6.6 Estimates of variety effects (vj), average heterosis (h) and variety heterosis (hj) effects for beta-carotene, dry matter, and sugar contents over three environments.

Parents	Traits					
	Beta-carotene (mg/100dDW)		Dry matter (%)		Sugars (%)	
	Variety effects (v_j)	Variety heterosis (h_j)	Variety effects (v_j)	Variety heterosis (h_j)	Variety effects (v_j)	Variety heterosis (h_j)
			Crosses			
Apomuden	19.08**	-5.06**	-0.09**	0.03**	14.77**	-4.81**
Ogyefo	-12.16**	-4.00**	0.05**	0.01^{ns}	-7.58**	-1.47^{ns}
Beauregard	7.53**	1.66^{ns}	-0.04**	-0.02**	-0.42^{ns}	4.69**
Histarch	-14.44**	7.40**	0.09**	-0.01^{ns}	-6.77**	1.59^{ns}
Std. error	1.19	1.03	0.01	0.01	1.03	0.89
Average Heterosis		-6.09±0.88**		-0.01 ± 0.01^{ns}		-0.62 ± 0.76^{ns}
			Reciprocals			
Apomuden	19.08**	-4.87**	-0.09**	0.02**	14.77**	-4.44**
Ogyefo	-12.16**	1.75*	0.05**	-0.03**	-7.58**	2.74**
Beauregard	7.53**	0.55^{ns}	-0.04**	-0.01^{ns}	-0.42^{ns}	3.47**
Histarch	-14.44**	2.58**	0.09**	0.02**	-6.77**	-1.77*
Std. error	1.01	0.87	0.01	0.01	0.79	0.68
Average Heterosis		-6.91±0.75**		0.02 ± 0.01^{ns}		-1.62±0.59**

***Significant at P<0.05; **Significant at P<0.01; ^{ns} Not significant.**

6.3.5. Estimates of variety effects and heterosis for starch, iron and zinc contents

Variety effect (v_j) was significant for starch content, iron content and zinc content for the crosses and their reciprocals (Table 6.7). Beauregard did not show significant ($P>0.05$) variety effect (v_j) for all the traits whereas Ogyefo also did not have significant ($P>0.05$) variety effect (v_j) for zinc content. Variety effect (v_j) for starch content ranged from -17.75% (Apomuden) to 9.50% (Histarch). The reverse was true for iron and zinc contents with Histarch producing the lowest values and Apomuden the highest values. Values for iron content and zinc content ranged from -0.47 mg/100gDW to 0.59 mg/100gDW and -0.269 mg/100gDW to 0.394 mg/100gDW, respectively.

Variety heterosis (h_j) was also significant for starch content, iron content and zinc content (Table 6.7). Again unlike the variety effect (v_j), the variety heterosis (v_j) effects varied not only in value but also in level of significance between the crosses and their reciprocals. For example, variety heterosis (v_j) effect for Ogyefo was not significant ($P>0.05$) for starch content for the crosses, but it was significant ($P<0.01$) for the reciprocals. Similarly, variety heterosis (v_j) effect for Ogyefo was not significant ($P>0.05$) for iron and zinc contents for the crosses, but it was significant ($P<0.05$) for the reciprocals. Values for starch content ranged from -4.79 (Beauregard) to 5.97 (Apomuden) and -4.35 (Beauregard) to 6.32 (Apomuden) for the crosses and the reciprocals, respectively. Those of iron content ranged from -0.25 (Apomuden) to 0.11 (Histarch) and -0.24 (Apomuden) to 0.22 (Ogyefo) for the crosses and the reciprocals. Values for the zinc content also ranged from -0.175 to 0.145 and these values were given by Apomuden and Ogyefo. Average heterosis for the traits was lower for the crosses than the reciprocals as shown in Table 6.7.

Table 6.7 Estimates of variety effects (vj), average heterosis (h) and variety heterosis (hj) effects for starch, iron, and zinc contents over three environments

Parents	Traits					
	Starch (%)		Iron (mg/100g)DW		Zinc (mg/100g)DW	
	Variety effects (V_j)	Variety heterosis (h_j)	Variety effects (V_j)	Variety heterosis (h_j)	Variety effects (V_j)	Variety heterosis (h_j)
			Crosses			
Apomuden	-17.75**	5.97**	0.59**	-0.25**	0.394**	-0.166*
Ogyefo	8.18**	0.96^{ns}	-0.28*	0.06^{ns}	-0.121^{ns}	0.072^{ns}
Beauregard	0.08^{ns}	-4.79**	0.16^{ns}	0.08^{ns}	-0.004^{ns}	0.055^{ns}
Histarch	9.50**	-2.13**	-0.47**	0.11^{ns}	-0.269**	0.039^{ns}
Std. error	1.04	0.90	0.10	0.09	0.08	0.07
Average Heterosis		1.71±0.77*		-0.28±0.08**		-0.127±0.06*
			Reciprocals			
Apomuden	-17.75**	6.32**	0.59**	-0.24**	0.394**	-0.175*
Ogyefo	8.18**	-3.87**	-0.28*	0.22*	-0.121^{ns}	0.145*
Beauregard	0.08^{ns}	-4.35**	0.16^{ns}	0.07^{ns}	-0.004^{ns}	0.048^{ns}
Histarch	9.50**	1.90**	-0.47**	-0.04^{ns}	-0.269**	-0.019^{ns}
Std. error	0.88	0.76	0.11	0.09	0.08	0.07
Average Heterosis		2.28±0.66**		-0.27±0.08**		-0.121±0.06*

***Significant at P<0.05; **Significant at P<0.01; ^{ns} Not significant.**

6.3.6. Heterosis for all crosses among the four parents over three environments for beta-carotene, dry matter and sugar contents

Better parent heterosis (h_{ij}) for beta-carotene ranged from -84% for the crosses Ogyefo x Beauregard to -22% for the crosses Histarch x Ogyefo. Mid-parent heterosis ($\hat{h}ij$) also ranged from -75% (Ogyefo x Beauregard) to 30% (Beauregard x Histarch). Specific heterosis (s_{ij}) was significant ($P<0.05$) for all the crosses among the parents except for the crosses involving Apomuden x Ogyefo, Histarch x Apomuden, Beauregard x Ogyefo, and Beauregard x Histarch (Table 6.8).

The results for the dry matter content are also shown in Table 6.8. Better parent heterosis (h_{ij}) ranged from -26% for the crosses Beauregard x Histarch to -5% for the crosses Ogyefo x Histarch. The mid-parent heterosis ($\hat{h}ij$) also ranged from -14% (Beauregard x Histarch and Beauregard x Ogyefo) to 9% (Histarch x Apomuden). Specific heterosis (s_{ij}) was significant ($P<0.05$) for only crosses involving Ogyefo x Apomuden, and Histarch x Beauregard.

Better parent heterosis (h_{ij}) for the sugar content was computed based on the low sugar content parent (Table 6.8). The values ranged from 3% (Ogyefo x Histarch) to 63% (Beauregard x Histarch). The mid-parent heterosis ($\hat{h}ij$) also ranged from -29% for crosses Histarch x Apomuden to 35% for crosses Beauregard x Histarch. Specific heterosis (s_{ij}) was significant ($P<0.05$) for only crosses involving Ogyefo x Apomuden, Beauregard x Apomuden, Histarch x Ogyefo, and Histarch x Beauregard, respectively.

Table 6.8 Estimates of heterosis effects as per cent of the better parent (h_{1j}) and mid-parent value ($\hat{h}ij$), and the specific heterosis (s_{ij}) for beta-carotene, dry matter and sugar contents over three environments

Cross	Trait								
	Beta-carotene (mg/100g)DW			Dry matter (%)			Sugars (%)		
	Heterosis effect (%)		Specific heterosis	Heterosis effect (%)		Specific heterosis	Heterosis effect (%)		Specific heterosis
	h_{ij}	$\hat{h}ij$	s_{ij}	h_{ij}	$\hat{h}ij$	s_{ij}	h_{ij}	$\hat{h}ij$	s_{ij}
Apomuden x Ogyefo	-79	-63	1.48^{ns}	-18	0	-0.012^{ns}	35	-24	0.69^{ns}
$Ogyefo x Apomuden	-76	-59	-2.74**	-18	0	0.013*	42	-20	-1.82**
Apomuden x Beauregard	-36	-24	1.92*	-10	-3	0.009^{ns}	34	-0.7	0.56^{ns}
$Beauregard x Apomuden	-39	-28	2.38**	-10	-3	-0.007^{ns}	30	-4	1.50**
Apomuden x Histarch	-64	-35	-3.39**	-16	3	0.003^{ns}	38	-19	-1.22^{ns}
$Histarch x Apomuden	-69	-43	0.36^{ns}	-12	9	-0.006^{ns}	22	-29	0.32^{ns}
Ogyefo x Beauregard	-84	-75	-3.39**	-18	-8	0.003^{ns}	35	8	-1.22^{ns}
$Beauregard x Ogyefo	-55	-27	2.38^{ns}	-23	-14	-0.006^{ns}	59	27	0.32^{ns}
Ogyefo x Histarch	-32	-16	1.92*	-5	-3	0.009^{ns}	3	0.2	0.53^{ns}
$Histarch x Ogyefo	-22	-4	2.38**	-7	-5	-0.007^{ns}	9	6	1.50**
Beauregard x Histarch	-26	30	1.48^{ns}	-26	-14	-0.012^{ns}	63	35	0.69^{ns}
$Histarch x Beauregard	-68	-45	-2.75**	-7	8	0.013*	10	-9	-1.82**
Std. error (direct crosses)			0.79			0.01			0.68
Std. error (Reciprocal crosses)			0.67			0.01			0.53

$Reciprocals; *Significant at P<0.05; **Significant at P<0.01; ^{ns}Not significant.

6.3.7. Heterosis for all crosses among the four parents over three environments for starch iron and zinc contents

Specific heterosis (s_{ij}) was not significant for any of the crosses for iron and zinc contents (Table 6.9). Crosses involving Ogyefo x Apomuden, Beauregard x Apomuden, Apomuden x Histarch, Ogyefo x Beauregard, Histarch x Ogyefo, and Histarch x Beauregard showed significant ($P<0.05$) specific heterosis (s_{ij}) for starch content.

Better parent heterosis (h_{ij}) for starch content ranged from -15% (Beauregard x Ogyefo and Beauregard x Histarch) to -1% (Ogyefo x Histarch). Mid-parent heterosis **(**$\hat{h}ij$) also ranged from -10% (Beauregard x Ogyefo) to 17% (Histarch x Apomuden).

For iron content, better parent heterosis (h_{ij}) ranged from -41% for the crosses Histarch x Apomuden to -1% for the crosses Beauregard x Histarch. Mid-parent heterosis **(**$\hat{h}ij$) also ranged from -25% for crosses Histarch x Apomuden to 3% for the crosses Beauregard x Ogyefo.

Better parent heterosis (h_{ij}) for zinc content had values which ranged from -41% for the crosses Histarch x Apomuden to 4% for the crosses Beauregard x Ogyefo. Its mid-parent heterosis **(**$\hat{h}ij$) also ranged from -25% for the crosses Histarch x Apomuden to 8% for the crosses Beauregard x Ogyefo (Table 6.9).

Table 6.9 Estimates of heterosis effects as per cent of the better parent (h_{1j}) and the mid-parent value ($\hat{h}ij$), and the specific heterosis (s_{ij}) for starch, iron, and zinc content over three environments

Cross	Trait								
	Starch (%)			Iron (mg/100g)DW			Zinc (mg/100g)DW		
	Heterosis effect (%)		Specific heterosis	Heterosis effect (%)		Specific heterosis	Heterosis effect (%)		Specific heterosis
	h_{ij}	$\hat{h}ij$	s_{ij}	h_{ij}	$\hat{h}ij$	s_{ij}	h_{ij}	$\hat{h}ij$	s_{ij}
Apomuden x Ogyefo	-7	14	-0.82^{ns}	-36	-22	0.004^{ns}	-31	-19	0.000^{ns}
$Ogyefo x Apomuden	-8	12	2.24**	-30	-16	-0.054^{ns}	-28	-15	-0.015^{ns}
Apomuden x Beauregard	-10	4	-0.56^{ns}	-27	-20	-0.011^{ns}	-29	-4	-0.005^{ns}
$Beauregard x Apomuden	-10	5	-1.59**	-25	-18	0.012^{ns}	-29	3	0.000^{ns}
Apomuden x Histarch	-9	12	1.38*	-37	-21	0.007^{ns}	-39	-22	0.005^{ns}
$Histarch x Apomuden	-5	17	-0.65^{ns}	-41	-25	0.042^{ns}	-41	-25	0.016^{ns}
Ogyefo x Beauregard	-7	-1	1.38*	-17	-7	0.007^{ns}	-4	1	0.005^{ns}
$Beauregard x Ogyefo	-15	-10	0.65^{ns}	-8	3	0.042^{ns}	4	8	0.016^{ns}
Ogyefo x Histarch	-1	-0	-0.56^{ns}	-13	-8	-0.011^{ns}	-9	-2	0.005^{ns}
$Histarch x Ogyefo	-3	-2	-1.59**	-10	-5	0.012^{ns}	-7	0	0.000^{ns}
Beauregard x Histarch	-15	-9	-0.82^{ns}	-1	-5	0.004^{ns}	-14	-4	0.000^{ns}
$Histarch x Beauregard	-4	3	2.24**	-29	-17	-0.055^{ns}	-21	-6	-0.016^{ns}
Std. error (direct crosses)			0.69			0.70			0.51
Std. error (Reciprocal crosses)			0.57			0.07			0.05

$Reciprocals; *Significant at P<0.05; **Significant at P<0.01; ^{ns}Not significant.

6.3.8. Mean performance of elite F_1 hybrids selected for low sugar content, moderate to high beta-carotene content, and high storage root yield

Mean performance of all the entries is shown in Appendix 6.1. Hybrids selected for low sugar content had sugar content which ranged from 12.93% to 14.88% (Table 6.10). These values were for Histarch x Apomuden -11 and Histarch x Ogyefo - 30. The beta-carotene content of these hybrids ranged from 1.60 mg/100gDW for Histarch x Beauregard-2 to 5.01 mg/100gDW for Ogyefo x Apomuden – 16. Their dry matter content also ranged from 40% (Histarch x Beauregard – 10, Histarch x Apomuden – 1 and Ogyefo x Apomuden -16) to 46% (Ogyefo x Histarch -14), whilst their storage root yield also ranged from 7.57 t/ha for Ogyefo x Histarch - 20 to 39.20 t/ha for Ogyefo x Histarch - 9. Hybrids selected for beta-carotene content had beta-carotene content which ranged from 13.55 mg/100gDW (Beauregard x Apomuden -11) to 41.71 mg/100gDW (Apomuden x Beauregard - 4) (Table 6.11). Their dry matter ranged from 23% for Apomuden x Beauregard - 4 to 39% for Histarch x Apomuden - 9. Their sugar content ranged from 17.62% to 36.71% whilst their storage root yield ranged from 15.47 t/ha to 59.57 t/ha. The lowest and highest values of sugar content were given by Histarch x Beauregard - 21 and Apomuden x Beauregard - 4. Similarly, those of the root yield were Histarch x Apomuden - 9 and Beauregard x Apomuden - 30. The F_1's selected based on the storage root yield in addition to the hybrids selected above (Table 6.12) had yield range from 22.12 t/ha for Ogyefo x Apomuden- 11 to 47.9 t/ha for Beauregard x Histarch -13. Their beta-carotene and dry matter contents ranged from 1.38 mg/100gDW (Beauregard x Apomuden -10) to 17.78 mg/100gDW (Beauregard x Apomuden - 6) and 29% (Ogyefo x Beauregard – 6) to 42% (Ogyefo x Histarch – 15 and Histarch x Beauregard -9). Their sugar content also ranged from 16.14% to 22.94%. These values were given by Histarch x Beauregard - 9 and Beauregard x Apomuden -6.

Table 6.10 Means of the elite F_1 hybrids selected based on low sugar performance relative to the low sugar parents over three environments

Genotype	Beta-carotene (mg/100g)DW	Dry matter (%)	Iron (mg/100g) DW	Starch (%)	Total sugars (%)	Zinc (mg/100g) DW	Mean root wt (kg)	Total root yield (t/ha)
87X50-11	2.39	44	1.29	75.57	12.93	0.77	0.22	21.20
61X87-14	4.82	46	1.30	74.48	13.01	0.90	0.13	9.03
87X82-14	3.93	42	1.53	71.37	13.45	0.93	0.09	15.34
87X82-10	2.93	40	1.44	72.81	13.66	0.85	0.19	18.15
61X87-3	4.02	42	1.23	73.58	13.78	0.84	0.20	26.27
87X61-34	4.76	43	1.41	72.77	13.83	0.82	0.10	18.40
87X61-24	1.99	41	1.42	72.57	13.86	0.90	0.09	7.95
87X50-1	4.75	40	1.43	73.96	14.10	0.79	0.26	33.73
87X61-4	3.26	42	1.36	72.59	14.28	0.89	0.22	29.44
61X50-16	5.01	40	1.51	72.91	14.36	1.07	0.19	23.50
Ogyefo (61)	5.95	39	1.69	71.37	14.36	1.01	0.22	15.35
61X87-9	4.54	45	1.64	72.24	14.39	0.98	0.22	39.20
61X87-20	4.75	41	1.47	72.45	14.67	0.93	0.16	7.57
87X82-2	1.60	41	1.69	71.43	14.73	0.99	0.13	24.08
87X61-30	4.57	41	1.42	72.31	14.88	0.88	0.19	17.69
Histarch (87)	3.67	43	1.49	72.70	15.17	0.86	0.20	24.39
***SEM (P<0.05)**	2.63	2.00	0.11	2.03	1.79	0.07	0.05	6.24
Grand mean	11.81	35	1.67	65.54	20.56	1.00	0.18	22.78
CV (%)	41.1	8.7	11.1	5.7	15.9	11.5	47.2	49.8

***SEM=Standard error of Mean**

Table 6.11 Means of the elite F_1 hybrids selected based on moderate to high beta-carotene content over three environments

Genotype	Beta-carotene (mg/100g)DW	Flesh colour	Dry matter (%)	Iron (mg/100g) DW	Starch (%)	Total sugars (%)	Zinc (mg/100g) DW	Mean root wt (kg)	Total root yield (t/ha)
50X82-4	41.71	Dark orange	23	2.09	47.04	36.35	1.20	0.14	22.78
Apomuden (50)	37.19	Dark orange	26	2.56	45.44	36.71	1.53	0.13	19.72
82X50-23	33.73	Dark orange	29	2.01	58.81	25.71	1.12	0.16	35.69
82X50-4	33.47	Dark orange	26	2.12	51.62	32.88	1.26	0.21	35.28
82X87-9	32.49	Dark orange	26	2.07	51.20	32.67	1.09	0.35	22.28
82X50-19	25.97	Intermediate orange	26	1.96	52.36	32.80	1.13	0.23	26.95
50X61-18	25.72	Intermediate orange	28	2.03	60.75	24.10	1.21	0.13	32.04
50X87-15	25.65	Intermediate orange	33	1.77	62.62	20.66	0.99	0.17	24.19
Beauregard (82)	25.64	Intermediate orange	31	2.12	63.27	21.51	1.13	0.32	37.53
82x50-17	25.47	Intermediate orange	27	1.85	56.75	28.85	0.96	0.22	26.76
82X87-5	24.98	Intermediate orange	36	1.59	67.83	18.03	0.89	0.16	22.14
82X87-7	23.20	Intermediate orange	29	1.82	55.36	31.80	1.07	0.22	32.31
82X87-4	23.00	Intermediate orange	32	1.67	62.90	22.78	0.91	0.41	29.89
82X50-30	22.49	Intermediate orange	30	1.90	58.27	27.35	1.06	0.25	59.57
87X82-21	19.55	Intermediate orange	35	1.71	68.50	17.62	0.90	0.16	17.30
87X50-9	19.03	Intermediate orange	39	1.44	68.49	19.04	0.82	0.18	15.47
61X50-19	18.62	Intermediate orange	30	1.96	58.83	26.05	1.14	0.16	20.48
50X87-14	18.16	Intermediate orange	32	1.72	63.47	23.72	0.95	0.21	21.99
82X87-6	14.86	Pale orange	35	1.48	63.28	24.04	0.86	0.18	35.85
82X50-11	13.55	Pale orange	36	1.60	65.97	19.34	0.97	0.18	29.12
***SEM (P<0.05)**	2.63		2.00	0.11	2.03	1.79	0.07	0.05	6.24
Grand mean	11.81		35	1.67	65.54	20.56	1.00	0.18	22.78
CV (%)	41.1		8.7	11.1	5.7	15.9	11.5	47.2	49.8

***SEM=Standard error of mean**

Table 6.12 Means of the elite F_1 hybrids selected based on storage root yield relative to their parents over three environments

Genotype	Beta-carotene (mg/100g)DW	Dry matter (%)	Iron (mg/100g) DW	Starch (%)	Total sugars (%)	Zinc (mg/100g) DW	Mean root wt. (kg)	Total root yield (t/ha)
82X87-13	3.40	35	1.86	67.40	18.66	1.04	0.38	47.90
61X87-15	6.21	42	1.56	69.98	17.09	0.94	0.20	38.79
82X50-29	2.20	33	1.56	65.79	20.36	0.94	0.34	38.21
61X82-4	6.37	30	2.05	64.84	20.50	1.29	0.17	38.11
Beauregard (82)	25.64	31	2.12	63.27	21.51	1.13	0.32	37.53
50X61-26	6.66	33	1.78	65.01	20.64	1.15	0.20	34.08
82X61-4	2.23	33	1.72	64.71	19.80	1.05	0.17	33.93
87X61-32	7.82	37	1.37	69.39	17.47	0.96	0.14	31.35
82X87-11	11.47	35	1.56	67.73	21.93	0.87	0.27	30.95
87X82-9	3.22	42	1.45	70.83	16.14	0.88	0.22	30.20
82X50-10	1.38	31	1.47	63.54	22.48	0.91	0.24	29.81
61X82-2	2.11	33	1.64	67.30	19.44	1.00	0.16	29.44
61X50-9	8.64	37	1.68	67.83	17.66	1.05	0.14	28.47
82X50-6	17.78	30	1.68	63.12	22.94	0.89	0.23	26.04
87X61-38	5.65	41	1.75	68.51	16.35	1.02	0.21	24.74
Histarch (87)	3.67	43	1.49	72.70	15.17	0.86	0.20	24.39
87X82-5	6.91	39	1.45	70.54	16.61	0.89	0.17	24.10
50X61-12	3.11	32	1.53	65.82	19.81	1.07	0.18	23.12
61X82-6	3.55	29	1.65	67.88	17.85	1.01	0.16	22.75
61X50-11	7.66	32	1.87	64.45	22.60	1.28	0.15	22.12
Apomuden (50)	37.19	26	2.56	45.44	36.71	1.53	0.13	19.72
Ogyefo (61)	5.95	39	1.69	71.37	14.36	1.01	0.22	15.35
SEM (P<0.05)	2.63	2.00	0.11	2.03	1.79	0.07	0.05	6.24
Grand mean	11.81	35	1.67	65.54	20.56	1.00	0.18	22.78
CV (%)	41.1	8.7	11.1	5.7	15.9	11.5	47.2	49.8

6.4. Discussion

A general model for estimating genetic effects proposed by Gardner (1965), Eberhart and Gardner (1966), and Gardner and Eberhart (1966), which can be applied to both inbred parents and non-inbred parents (varieties and/or populations) was used for this study. Coefficient of variation (CV) produced from the Gardner and Eberhart (1966) Analysis II (GEAN II) for the respective traits were all less than 24%. In addition, the R-square values which ranged from 0.65 to 0.98 were larger than the expected minimum of 0.50 indicating a high precision of the results generated by the analysis. Differences were found between the results for the crosses and their reciprocals. For instance, genotype (entry) x environment interactions (G x E) were not significant for any of the traits for the crosses except zinc content, but, G x E was significant for all the traits for the reciprocals except dry matter and starch contents. Whilst there was no significant ($P>0.05$) effect of environment on beta-carotene and dry matter contents for the crosses, only dry matter did not show significant ($P>0.05$) variation across the environments for the reciprocals. Overall heterosis was significant for all the traits for both the crosses and their reciprocals except zinc content in the case of the crosses. Similarly, average heterosis was also significant ($P<0.05$) for all the traits except dry matter content and sugar content for the crosses and only dry matter content for the reciprocals. Variety heterosis on the other hand was significant ($P<0.05$) for all the traits for both the crosses and their reciprocals except iron and zinc contents for the crosses. Specific combining ability (SCA) was significant ($P<0.01$) for only beta-carotene content for the crosses and beta-carotene content, sugar content and starch content for the reciprocals. These differences between the crosses and their reciprocals may be attributed to maternal effects. Maternal effects are influences of parents on offspring phenotype occurring through pathways other than inherited DNA (Adkins-Regan *et al.*, 2013). Phenotypes that are

controlled by cytoplasmic factors found in the female parent are said to express a maternal effect.

Variety effect (vj) and variety heterosis (hj) were significant for all the traits studied. Variety effects are calculated from the performance of parents (Harold *et al.*, 2001). It is the difference between the mean of a parent and the mean of all parents (Gardner, 1967). Variety heterosis (hj) effects was defined by Harold *et al.* (2001), as the deviations in performance of crosses from the performance mid-point of their respective parents. However, Gardner (1967), defined variety heterosis (hj) as the contribution of heterosis by variety j in its crosses measured as a deviation from average heterosis. According to the author, it is calculated as a function of the difference between the mean of a parent in crosses and the average of all crosses and the difference between a parent's mean and the average of all parents. Although specific combining ability (SCA) was significant for some traits, the SCA accounted for a less sizeable portion of the total sum of squares for all the traits compared to the variety heterosis. It suggests that both additive and non-additive effects are involved in the expression of some traits. However, additive effects were more important than non-additive effects for all the traits studied. Oduro (2013) also found additive effects more important than non-additive effects for all these traits on different sweetpotato genotypes studied. Shumbusha *et al.* (2014) also made a similar observation in a study on sweetpotato storage root dry matter. This observation was also made on a diallel of maize on various traits (Crossa *et al.*, 1987; Adam *et al.*, 2001; Harold *et al.*, 2001). This shows that majority of the total sum of squares of the traits due to differences among generation means could be explained by variety effects (vj) and variety heterosis. This means that variety effects for the parents were important predictors of cross performance. However, average heterosis (h) was the most important of the three heterosis (hij) for beta-carotene, iron, and zinc contents. The

average heterosis (h) contributed by a particular set of parents used in crosses is the difference between the mean of all crosses and the mean of all parents (Gardner, 1967). Average heterosis effects (h) are observed in diversity analysis as a separation of parents in different directions away from the origin (Harold *et al.*, 2001). Negative variety heterosis (h_j) can be expected to move a parent's position closer to the origin, and positive variety heterosis (h_j) expected to move a parent further away from all the other parents.

The high values of variety heterosis (h_j) of Histarch for beta-carotene content, Apomuden for dry matter content and starch content, Beauregard for sugar content, and Ogyefo for zinc and iron content indicates that these varieties have excellent general combining ability for the respective traits. High variety heterosis (h_j) indicates differences in frequencies of dominant alleles between them and the other parents (Crossa *et al.*, 1987). The negative values obtained for the variety heterosis (h_{ij}) may be attributed to the unrealized performance expectation of the parents in the hybrids. According to Harold *et al.* (2001), negative values of variety heterosis for breeding varieties/population appear to represent an unfulfilling of performance expectation arising from high variety effects (v_j) and high average heterosis effect (h).

Apomuden and Beauregard had the highest beta-carotene content, sugar content, iron content and zinc content as reflected by their positive values for variety effects (v_j) except for iron. Ogyefo and Histarch had the highest dry matter content and starch content and this is reflected by their positive values for variety effects (v_j). Ogyefo and Histarch contributed positively to increase dry matter and starch content and decreased sugar content in the hybrids. Apomuden on the other hand also contributed to increase beta-carotene, sugar, iron and zinc contents in the hybrids whilst Beauregard was the same as Apomuden except for zinc content.

SCA is important in choosing parents to be used in a breeding programme where the superiority of F_1 progenies over the parents (specific heterosis) will be exploited for genetic improvement. Specific heterosis (s_{ij}) is the deviation between the observed performance of specific cross and its expected performance based on variety effect (v_j), average heterosis (h), and variety heterosis (h_j) (Crossa *et al.*, 1987). It is calculated as a function of the sum between the mean of a cross and the average of all crosses and the sum of the mean of all crosses of varieties j and j'(Gardner, 1967). In diversity analysis, it is observed as adjustments in distances between parent pairs (Harold *et al.*, 2001). It provides an estimate of genetic variability which is an important consideration in choosing germplasm pools to be used in recurrent selection programmes (Crossa *et al.*, 1987). The crosses Ogyefo x Apomuden and Histarch x Beauregard showed consistently high heterosis effects for beta-carotene content, dry matter content, sugar content and starch content. This is because their values for heterosis (h_{ij}), expressed as a percentage of the better parent and mid-parent were also consistently relatively high indicating high SCA. The good performance in these crosses is not only due in part to their high variety heterosis (h_j), but mainly by their high specific heterosis (s_{ij}). This suggests that it is possible to breed a sweetpotato variety that has appreciable content of beta-carotene, dry matter and low sugar using the hybrids developed from the current study.

The values obtained from the combined ANOVA for the beta-carotene, dry matter, sugar and starch contents were in the range reported by Grüneberg *et al.* (2009). However, the values obtained for iron and zinc contents were less than those reported. Values for dry matter content were also comparable to those reported by Shumbusha *et al.* (2014), and sugar contents were in agreement with Kays *et al.* (2005). They classified sugar content in sweetpotato based upon the concentration and relative sweetness of individual sugars,

expressed numerically as sucrose equivalents per 100 g dry mass as very high ≥38%; high 29-37%; moderate 21-28%; low 12-20%; and non-sweet ≤12%, and the hybrids were classified based on this. Hybrids selected from this work based upon sugar content were in the low-sugar content category since their sugar content ranged from 12.93 – 14.88%. Among the selected hybrids, seven hybrids Histarch x Apomuden -11, Ogyefo x Histarch-3, Histarch x Apomuden-1, Histarch x Ogyefo-4, Ogyefo x Apomuden-16, Ogyefo x Histarch-9, and Histarch x Beauregard-2 had high dry matter content and storage root yield. They will be further tested for potential release to farmers. These hybrids were selected because their sugar content and dry matter content were comparable to the low sugar parents, but they out yielded these parents. Three hybrids namely Apomuden x Histarch-15, Beauregard x Histarch-5, and Beauregard x Histarch-4 are also superior hybrids based on beta-carotene content. These hybrids are also proposed for further testing for potential release since they have moderate beta-carotene, low sugar and high dry matter contents compared to Apomuden, the only released orange-flesh sweetpotato variety in Ghana. Their sugar content ranged from 18.03 – 22.78% whilst Apomuden had sugar content of 36.71%. They also out yielded Apomuden. Some important uses of sweetpotato discovered through the PRA included use of sweetpotato flour as substitute for normal sugar in porridge and other local dishes such as *aboolo*. For this reason, 18 other hybrids with higher yields but mostly having high sugar content have been also considered for advance trials. These hybrids are presented in Table 6.12 and have storage root yield range from 22.12 t/ha to 47.90 t/ha, beta-carotene and dry matter contents ranged from 1.38 mg/100gDW to 17.78 mg/100gDW and 29% to 42%, respectively. Their sugar also content ranged from 16.14% to 22.94%.

6.5. Conclusion

The results of this study showed that genetic variability exists for the traits studied, and much of this genetic variation is additive in nature. This indicates that the parents used can be inter-crossed to develop elite genotypes with sufficient genetic variability for successful exploitation in future breeding programs. Ten promising hybrids were selected based on low sugar and high beta-carotene content. These were Histarch x Apomuden -11, Ogyefo x Histarch-3, Histarch x Apomuden-1, Histarch x Ogyefo-4, Ogyefo x Apomuden-16, Ogyefo x Histarch-9, Histarch x Beauregard-2, Apomuden x Histarch-15, Beauregard x Histarch-5, and Beauregard x Histarch-4. Furthermore, the 18 hybrids shown in Table 6.12 which were selected based on storage root yield performance should be further tested multi-locational on-farm for potential release to farmers.

CHAPTER SEVEN

7.0 ESTIMATE OF HETEROSIS FOR END-USER TRAITS OF SWEETPOTATO

7.1. Introduction

Sweetpotato is the fourth most important root and tuber crop in Ghana, in terms of production, after cassava, yam and cocoyam. Annual production is estimated at 135, 000 tonnes, representing just under 0.6% of all root and tuber crops produced in Ghana (FAOSTAT, 2013). The attainment of maximum sweetpotato utilization in Ghana has become an important objective in its breeding programme recently. The major emphasis in breeding is on the development of farmer/consumer preferred improved varieties. Consumers in Ghana prefer non-sweet (bland taste), high dry matter sweetpotatoes for staple food. Significant efforts have been made to find the economically feasible breeding systems for the development of such varieties with high beta-carotene content (orange-flesh sweetpotato) as well.

Many sweetpotato traits are quantitatively inherited (Jones, 1986). These include beta-carotene content, dry matter content, sugar content and storage root yield. The attainment of maximum crop yield is an important objective in most breeding programmes (Rausul *et al.*, 2002), and another major emphasis in sweetpotato breeding is on the development of end-user preferred improved varieties. Significant efforts have been made to find the economically feasible systems for the development of such varieties. Exploitation of heterosis (advantage of F_1 hybrids over their parents) in sweetpotato continues to be an important choice. The choice of parental material used in the hybridization scheme does contribute significantly for the development of a suitable genotypes (Rausul *et al.*, 2002). The objective of this study was to estimate the level of heterosis and heterobeltiosis among F_1 hybrids

obtained from crosses among four low sugar sweetpotato parents and also among five high beta-carotene sweetpotato parents.

7.2. Materials and Methods

7.2.1. Experimental sites

The hybridization blocks were established at the research field of the Crops Research Institute of the Council for Scientific and Industrial Research, Ghana (CSIR-CRI), at Fumesua in the minor cropping season in 2012. The F_1 progenies and their parents were evaluated at three locations across three ecozones of Ghana. The locations were the CSIR-CRI research station at Fumesua (forest ecozone), the National Agricultural Research Stations at Wenchi (transition ecozone) and Pokuase (coastal savanna ecozone).

7.2.2. Genetic materials used

The sweetpotato genotypes used as parents to develop the low sugar population were two released varieties (Histarch and Ogyefo) and two breeding lines (AAT-03-025 and CIP 442264). Those used for the development of the high beta-carotene population were one released variety (Apomuden) and four breeding lines which were Beauregard, Resisto, CIP 442850 and CIP 443035. These genotypes were among the best genotypes selected from the base population which was developed from the sweetpotato germplasm collected and evaluated in Chapter Four of this thesis. Their selection as parents was based on high beta-carotene content or low sugar content and their amenability to produce viable seeds when crossed as presented in Chapters Four and Five of this thesis. The attributes of the sweetpotato parents are presented in Table 7.1.

Table 7.1 Genetic materials used and their characteristics

Parents	Dry matter content (%)	Beta-carotene content (mg/100g)DW	Sugar content (%)
Histarch	45	9.85	10.13
Ogyefo	42	6.83	11.67
AAT – 03 – 025	39	10.98	12.26
CIP 442264	45	7.74	11.06
***Resisto**	38	27.53	18.53
***Beauregard**	32	24.31	22.90
***Apomuden**	27	33.67	28.97
***CIP 443035**	36	19.75	14.98
***CIP 442850**	27	20.21	30.34

*** Parents used for the development of high beta-carotene population**

7.2.3. Experimental layout

Two experiments were run. One involved the use of four low sugar parents for the development of low sugar population whilst the other involved five high beta-carotene parents for the development of high beta-carotene population. The parents were crossed among themselves using the full diallel mating scheme. In all 111 F_1 progenies were obtained for each experiment (Tables 7.2a and 7.2b). Due to poor vigour of some progenies, only 92 were evaluated alongside their parents at the three locations for the low sugar population. Similarly, only 99 were evaluated alongside their parents at the three locations for the high beta-carotene population. Field evaluations were done in the minor cropping season in 2013 using an alpha lattice design with two replications. All entries were planted in a single row on ridges at five plants per progeny at planting distance of 0.3 m within row and 1m between rows in two replications. Four node vines from the middle portion to the tip were used for planting. Genotypes within family were randomised into adjacent plots.

Table 7.2a Full-diallel mating representation for the low sugar parents (number of F_1 hybrids for evaluation highlighted)

*Parents	Histarch	Ogyefo	AAT – 03 – 025	CIP 442264
Histarch	P87	**80**	**5**	**2**
Ogyefo	**20**	P61	**0**	**0**
AAT – 03 – 025	**0**	**0**	P72	**0**
CIP 442264	**4**	**0**	**0**	P64

***[P87 (Histarch); P61 (Ogyefo); P72 (AAT – 03 - 025); P64 (CIP 442264)]**

Table 7.2b Full-diallel mating representation for the high beta-carotene parents (number of F_1 hybrids for evaluation highlighted)

*Parents	Apomuden	Beauregard	Resisto	CIP 443035	CIP 442850
Apomuden	P50	**13**	**5**	**4**	**13**
Beauregard	**31**	P82	**0**	**4**	**1**
Resisto	**3**	**0**	P21	**0**	**0**
CIP 443035	**16**	**10**	**2**	P79	**3**
CIP 442850	**2**	**4**	**0**	**0**	P109

***[P50 (Apomuden); P82 (Beauregard); P21 (Resisto), P79 (CIP 443035); P109 (CIP 442850)]**

7.2.4. Data collection

Harvesting was done at three and half months after planting. The three middle plants for each progeny row were harvested, and one large, one medium, and one small, storage roots were randomly selected for physico-chemical analysis after yield data were taken. Storage roots taken for the yield data were those approximately over 3 cm in diameter and without cracks, insect damage or rotten parts (Ekanayake *et al.*, 1990). The yield data recorded were mean root weight and root yield. The physico-chemical traits determined were beta-carotene content, dry matter content, total sugar (fructose, glucose and sucrose) content, starch

content, and iron and zinc contents. This was done at the Quality and Nutrition Laboratory of International Potato Centre (CIP) at CSIR-CRI, Fumesua, Ghana. The physico-chemical traits except dry matter content were determined using the Workflow for Sample Preparation and NIRS analysis of sweetpotato developed by the Quality and Nutrition Laboratory of the International Potato Centre (CIP), Lima, Peru. Fifty grams fresh sample was used. The fresh sample was freeze-dried using a freeze dryer for 72 hours. The dry matter content was calculated as the ratio of the weight of the dry sample to that of the wet sample expressed as a percentage.

7.2.5. Data analysis

Hybrids with missing data were eliminated from the analysis. Therefore, data for 97 F_1 clones out of 99 were used for the analysis for the high beta-carotene population alongside their five parents making a total of 102 entries. Analysis of Variance (ANOVA) was performed on the combined data of all parents and their F_1 derived individuals for each of the experiments to ascertain the performance among and between the F_1s and their parents within and between the families. Data used for this analysis were mean data from each of the three locations obtained from ANOVA as employed by Buerstmayr *et al.* (2007). The ANOVA was carried out in an 8 x 12 alpha lattice design for the low sugar experiment, and in a 6 x 17 alpha lattice design for the high beta-carotene experiment. After this, data for genotypes within family were analysed separately with their parents for each of the experiments to estimate heterosis. The relative efficiency (RE) of an alpha lattice design over randomized complete block design (RCBD) were determined for the different within family data as shown below.

$$RE = \frac{S.E_{RCBD}}{S.E_{\alpha\text{-lattice}}} \quad \text{OR} \quad RE = \frac{MSe_{RCBD}}{MSe_{\alpha\text{-lattice}}}$$

Where: S.E = standard error; MSe = Error means square; RE is significant if the ratio is >1 and vice versa.

All the family analyses were carried out in a randomized complete block design (RCBD) except for the crosses between Histarch and Ogyefo which was done using an 8 x 11 alpha lattice design. This was because the relative efficiency (RE) of alpha lattice design over randomized complete block design (RCBD) was significant for the data involving crosses between Histarch and Ogyefo. The analysis was done using Genstat version 9.2.0.152 (Genstat, 2007). The percent increase or decrease of F_1 hybrids over mid-parent as well as better parent was calculated to estimate heterosis for the traits studied (Fonseca and Patterson, 1968). This was done as shown below;

$$Ht\ (\%) = \frac{F_1 - MP}{MP} \times 100; \qquad Hbt\ (\%) = \frac{F_1 - BP}{BP} \times 100$$

Where, Ht = Heterosis; Hbt = Heterobeltiosis; MP = Mid-Parent Value; BP = Better Parent Value; $F_{1=}$ F_1 hybrid value.

The 't' test was used to determine whether F_1 hybrid means were statistically different from mid-parent and better parent means (Wynne *et al.*, 1970), as follows;

$$tij = \frac{F_{1ij} - MP_{ij}}{\sqrt{3/8EMS}} \qquad tij = \frac{F_{1ij} - BP_{ij}}{\sqrt{1/2EMS}}$$

Where,

F_{1ij} = Mean of the ijth F_1 cross; MP_{ij} = Mid-parent value for the ijth cross

BP_{ij} = Better parent value for ijth cross; EMS = Error mean square

7.3. Results

Numerous ANOVA tables were obtained because numerous ANOVA were carried out for the separate analysis involving genotypes within family (to estimate mid-parent and better parent heterosis). As a result, only ANOVA tables from the combined analysis (i.e. involving all the genotypes irrespective of family and the parents) were reported. The results are presented separately for the low sugar population and the high beta-carotene population as follows.

7.3.1. Performance of low sugar population

The mean square values obtained from the combined ANOVA showed highly significant ($p < 0.01$) differences among the genotypes for all the traits except sugar content (Table 7.3). The mean performance for the population is shown in Appendix 7.1. Range of values for the traits were 36 – 48% for dry matter content, 9.01 – 17.53% for sugar content, 68.27 – 76.25% for starch content, 1.99 – 5.16% for protein content, 1.63 – 8.23 mg/100g DW for beta-carotene content, 1.21 – 1.82 mg/100gDW for iron content, and 0.82 – 1.17 mg/100gDW for zinc content. Some genotypes did not produce storage roots. The highest values for harvest index, mean root weight and root yield were 0.55, 0.49 Kg, and 36.31 t/ha, respectively. The mean values for the traits were 43% (dry matter content), 13.45% (sugar content), 72.64% (starch content), 3.02% (protein content), 4.25 mg/100gDW (beta-carotene content), 1.45 mg/100gDW (iron content), 0.95 mg/100gDW (zinc content), 0.33 (harvest index), 0.17 Kg (mean root weight), and 16.04 t/ha (root yield). Their coefficient of variation were 6.3% (dry matter content), 20.7% (sugar content), 2.9% (starch content), 20.0% (protein content), 55.3% (beta-carotene content), 12.0% (iron content), 9.3% (zinc content), 35.6% (harvest index), 59.2% (mean root weight), and 46.9% (root yield).

Table 7.3 Mean squares from combined Analysis of Variance for the low sugar population

Source of variation	Df	Total sugar (%)	Dry matter (%)	Starch (%)	β-carotene (mg/100g) DW	Iron (mg/100g) DW	Zinc (mg/100g) DW	Protein (%)	Harvest Index	mean root weight (kg)	Total root yield (t/ha)
Rep stratum	2	15.41	0.0002	198.04	11.22	4.58	0.62	27.47	0.93	0.21	2040.33
Rep.Blk. Stratum											
Genotype	7	8.54^{ns}	0.0023^{ns}	11.03^{ns}	6.42^{ns}	0.09^{ns}	0.01^{ns}	1.65^{ns}	0.02^{ns}	0.02^{ns}	301.61**
Residual	14	8.06	0.0010	6.40	5.06	0.04	0.02	0.79	0.03	0.01	65.13
Rep.Blk.Plot Stratum											
Genotype	74	10.13^{ns}	0.0018**	7.55**	9.08**	0.05**	0.02**	0.97**	0.03**	0.02**	142.90**
Residual	190	7.77	0.0007	4.42	5.57	0.03	0.01	0.37	0.01	0.01	55.17

**** Significant at P<0.01; ^{ns} not significant at P>0.05.**

7.3.2. Estimation of heterosis for low sugar sweetpotato population

Significant variation ($P<0.05$) existed among the parents, the F_1 hybrids and between the parents and the F_1 hybrids for all the traits in the crosses between Histarch and Ogyefo (Table 7.4). Fifty-five per cent of the F_1 hybrids had sugar content lower than the parent with the lowest sugar content, Ogyefo (13.58%). The higher sugar content parent Histarch (16.33%) had lower sugar content than only two of the F_1 hybrids, Histarch x Ogyefo-46 and Histarch x Ogyefo-57, which had sugar contents of 17.18% and 17.53%, respectively. Crosses between Histarch and CIP 442264 had significant differences ($P<0.05$) for only dry matter content, protein content, zinc content and root yield (Table 7.6). Similarly, significant differences were found for only dry matter content, protein content, beta-carotene content and root yield for the crosses involving Histarch and AAT-03-025 (Table 7.8).

Heterosis was significant for some hybrids for some of the traits for all the crosses except for Histarch x CIP 442264 (Tables 7.5, 7.7 and 7.9). Both positive and negative heterosis were found. For example, Histarch x Ogyefo-26 had significant negative mid-parent and better parent heterosis for dry matter content (-14% and -18%), and also sugar content (-39.1% and -33.0%) but positive heterosis for protein content (86.4% and 80.5%). It also had positive mid-parent heterosis of 19.5% and 18.7% for iron and zinc content, respectively.

Table 7.4 Performance of Histarch and Ogyefo, and their F_1 hybrids

Genotype	Dry matter (%)	Total Sugars (%)	Starch (%)	Protein (%)	β-carotene (mg/100g)DW	Iron (mg/100g)DW	Zinc (mg/100)DW	Root yield (t/ha)
61x87-11	45	9.01	75.14	3.51	5.66	1.36	0.98	16.03
87x61-26	38	9.13	70.22	5.16	6.82	1.82	1.08	-
87x61-13	45	9.50	76.25	2.97	2.27	1.52	0.92	16.53
87x61-21	44	9.94	72.92	3.92	2.72	1.64	1.05	12.08
87x61-37	43	10.79	72.56	2.85	5.09	1.40	0.98	28.26
87x61-65	45	11.18	74.13	2.89	3.40	1.40	0.94	14.94
87x61-87	42	11.72	72.05	3.97	6.46	1.65	1.04	7.57
87x61-88	44	11.76	74.27	2.95	3.33	1.37	0.98	14.54
‘’	‘’	‘’	‘’	‘’	‘’	‘’	‘’	‘’
Ogyefo (61)	41	13.62	72.92	2.86	3.75	1.48	0.95	13.61
‘’	‘’	‘’	‘’	‘’	‘’	‘’	‘’	‘’
87x61-20	42	15.32	72.38	3.40	6.44	1.35	0.96	15.22
61x87-15	42	15.33	71.75	2.55	4.86	1.38	0.89	8.21
61x87-6	39	15.63	68.34	2.56	4.45	1.46	0.92	9.64
87x61-77	38	15.64	72.20	3.59	5.49	1.35	1.00	21.97
87x61-42	41	15.95	70.54	2.22	3.90	1.30	0.85	11.53
61x87-4	40	16.26	72.23	2.51	3.17	1.43	0.86	22.47
87x61-47	40	16.29	71.37	2.77	3.92	1.42	0.93	19.17
Histarch (87)	46	16.33	72.82	2.68	4.74	1.56	0.87	20.71
87x61-46	40	17.18	70.30	2.31	6.43	1.32	0.88	3.56
***SEM (5%)**	1.33	1.48	0.97	0.36	1.19	0.09	0.05	4.08
Grand mean	42	13.41	72.77	2.99	4.08	1.44	0.95	16.30
Range	36 – 48	9.01 - 17.53	68.34 - 76.25	1.99 - 5.16	1.63 - 8.23	1.21 - 1.82	0.83 - 1.17	7.57 - 36.31
CV (%)	6.8	20.4	2.5	21.6	54.0	12.3	9.9	46.4

***SEM =Standard error of mean**

Table 7.5 Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for the F_1 hybrids of Histarch (87) and Ogyefo (61)

Genotype	Dry matter		Total sugars		Starch		Protein		β-carotene		Iron		Zinc		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
61x87-11	3^{ns}	-3^{ns}	-39.9*	-33.9*	3.1^{ns}	3.0^{ns}	26.6^{ns}	22.6^{ns}	33.2^{ns}	19.4^{ns}	-10.8^{ns}	-13.1^{ns}	7.9^{ns}	3.3^{ns}	-6.6^{ns}	-22.6^{ns}
87x61-26	-14*	-18*	-39.1*	-33.0*	-3.6^{ns}	-3.7^{ns}	86.4**	80.5**	60.5^{ns}	43.9^{ns}	19.5*	16.5^{ns}	18.7*	13.7^{ns}	-	-
87x61-13	3^{ns}	-2^{ns}	-36.6*	-30.3*	4.6*	4.6*	7.3^{ns}	4.0^{ns}	-46.6^{ns}	-52.1^{ns}	-0.3^{ns}	-2.9^{ns}	0.63^{ns}	-3.6^{ns}	-4.0^{ns}	-20.2^{ns}
87x61-21	1^{ns}	-4^{ns}	-33.6*	-27.0*	0.1^{ns}	0.0^{ns}	41.6*	37.2^{ns}	-36.0^{ns}	-42.6^{ns}	7.6^{ns}	4.8^{ns}	15.3^{ns}	10.4^{ns}	-29.6^{ns}	-41.7^{ns}
87x61-37	-1^{ns}	-6^{ns}	-28.0*	-20.8*	-0.4^{ns}	-0.5^{ns}	3.0^{ns}	-0.2^{ns}	19.8^{ns}	7.4^{ns}	-7.8^{ns}	-10.1^{ns}	7.2^{ns}	2.6^{ns}	64.7^{ns}	36.5^{ns}
87x61-65	2^{ns}	-3^{ns}	-25.4^{ns}	-17.9*	1.7^{ns}	1.7^{ns}	4.5^{ns}	1.2^{ns}	-20.0^{ns}	-28.3^{ns}	-7.6^{ns}	-10.0^{ns}	3.2^{ns}	-1.2^{ns}	-12.9^{ns}	-27.9^{ns}
87x61-87	-4^{ns}	-9^{ns}	-21.8^{ns}	-14.0^{ns}	-1.1^{ns}	-1.2^{ns}	43.3*	38.8^{ns}	52.0^{ns}	36.3^{ns}	8.4^{ns}	5.6^{ns}	14.8^{ns}	9.9^{ns}	-55.9^{ns}	-63.5*
87x61-88	1^{ns}	-4^{ns}	-21.5^{ns}	-13.7^{ns}	1.9^{ns}	1.9^{ns}	6.5^{ns}	3.2^{ns}	-21.7^{ns}	-29.8^{ns}	-9.8^{ns}	-12.1^{ns}	7.45^{ns}	2.9^{ns}	-15.3^{ns}	-29.8^{ns}
“	“	“	“	“	“	“	“	“	“	“	“	“	“	“	“	“
87x61-20	-3^{ns}	-8^{ns}	2.3^{ns}	12.5^{ns}	-0.7^{ns}	-0.7^{ns}	22.6^{ns}	18.7^{ns}	51.5^{ns}	35.9^{ns}	-10.9^{ns}	-13.2^{ns}	5.3^{ns}	0.8^{ns}	-11.3^{ns}	-26.5^{ns}
61x87-15	-3^{ns}	-9^{ns}	2.3^{ns}	12.6^{ns}	-1.5^{ns}	-1.6^{ns}	-8.1^{ns}	-11.0^{ns}	14.4^{ns}	2.5^{ns}	-9.1^{ns}	-11.5^{ns}	-1.7^{ns}	-5.8^{ns}	-52.2^{ns}	-60.4^{ns}
61x87-6	-11*	-16^{ns}	4.3^{ns}	14.8^{ns}	-6.2*	-6.3*	-7.7^{ns}	-10.6^{ns}	4.7^{ns}	-6.1^{ns}	-4.1^{ns}	-6.5^{ns}	0.9^{ns}	-3.3^{ns}	-43.8^{ns}	-53.5^{ns}
87x61-77	-12*	-16^{ns}	4.4^{ns}	14.8^{ns}	-0.9^{ns}	-1.0^{ns}	29.6^{ns}	25.5^{ns}	29.2^{ns}	15.8^{ns}	-10.9^{ns}	-13.2^{ns}	10.4^{ns}	5.7^{ns}	28.0^{ns}	6.1^{ns}
87x61-42	-6^{ns}	-11^{ns}	6.5^{ns}	17.1^{ns}	-3.2^{ns}	-3.3^{ns}	-19.9^{ns}	-22.4^{ns}	-8.2^{ns}	-17.7^{ns}	-14.3^{ns}	-16.5^{ns}	-6.8^{ns}	-10.7^{ns}	-32.8^{ns}	-44.3^{ns}
61x87-4	-7^{ns}	-12^{ns}	8.5^{ns}	19.4^{ns}	-0.9^{ns}	-1.0^{ns}	-9.4^{ns}	-12.2^{ns}	-25.4^{ns}	-33.1^{ns}	-6.3^{ns}	-8.7^{ns}	-5.4^{ns}	-9.4^{ns}	30.9^{ns}	8.5^{ns}
87x61-47	-9^{ns}	-14^{ns}	8.7^{ns}	19.6^{ns}	-2.1^{ns}	-2.1^{ns}	-0.1^{ns}	-3.3^{ns}	-7.8^{ns}	-17.3^{ns}	-6.3^{ns}	-8.7^{ns}	2.7^{ns}	-1.6^{ns}	11.7^{ns}	-7.4^{ns}
87x61-46	-8^{ns}	-13^{ns}	14.7^{ns}	26.1^{ns}	-3.5^{ns}	-3.6^{ns}	-16.7^{ns}	-19.3^{ns}	51.3^{ns}	35.7^{ns}	-13.0^{ns}	-15.3^{ns}	-3.1^{ns}	-7.2^{ns}	-79.3*	-82.8*
87x61-57	-9^{ns}	-14^{ns}	17.0^{ns}	28.7^{ns}	-4.2*	-4.3^{ns}	13.7^{ns}	10.1^{ns}	-39.8^{ns}	-46.0^{ns}	-2.5^{ns}	-5.0^{ns}	9.4^{ns}	4.8^{ns}	17.7^{ns}	-2.5^{ns}

***Significant at P<0.05; **Significant at P<0.01; ^{ns}Not significant at P<0.05**

Table 7.6 Performance of Histarch and CIP 442264, and their F_1 hybrids

Genotype	Dry matter (%)	Total Sugars (%)	Starch (%)	Protein (%)	B-carotene (mg/100g)DW	Iron (mg/100g)DW	Zinc (mg/100g)DW	Root yield (t/ha)
Histarch (87)	46	16.33	72.82	2.68	4.74	1.56	0.87	20.71
CIP 442264 (64)	42	10.80	68.27	3.82	6.37	1.77	1.00	5.07
64x87-1	48	14.29	72.06	3.93	5.96	1.79	1.02	13.31
64x87-2	48	12.59	72.96	4.01	4.97	1.69	1.06	12.04
64x87-3	46	12.25	72.94	3.27	7.90	1.40	0.91	0.00
87x64-1	46	15.44	69.74	3.78	7.44	1.65	1.09	13.57
87x64-2	48	14.14	72.59	3.33	7.00	1.72	0.97	15.93
SED (5%)	2	3.38	4.33	0.44	3.63	0.22	0.1	6.13
Grand mean	46	13.69	71.6	3.54	6.34	1.65	0.99	11.50
Range	42 – 48	10.80 – 16.33	68.27 - 72.96	2.68 - 4.01	4.74 - 7.90	1.40 - 1.79	0.87 - 1.09	0.00 – 20.71
CV (%)	4.6	30.2	7.4	15.2	70.1	16.5	12.1	65.2

Table 7.7 Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for the F_1 hybrids of Histarch (87) and CIP 442264 (64)

Genotype	Dry matter		Total sugars		Starch		Protein		β-carotene		Iron		Zinc		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
64x87-1	10^{ns}	5^{ns}	5.4^{ns}	32.3^{ns}	2.5^{ns}	-1.0^{ns}	5.2^{ns}	2.8^{ns}	7.2^{ns}	-6.4^{ns}	7.1^{ns}	1.1^{ns}	8.5^{ns}	2.0^{ns}	3.3^{ns}	-35.7^{ns}
64x87-2	10^{ns}	5^{ns}	-7.2^{ns}	16.6^{ns}	3.8^{ns}	0.2^{ns}	5.9^{ns}	5.0^{ns}	-10.6^{ns}	-22.0^{ns}	1.3^{ns}	-4.5^{ns}	12.8^{ns}	6.1^{ns}	-6.6^{ns}	-41.9^{ns}
64x87-3	4^{ns}	-1^{ns}	-9.7^{ns}	13.4^{ns}	3.8^{ns}	0.2^{ns}	0.1^{ns}	-14.5^{ns}	42.1^{ns}	24.0^{ns}	-16.3^{ns}	-21.1^{ns}	-3.7^{ns}	-9.5^{ns}	-	-
87x64-1	4^{ns}	-1^{ns}	13.9^{ns}	43.0^{ns}	-0.8^{ns}	-4.2^{ns}	4.1^{ns}	-1.1^{ns}	33.8^{ns}	16.8^{ns}	-1.4^{ns}	-6.9^{ns}	15.8^{ns}	8.9^{ns}	5.3^{ns}	-34.5^{ns}
87x64-2	10^{ns}	5^{ns}	4.3^{ns}	30.9^{ns}	3.3^{ns}	-0.3^{ns}	0.6^{ns}	-12.7^{ns}	25.9^{ns}	9.9^{ns}	2.7^{ns}	-3.1^{ns}	3.4^{ns}	-2.8^{ns}	23.6^{ns}	-23.1^{ns}

^{ns}Not significant at P<0.05

Table 7.8 Performance of Histarch and AAT-03-025, and their F_1 hybrids

Genotype	Dry matter (%)	Total Sugars (%)	Starch (%)	Protein (%)	B-carotene (mg/100g)DW	Iron (mg/100g)DW	Zinc (mg/100g)DW	Root yield (t/ha)
Histarch (87)	46	16.33	72.82	2.68	4.74	1.56	0.87	20.71
AAT-03-025 (72)	43	12.47	72.32	2.27	2.41	1.31	0.82	19.87
87x72-1	43	16.90	71.25	2.96	7.31	1.43	0.96	17.36
87x72-2	40	16.16	70.36	2.72	5.59	1.47	0.85	6.89
LSD (5%)	4	5.7	2.90	0.68	4.02	0.32	0.16	13.74
Grand mean	43	15.5	71.69	2.66	5.01	1.44	0.88	13.20
Range	40 – 46	12.47 - 16.90	70.36 – 72.82	2.27 - 2.96	2.41 - 7.31	1.31 - 1.56	0.85 - 0.96	6.89 – 20.71
CV (%)	4.2	22.6	2.5	15.4	49.2	13.8	11.2	63.5

Table 7.9 Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for the F_1 hybrids of Histarch (87) and AAT-03-025 (72)

Genotype	Dry matter		Total sugars		Starch		Protein		β-carotene		Iron		Zinc		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
87x72-1	-6^{ns}	-7*	17.4^{ns}	35.5^{ns}	-1.8^{ns}	-2.2^{ns}	20.0^{ns}	10.6^{ns}	104.2^{ns}	54.2^{ns}	0.0^{ns}	-8.2^{ns}	13.4^{ns}	10.2^{ns}	-14.4^{ns}	-16.2^{ns}
87x72-2	-11**	-12**	12.2^{ns}	29.6^{ns}	-3.0^{ns}	-3.4^{ns}	10.2^{ns}	1.6^{ns}	56.1^{ns}	17.9^{ns}	2.7^{ns}	-6.0^{ns}	0.0^{ns}	-3.0^{ns}	-66.4*	-66.7^{ns}

***Significant at P<0.05; **Significant at P<0.01; ^{ns}Not significant at P<0.05**

7.3.3. Performance of high beta-carotene population

There were highly significant ($p < 0.01$) differences among the genotypes for all the traits (Table 7.10). The mean performance of this population is presented in Appendix 7.2. The means and range of values were 24.13 mg/100gDW and 2.72 – 44.05 mg/100gDW for beta-carotene content, 29% and 22 – 38% for dry matter content, 29.41% and 16.43 – 46.34% for sugar content, 56.39% and 39.05 – 68.96% for starch content, 3.11% and 1.89 – 6.07% for protein content, 1.90 mg/100gDW and 1.34 – 2.81 mg/100gDW for iron content, 1.11 mg/100gDW and 0.78 – 1.77 mg/100gDW for zinc content, 0.54 and 0.26 – 0.76 for harvest index, 0.16 Kg and 0.07 – 0.40 Kg for mean root weight, and 30.67 t/ha and 3.65 – 69.52 t/ha for root yield. The CV's ranged from 10.3% to 48.6%. Results for the individual families are presented in Tables 7.11, 7.13, 7.15, 7.17, 7.19, 7.21, 7.23 and 7.25, respectively.

Table 7.10 Combined Analysis of variance (Mean square) for the high beta-carotene population

Source of variation	Df	Total sugar (%)	Dry matter (%)	Starch (%)	β-carotene (mg/100g) DW	Iron (mg/100g) DW	Zinc (mg/100g) DW	Protein (%)	Harvest Index	mean root weight (kg)	Total root yield (t/ha)
Rep stratum	2	57.14	0.031	775.12	664.6	5.46	4.65	67.03	1.68	0.02	2145.26
Rep.Blk. Stratum											
Genotype	5	569.82**	0.023**	6.46.35**	841.8**	0.77**	0.38**	3.59*	0.07**	0.01^{ns}	737.85**
Residual	10	9.20	0.001	10.16	47.0	0.04	0.02	0.70	0.01	0.01	156.12
Rep.Blk.Plot Stratum											
Genotype	86	131.90**	0.004**	142.33**	318.1**	0.18**	0.09**	0.95**	0.03**	0.01**	370.81**
Residual	202	25.58	0.001	33.80	103.7	0.06	0.03	0.47	0.01	0.01	93.78

***Significant at P<0.05; ** Significant at P<0.01; ^{ns} not significant at P>0.05.**

7.3.4. Estimation of heterosis for high beta-carotene population

Significant differences (P<0.05) were established among the genotypes for crosses involving Apomuden and Beauregard (Table 7.11). In all, 57% of the hybrids were not significantly different (P>0.05) for beta-carotene content from the highest beta-carotene content parent, Apomuden (40.67 mg/100gDW). Nine of these hybrids had equal or higher dry matter content than Apomuden (dry matter content of 28%). Two of these hybrids, namely Beauregard x Apomuden-7 (sugar content of 24.85%) and Beauregard x Apomuden-19 (sugar content of 25.34%) had lower sugar content than Apomuden (sugar content of 31.63%). Eleven hybrids including Beauregard x Apomuden-7 (root yield of 33.11 t/ha) had root yield that was not significantly different (P>0.05) from that of Apomuden (34.00 t/ha). Similarly, significant variation (P<0.05) was found among the genotypes for all the traits for all the other cross combinations (Tables 7.13, 7.15, 7.19, 7.21, 7.23 and 7.25) except crosses between CIP 443035 and CIP 442850 which did not show significant (P>0.05) difference for beta-carotene and zinc contents (Table 7.17).

Significant heterosis existed for some hybrids for some of the traits for all the cross combinations (Table 7.12, 7.14, 7.16, 7.18, 7.20, 7.22, 7.24, and 7.26). For example, whilst CIP 443035 x Beauregard-10 had significant heterosis (better parent) for only starch content (3.6%), significant heterosis was found for CIP 443035 x Beauregard-1 for all the traits except sugar content and root yield (Table 7.14). CIP 443035 x Apomuden-7 also expressed heterosis for all the traits except sugar content, zinc content, and root yield (Table 7.16).

Table 7.11 Performance of Apomuden and Beauregard, and their F_1 hybrids

Genotype	β-carotene (mg/100g)DW	Dry matter (%)	Total sugars (%)	Starch (%)	Protein (%)	Iron (mg/100g)DW	Zinc (mg/100g)DW	Root yield (t/ha)
Apomuden (50)	40.67	28	31.63	49.35	4.06	2.30	1.52	34.00
Beauregard (82)	26.24	30	26.49	59.87	3.99	2.03	1.11	26.59
82x50-13	44.05	23	41.32	43.38	3.20	2.17	1.23	38.41
50x82-1	41.91	22	34.33	40.37	6.07	2.81	1.77	19.00
82x50-27	41.66	25	39.21	50.51	3.03	2.01	1.16	48.35
50x82-4	41.00	24	44.75	43.63	2.72	2.08	1.21	18.00
50x82-12	39.65	28	34.21	48.81	4.11	2.50	1.57	19.22
82x50-14	39.10	22	32.66	46.53	2.68	1.99	1.09	69.52
82x50-4	38.70	25	38.45	47.05	3.43	2.23	1.38	44.11
82x50-17	37.92	24	30.95	51.06	3.13	2.06	1.12	42.52
“	“	“	“	“	“	“	“	“
“	“	“	“	“	“	“	“	“
82x50-2	16.39	28	27.96	58.06	2.75	1.75	1.03	33.00
82x50-32	16.37	33	31.97	60.28	2.38	1.63	0.94	43.26
50x82-9	12.96	28	30.92	58.60	3.16	1.86	0.99	31.96
50x82-8	11.65	23	28.11	57.90	1.89	1.51	0.79	34.07
82x50-9	11.06	32	23.73	64.48	2.40	1.57	0.85	41.19
82x50-11	10.62	32	27.83	63.56	2.51	1.50	0.88	27.49
82x50-8	10.00	29	26.38	61.79	2.90	1.61	0.90	43.94
82x50-1	8.89	28	28.05	59.79	3.20	1.82	1.06	35.66
82x50-10	8.26	29	25.21	60.20	2.71	1.61	0.97	41.09
SED (5%)	9.32	3	4.66	5.59	0.69	0.24	0.17	8.89
Grand mean	26.30	28	31.41	54.85	3.19	1.93	1.12	34.39
Range	8.26 - 44.05	22 - 34	22.69 - 44.75	40.37 - 64.48	1.89 - 6.07	1.50 - 2.81	0.79 - 1.77	12.74 - 69.52
CV (%)	43.5	13.0	18.2	12.5	26.6	15.2	19.0	31.7

Table 7.12 Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for the F_1 hybrids of Apomuden (50) and Beauregard (82)

Genotype	β-carotene		Dry matter		Total sugars		Starch		Protein		Iron		Zinc		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
82x50-13	31.7^{ns}	8.3^{ns}	-21*	-23*	42.2*	56.0*	-20.6*	-12.1*	-20.4^{ns}	-21.1^{ns}	0.2^{ns}	-5.9^{ns}	-6.4^{ns}	-19.3^{ns}	-36.7^{ns}	-44.1^{ns}
50x82-1	25.3^{ns}	3.1^{ns}	-24*	-27*	18.1^{ns}	29.6^{ns}	-26.1*	-18.2*	51.0*	49.5*	29.9*	22.0^{ns}	34.9*	16.3^{ns}	0.0^{ns}	-11.8^{ns}
82x50-27	24.5^{ns}	2.43^{ns}	-14^{ns}	-17^{ns}	34.9*	48.0*	-7.5^{ns}	2.4^{ns}	-24.7^{ns}	-25.4^{ns}	-7.0^{ns}	-12.7^{ns}	-11.4^{ns}	-23.6^{ns}	-11.1^{ns}	-21.5^{ns}
50x82-4	22.5^{ns}	0.81^{ns}	-17*	-20*	54.0**	68.9**	-20.1*	-11.6*	-32.3^{ns}	-33.0^{ns}	-3.7^{ns}	-9.5^{ns}	-7.7^{ns}	-20.5^{ns}	-35.9^{ns}	-43.5^{ns}
50x82-12	18.5^{ns}	-2.5^{ns}	-3^{ns}	-7^{ns}	17.7^{ns}	29.1^{ns}	-10.6^{ns}	-1.09^{ns}	2.3^{ns}	1.31^{ns}	15.5^{ns}	8.5^{ns}	19.5^{ns}	3.0^{ns}	-14.8^{ns}	-24.9^{ns}
82x50-14	16.9^{ns}	-3.9^{ns}	-24*	-27*	12.4^{ns}	23.3^{ns}	-14.8^{ns}	-5.7*	-33.3*	-33.9^{ns}	-7.7^{ns}	-13.3^{ns}	-16.8^{ns}	-28.3*	-40.0^{ns}	-47.1^{ns}
82x50-4	15.7^{ns}	-4.8^{ns}	-14^{ns}	-17^{ns}	32.3*	45.15*	-13.8^{ns}	-4.7*	-14.8^{ns}	-15.6^{ns}	3.0^{ns}	-3.3^{ns}	5.4^{ns}	-9.1^{ns}	57.0*	38.6^{ns}
82x50-17	13.3^{ns}	-6.8^{ns}	-17*	-20*	6.5^{ns}	16.8^{ns}	-6.5^{ns}	3.5^{ns}	-22.3^{ns}	-23.0^{ns}	-4.5^{ns}	-10.3^{ns}	-14.6^{ns}	-26.4^{ns}	26.6^{ns}	11.7^{ns}
“	“	“	“	“	“	“	“	“	“	“	“	“	“	“	“	“
82x50-2	-51.0^{ns}	-59.7*	-3^{ns}	-7^{ns}	-3.8^{ns}	5.6^{ns}	6.3^{ns}	17.7^{ns}	-31.7^{ns}	-32.3^{ns}	-19.2^{ns}	-24.1*	-21.5^{ns}	-32.4*	-17.9^{ns}	-27.6^{ns}
82x50-32	-51.1^{ns}	-59.8*	14^{ns}	10^{ns}	10.0^{ns}	20.7^{ns}	10.4^{ns}	22.2^{ns}	-40.8*	-41.4*	-24.5*	-29.1*	-28.6*	-38.4*	-21.1^{ns}	-30.4^{ns}
50x82-9	-61.3*	-68.1*	-3^{ns}	-7^{ns}	6.4^{ns}	16.7^{ns}	7.3^{ns}	18.7^{ns}	-21.4^{ns}	-22.2^{ns}	-14.1^{ns}	-19.3^{ns}	-24.5^{ns}	-34.9*	44.2^{ns}	27.2^{ns}
50x82-8	-65.2*	-71.4*	-21*	-23*	-3.3^{ns}	6.1^{ns}	6.0^{ns}	17.3^{ns}	-52.9**	-53.4*	-30.3*	-34.6*	-39.5*	-47.9**	47.0^{ns}	29.7^{ns}
82x50-9	-67.0*	-72.8*	10^{ns}	7^{ns}	-18.3^{ns}	-10.4^{ns}	18.1^{ns}	30.7^{ns}	-40.3*	-40.9*	-27.2*	-31.7*	-34.8*	-43.8**	-37.5^{ns}	-44.9^{ns}
82x50-11	-68.3*	-73.9*	10^{ns}	7^{ns}	-4.2^{ns}	5.1^{ns}	16.4^{ns}	28.8^{ns}	-37.6*	-38.2*	-30.6*	-34.8*	-32.7*	-42.0**	38.3^{ns}	22.0^{ns}
82x50-8	-70.1*	-75.4*	0^{ns}	-3^{ns}	-9.2^{ns}	-0.4^{ns}	13.2^{ns}	25.2^{ns}	-27.8^{ns}	-28.6^{ns}	-25.7*	-30.2*	-31.5*	-40.9*	10.4^{ns}	-2.6^{ns}
82x50-1	-73.4*	-78.1*	-3^{ns}	-7^{ns}	-3.5^{ns}	5.9^{ns}	9.5^{ns}	21.2^{ns}	-20.4^{ns}	-21.21^{ns}	-15.7^{ns}	-20.8^{ns}	-19.1^{ns}	-30.3*	46.5^{ns}	29.2^{ns}
82X50-10	-75.3*	-79.7*	0^{ns}	-3^{ns}	-13.3^{ns}	-4.8^{ns}	10.2^{ns}	22.0^{ns}	-32.6^{ns}	-33.3^{ns}	-25.3*	-29.9*	-26.2^{ns}	-36.4*	37.3^{ns}	21.2^{ns}

***Significant at P<0.05; **Significant at P<0.01; ^{ns}Not significant at P<0.05**

Table 7.13 Performance of CIP 443035 and Beauregard, and their F_1 hybrids

Genotype	β-carotene (mg/100g)DW	Dry matter (%)	Total sugars (%)	Starch (%)	Protein (%)	Iron (mg/100g)DW	Zinc (mg/100g)DW	Root yield (t/ha)
CIP 443035 (79)	22.66	30	24.39	58.91	3.44	2.00	1.17	3.56
Beauregard (82)	26.24	30	26.49	59.87	3.99	2.03	1.11	26.59
82x79-4	28.95	27	29.74	57.44	2.59	1.77	1.00	18.28
82x79-3	7.70	33	22.30	64.67	2.97	1.52	0.94	21.13
82x79-2	3.90	32	18.32	66.68	2.70	1.51	0.95	20.78
82x79-1	25.38	30	20.32	59.66	3.12	1.81	1.09	30.94
79x82-5	15.50	33	19.92	64.89	2.98	1.65	0.99	21.00
79x82-4	28.35	30	23.34	61.39	2.64	1.81	0.98	30.04
79x82-3	26.63	31	22.53	62.34	2.92	1.73	0.96	30.70
79x82-2	28.85	31	23.42	60.88	2.60	1.81	1.01	28.64
79x82-10	14.76	32	22.83	62.00	3.15	1.71	1.01	17.71
79x82-1	7.24	35	19.74	68.96	2.54	1.34	0.78	19.52
SED (5%)	7.90	3	3.16	3.28	0.50	0.16	0.08	6.22
Grand mean	18.6	32	22.89	62.45	2.95	1.71	1.00	21.00
Range	7.24 - 28.95	27 – 35	18.32 - 29.74	57.44 - 68.96	2.54 - 3.99	1.34 -2.03	0.78 - 1.17	3.56 - 30.94
CV (%)	52.2	10.8	16.9	2.5	20.5	11.5	9.6	36.2

Table 7.14 Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for the F_1 hybrids of CIP 443035 (79) and Beauregard (82)

Genotype	β-carotene		Dry matter		Total sugars		Starch		Protein		Iron		Zinc		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
82x79-4	18.4^{ns}	10.3^{ns}	-10^{ns}	-10^{ns}	16.9^{ns}	21.9^{ns}	-3.3^{ns}	-4.1^{ns}	-30.2*	-35.1*	-12.2^{ns}	-13.1^{ns}	-12.0^{ns}	-14.3^{ns}	21.2^{ns}	-31.3^{ns}
82x79-3	-68.5*	-70.7*	10^{ns}	10^{ns}	-12.3^{ns}	-8.6^{ns}	8.9^{ns}	8.0**	-19.9^{ns}	-25.5^{ns}	-24.3*	-25.1*	-17.9*	-20.0*	40.1^{ns}	-20.5^{ns}
82x79-2	-84.0*	-85.1*	7^{ns}	7^{ns}	-28.0*	-24.9^{ns}	12.3*	11.4**	-27.3*	-32.4*	-24.9**	-25.7*	-16.3*	-18.5*	38.8^{ns}	-21.9^{ns}
82x79-1	3.8^{ns}	-3.3^{ns}	0^{ns}	0^{ns}	-20.1^{ns}	-16.7^{ns}	0.5^{ns}	-0.4^{ns}	-15.9^{ns}	-21.8^{ns}	-9.9^{ns}	-10.7^{ns}	-4.2^{ns}	-6.7^{ns}	105.2*	16.4^{ns}
79x82-5	-36.6^{ns}	-40.9^{ns}	10^{ns}	10^{ns}	-21.7^{ns}	-18.3^{ns}	9.3^{ns}	8.4**	-19.6^{ns}	-25.3^{ns}	-17.7*	-18.5*	-12.8^{ns}	-15.1*	39.3^{ns}	-21.0^{ns}
79x82-4	16.0^{ns}	8.0^{ns}	0^{ns}	0^{ns}	-8.3^{ns}	-4.3^{ns}	3.4^{ns}	2.5**	-28.9*	-33.9*	-9.8^{ns}	-10.6^{ns}	-13.8*	-16.0*	99.2*	13.0^{ns}
79x82-3	8.9^{ns}	1.5^{ns}	3^{ns}	3^{ns}	-11.4^{ns}	-7.6^{ns}	5.0^{ns}	4.1**	-21.2^{ns}	-26.7^{ns}	-13.9^{ns}	-14.7^{ns}	-16.1*	-18.3*	103.6*	15.5^{ns}
79x82-2	18.0^{ns}	9.9^{ns}	3^{ns}	3^{ns}	-7.9^{ns}	-4.0^{ns}	2.5^{ns}	1.7**	-29.9*	-34.8*	-10.0^{ns}	-10.9^{ns}	-11.6^{ns}	-13.8^{ns}	89.9*	7.7^{ns}
79x82-10	-39.6^{ns}	-43.8^{ns}	7^{ns}	7^{ns}	-10.3^{ns}	-6.4^{ns}	4.4^{ns}	3.6**	-15.2^{ns}	-21.1^{ns}	-15.1^{ns}	-16.0^{ns}	-11.3^{ns}	-13.6^{ns}	17.4^{ns}	-33.4^{ns}
79x82-1	-70.4*	-72.4*	17*	17^{ns}	-22.4^{ns}	-19.1^{ns}	16.1*	15.2*	-31.6**	-36.4*	-33.5**	-34.2**	-32.0**	-33.7**	29.4^{ns}	-26.6^{ns}

***Significant at P<0.05; **Significant at P<0.01; ^{ns}Not significant at P<0.05**

Table 7.15 Performance of Apomuden and CIP 443035, and their F_1 hybrids

Genotype	β-carotene (mg/100g)DW	Dry matter (%)	Total sugars (%)	Starch (%)	Protein (%)	Iron (mg/100g)DW	Zinc (mg/100g)DW	Root yield (t/ha)
Apomuden (50)	40.67	28	31.63	49.35	4.06	2.30	1.52	34.00
CIP 443035 (79)	22.66	30	24.39	58.91	3.44	2.00	1.17	3.56
50x79-2	31.01	30	27.99	57.98	3.64	2.09	1.22	29.89
50x79-4	42.50	25	36.93	47.36	4.05	2.47	1.57	22.37
79x50-1	30.96	28	32.32	54.30	3.21	1.93	1.19	32.26
79x50-10	33.07	31	37.61	48.92	3.52	2.32	1.47	35.89
79x50-12	21.87	31	33.88	57.93	2.81	1.70	0.99	30.11
79x50-13	36.70	27	39.03	47.49	3.54	2.12	1.29	27.07
79x50-14	34.43	27	31.73	51.02	3.72	2.17	1.36	9.44
79x50-2	22.09	30	21.06	59.86	2.98	1.82	1.12	18.50
79x50-3	14.16	32	21.87	65.58	2.85	1.77	1.05	31.00
79x50-4	28.39	31	22.30	60.16	3.23	1.93	1.13	32.44
79x50-5	21.84	33	24.21	61.01	3.30	1.97	1.14	32.15
79x50-6	22.63	35	20.82	63.60	3.20	1.89	1.12	26.41
79x50-7	12.68	38	26.56	66.49	3.32	1.59	0.92	29.07
79x50-8	16.37	38	18.09	65.60	3.74	1.86	1.14	42.09
79x50-9	17.55	36	22.65	63.68	3.39	1.78	1.08	17.07
SED (5%)	10.10	3	4.61	5.32	0.54	0.23	0.16	7.29
Grand mean	26.4	31	27.83	57.60	3.41	1.98	1.20	27.60
Range	12.68- 42.50	25 - 38	18.09 - 39.03	47.36 - 66.49	2.81 - 4.06	1.59 - 2.47	0.92 - 1.57	3.56 - 42.09
CV (%)	46.8	12.5	20.3	11.3	19.5	14.3	16.2	32.3

Table 7.16 Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for the F_1 hybrids of Apomuden (50) and CIP 443035 (79)

Genotype	β-carotene		Dry matter		Total sugars		Starch		Protein		Iron		Zinc		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
50x79-2	-2.1^{ns}	-23.8^{ns}	3^{ns}	0^{ns}	-0.1^{ns}	14.8^{ns}	7.1^{ns}	-1.6^{ns}	-2.9^{ns}	-1.0^{ns}	-3.0^{ns}	-9.3^{ns}	-9.1^{ns}	-19.9^{ns}	59.2^{ns}	-12.1^{ns}
50x79-4	34.2^{ns}	4.5^{ns}	-14^{ns}	-17^{ns}	31.8*	51.4^{ns}	-12.5^{ns}	-19.6^{ns}	8.0^{ns}	0.0^{ns}	14.9^{ns}	7.4^{ns}	16.9^{ns}	3.1^{ns}	19.1^{ns}	-34.2^{ns}
79x50-1	-2.2^{ns}	-23.9^{ns}	-3^{ns}	-7^{ns}	15.4^{ns}	32.5^{ns}	0.3^{ns}	-7.8^{ns}	-14.4^{ns}	-2.1^{ns}	-10.3^{ns}	-16.2^{ns}	-11.2^{ns}	-21.7^{ns}	72.8^{ns}	-5.1^{ns}
79x50-10	4.4^{ns}	-18.7^{ns}	7^{ns}	3^{ns}	34.3*	54.2^{ns}	-9.6^{ns}	-17.0^{ns}	-6.2^{ns}	-1.4^{ns}	7.7^{ns}	0.7^{ns}	9.6^{ns}	-3.4^{ns}	91.1*	2.6^{ns}
79x50-12	-30.9^{ns}	-46.2^{ns}	7^{ns}	3^{ns}	21.0^{ns}	38.9^{ns}	7.0^{ns}	-1.7^{ns}	-25.0^{ns}	-3.1*	-21.0*	-26.1*	-25.8*	-34.6*	60.3^{ns}	-11.4^{ns}
79x50-13	15.9^{ns}	-9.8^{ns}	-7^{ns}	-10^{ns}	39.3*	60.0*	-12.3^{ns}	-19.4^{ns}	-5.7^{ns}	-1.3^{ns}	-1.6$_{ns}$	-8.0^{ns}	-3.7^{ns}	-15.1^{ns}	44.1^{ns}	-20.4^{ns}
79x50-14	8.7^{ns}	-15.3^{ns}	-7^{ns}	-10^{ns}	13.3^{ns}	30.1^{ns}	-5.7^{ns}	-13.4^{ns}	-0.9^{ns}	-0.9^{ns}	0.7^{ns}	-5.9^{ns}	1.6^{ns}	-10.4^{ns}	-49.7^{ns}	-72.2*
79x50-2	-30.2^{ns}	-45.7^{ns}	3^{ns}	0.0^{ns}	-24.8^{ns}	-13.7^{ns}	10.6^{ns}	1.6^{ns}	-20.7^{ns}	-2.7^{ns}	-15.3^{ns}	-20.8^{ns}	-16.7^{ns}	-26.6*	-1.5^{ns}	-45.6^{ns}
79x50-3	-55.3^{ns}	-65.2*	10^{ns}	7^{ns}	-21.9$^{n\ s}$	-10.3^{ns}	21.2*	11.3^{ns}	-23.9^{ns}	-3.0*	-17.7^{ns}	-23.0*	-21.4^{ns}	-30.7*	65.1^{ns}	-8.8^{ns}
79x50-4	-10.4^{ns}	-30.2^{ns}	7^{ns}	3^{ns}	-20.4^{ns}	-8.6^{ns}	11.1^{ns}	2.1^{ns}	-13.8^{ns}	-2.1^{ns}	-10.3^{ns}	-16.1^{ns}	-15.9^{ns}	-25.9*	72.7^{ns}	-4.6^{ns}
79x50-5	-31.0^{ns}	-46.3^{ns}	14^{ns}	10^{ns}	-13.6^{ns}	-0.7^{ns}	12.7^{ns}	3.6^{ns}	-12.0^{ns}	-1.9^{ns}	-8.5^{ns}	-14.4^{ns}	-15.1^{ns}	-25.2*	71.1^{ns}	-5.4^{ns}
79x50-6	-28.5^{ns}	-44.4^{ns}	21^{ns}	17^{ns}	-25.7^{ns}	-14.6^{ns}	17.5^{ns}	8.0^{ns}	-14.7^{ns}	-2.2^{ns}	-12.1^{ns}	-17.8^{ns}	-16.5^{ns}	-26.4*	40.6^{ns}	-22.3^{ns}
79x50-7	-60.0^{ns}	-68.8*	31*	27^{ns}	-5.2^{ns}	8.9^{ns}	22.8*	12.9^{ns}	-11.6^{ns}	-1.9^{ns}	-26.2*	-31.0*	-31.1*	-39.3**	54.8^{ns}	-14.5^{ns}
79x50-8	-48.3^{ns}	-59.7*	31*	27^{ns}	-35.4*	-25.8^{ns}	21.2*	11.4^{ns}	-0.3^{ns}	-0.8^{ns}	-13.4^{ns}	-19.1^{ns}	-14.7^{ns}	-24.8*	124.1**	23.8^{ns}
79x50-9	-44.6^{ns}	-56.8*	24^{ns}	20^{ns}	-19.1^{ns}	-7.1^{ns}	17.6^{ns}	8.1^{ns}	-9.6^{ns}	-1.7^{ns}	-17.3^{ns}	-22.7*	-19.4^{ns}	-29.0*	-9.1^{ns}	-49.8^{ns}

***Significant at P<0.05; **Significant at P<0.01; ^{ns}Not significant at P<0.05**

Table 7.17 Performance of CIP 443035 and CIP 442850, and their F_1 hybrids

Genotype	β-carotene (mg/100g)DW	Dry matter (%)	Total sugars (%)	Starch (%)	Protein (%)	Iron (mg/100g)DW	Zinc (mg/100g)DW	Root yield (t/ha)
CIP 443035 (79)	22.66	30	24.39	58.91	3.44	2.00	1.17	3.56
CIP 442850 (109)	24.12	25	38.22	49.41	3.17	2.04	1.20	35.33
79x109-3	21.66	30	25.36	57.10	3.40	2.09	1.17	26.07
79x109-2	19.95	31	33.45	51.64	4.32	2.24	1.27	13.00
79x109-1	26.33	28	31.37	53.60	4.27	2.12	1.17	23.31
LSD (5%)	6.41	2	4.56	4.27	0.56	0.17	0.10	5.54
Grand mean	22.9	29	30.60	54.10	3.72	2.10	1.20	20.30
Range	19.95 - 26.33	25 - 31	24.39 - 38.22	49.41 - 58.91	3.17 – 4.32	2.00 - 2.24	1.17 - 1.27	3.56 - 35.33
CV (%)	34.2	8.5	18.3	9.7	18.5	9.8	9.9	33.5

Table 7.18 Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for the F_1 hybrids of CIP 443035 (79) and CIP 442850 (109)

Genotype	β-carotene		Dry matter		Total sugars		Starch		Protein		Iron		Zinc		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
79x109-3	-7.4^{ns}	-10.2^{ns}	9^{ns}	0^{ns}	-19.0^{ns}	4.0^{ns}	5.4^{ns}	-3.1^{ns}	3.1^{ns}	$.1.1^{ns}$	3.3^{ns}	2.3^{ns}	-0.5^{ns}	-2.1^{ns}	34.11^{ns}	-26.2^{ns}
79x109-2	-14.7^{ns}	-17.3^{ns}	13^{ns}	3^{ns}	6.8^{ns}	37.1^{ns}	-4.7^{ns}	-12.3^{ns}	30.9^{ns}	25.6^{ns}	11.0^{ns}	9.9^{ns}	7.3^{ns}	5.5^{ns}	-33.13^{ns}	-63.2**
79x109-1	12.6^{ns}	9.2^{ns}	2^{ns}	-7^{ns}	0.2^{ns}	28.6^{ns}	-1.0^{ns}	-9.0^{ns}	29.5^{ns}	24.2^{ns}	5.1^{ns}	4.1^{ns}	-0.8^{ns}	-2.5^{ns}	19.91^{ns}	-34.0^{ns}

****Significant at P<0.01; ^{ns}Not significant at P<0.05**

Table 7.19 Performance of Resisto and Apomuden, and their F_1 hybrids

Genotype	β-carotene (mg/100g)DW	Dry matter (%)	Total sugars (%)	Starch (%)	Protein (%)	Iron (mg/100g)DW	Zinc (mg/100g)DW	Root yield (t/ha)
Resisto (21)	27.53	38	18.53	65.43	5.62	2.34	1.22	3.25
Apomuden (50)	40.67	28	31.63	49.35	4.06	2.30	1.52	34.00
21x50-1	21.18	32	22.45	62.45	3.07	1.94	1.17	35.89
21x50-2	33.17	29	32.96	55.62	2.98	1.95	1.08	34.41
50x21-1	31.18	26	42.50	47.16	3.20	2.13	1.30	36.67
50x21-4	2.72	32	19.42	66.16	3.22	1.65	1.08	19.70
50x21-5	6.32	33	17.44	63.35	3.42	1.84	1.11	31.85
SED (5%)	3.78	3	3.93	4.40	0.59	0.18	0.15	6.86
Grand mean	22.5	30	27.70	57.30	3.32	1.97	1.21	30.90
Range	2.72 - 40.67	26 - 38	17.44 - 42.50	47.16 - 66.16	2.98 - 5.62	1.65 - 2.34	1.08 - 1.52	3.25 - 36.67
CV (%)	20.5	11.1	17.4	9.4	21.9	11.3	15.2	27.2

Table 7.20 Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for the F_1 hybrids of Resisto (21) and Apomuden (50)

Genotype	β-carotene		Dry matter		Total sugars		Starch		Protein		Iron		Zinc		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
21x50-1	-37.9**	-47.9**	-3^{ns}	-16*	-10.5^{ns}	21.2^{ns}	8.8^{ns}	-4.6^{ns}	-36.6*	-45.4**	-16.4*	-17.1*	-14.7^{ns}	-23.1^{ns}	92.7*	5.6^{ns}
21x50-2	-2.7^{ns}	-18.4^{ns}	-12^{ns}	-24**	31.4*	77.9**	-3.1^{ns}	-15.0*	-38.5**	-47.0**	-15.9*	-16.7*	-21.2*	-29.0*	84.7*	1.2^{ns}
50x21-1	-8.6^{ns}	-23.3*	-21*	-32**	69.5**	129.4**	-17.8*	-27.9**	-33.9*	-43.1**	-8.1^{ns}	-8.9^{ns}	-5.0^{ns}	-14.3^{ns}	96.8*	7.9^{ns}
50x21-4	-92.0**	-93.3**	-3^{ns}	-16*	-22.6^{ns}	4.8^{ns}	15.3*	1.1^{ns}	-33.5*	-42.7**	-28.9**	-29.5**	-21.4*	-29.1*	5.7^{ns}	-42.1^{ns}
50x21-5	-81.5**	-84.5**	0^{ns}	-13^{ns}	-30.5*	-5.9^{ns}	10.4^{ns}	-3.2^{ns}	-29.3*	-39.1**	-20.8*	-21.5*	-18.6^{ns}	-26.7^{ns}	71.0*	-6.3^{ns}

***Significant at P<0.05; **Significant at P<0.01; ^{ns}Not significant at P<0.05**

Table 7.21 Performance of Apomuden and CIP 442850, and their F_1 hybrids

Genotype	β-carotene (mg/100g)DW	Dry matter (%)	Total sugars (%)	Starch (%)	Protein (%)	Iron (mg/100g)DW	Zinc (mg/100g)DW	Root yield (t/ha)
Apomuden (50)	40.67	28	31.63	49.35	4.06	2.30	1.52	34.00
CIP 442850 (109)	24.12	25	38.22	49.41	3.17	2.04	1.20	35.33
109x50-1	10.06	27	29.22	58.48	2.63	1.76	0.94	45.65
109x50-2	16.84	33	24.72	59.52	3.53	1.93	1.15	39.50
50x109-1	34.45	24	39.48	48.17	2.60	1.92	1.02	47.26
50x109-11	10.15	35	23.25	66.06	1.96	1.54	0.95	30.30
50x109-12	34.86	24	39.62	45.47	2.56	2.06	1.25	24.74
50x109-13	33.57	24	35.19	51.51	3.41	2.20	1.37	18.52
50x109-14	17.13	29	28.10	58.25	2.23	1.71	0.97	45.17
50x109-3	40.00	23	41.56	42.53	2.91	2.07	1.17	31.20
50x109-4	29.19	22	30.74	48.71	2.52	1.97	1.10	26.50
50x109-5	28.28	23	46.34	39.05	2.63	2.18	1.31	23.37
50x109-7	30.24	22	41.25	40.68	2.66	2.18	1.35	27.22
50x109-8	30.15	23	38.07	44.05	3.53	2.42	1.55	28.48
50x109-9	36.19	23	39.00	44.87	3.38	2.33	1.45	33.11
SED (5%)	4.98	2.00	3.03	3.57	0.53	0.17	0.12	8.20
Grand mean	27.73	26	35.09	49.74	2.92	2.04	1.22	32.90
Range	10.06 - 40.67	22 – 35	23.25 - 46.34	39.05 -66.06	1.96 - 4.06	1.54 - 2.42	0.94 - 1.55	18.52 - 47.26
CV (%)	22	12.5	10.6	8.8	22.0	10.4	12.2	30.5

Table 7.22 Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for the F_1 hybrids of Apomuden (50) and CIP 442850 (109)

Genotype	β-carotene		Dry matter		Total sugars		Starch		Protein		Iron		Zinc		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
109x50-1	-69.0**	-75.3**	0^{ns}	-4^{ns}	-16.3^{ns}	-7.6^{ns}	18.4*	17.7*	-27.1^{ns}	-35.2*	-18.7*	-23.3*	-31.2**	-38.4**	31.7^{ns}	29.2^{ns}
109x50-2	-48.0**	-58.6**	22*	18^{ns}	-29.2**	-21.8*	20.5*	19.9*	-2.3^{ns}	-13.1^{ns}	-11.1^{ns}	-16.1^{ns}	-15.3^{ns}	-24.2*	13.9^{ns}	11.8^{ns}
50x109-1	6.3^{ns}	-15.3^{ns}	-11^{ns}	-14^{ns}	13.0^{ns}	24.8*	-2.5^{ns}	-3.1^{ns}	-27.9*	-35.9*	-11.8^{ns}	-16.7*	-24.7*	-32.6**	36.3^{ns}	33.8^{ns}
50x109-11	-68.7**	-75.0**	30**	25*	-33.4**	-26.5*	33.8**	33.1**	-45.6**	-51.7**	-29.1**	-33.1**	-30.1**	-37.5**	-12.6^{ns}	-14.2^{ns}
50x109-12	7.6^{ns}	-14.3^{ns}	-11^{ns}	-14^{ns}	13.4^{ns}	25.3*	-7.9^{ns}	-8.6^{ns}	-29.0*	-36.9*	-5.1^{ns}	-10.4^{ns}	-8.2^{ns}	-17.8**	-28.6^{ns}	-30.0^{ns}
50x109-13	3.6^{ns}	-17.5^{ns}	-11^{ns}	-14^{ns}	0.7^{ns}	11.3^{ns}	4.3^{ns}	3.6^{ns}	-5.7^{ns}	-16.1^{ns}	1.3^{ns}	-4.4^{ns}	0.5^{ns}	-10.0^{ns}	-46.6*	-47.6*
50x109-14	-47.1**	-57.9**	7^{ns}	3.6^{ns}	-19.6*	-11.2^{ns}	18.0*	17.3*	-38.3*	-45.1**	-21.3*	-25.8*	-28.4**	-35.9**	30.3^{ns}	27.9^{ns}
50x109-3	23.5^{ns}	-1.6^{ns}	-15^{ns}	-18^{ns}	19.0*	31.4*	-13.9^{ns}	-14.5^{ns}	-19.5^{ns}	-28.4^{ns}	-4.7^{ns}	-10.0^{ns}	-13.6^{ns}	-22.7*	-10.0^{ns}	-11.7^{ns}
50x109-4	-9.9^{ns}	-28.2*	-19*	-21^{*}	-12.0^{ns}	-2.8^{ns}	-1.4^{ns}	-2.0^{ns}	-30.1*	-37.9*	-9.4^{ns}	-14.5^{ns}	-19.4*	-27.8**	-23.57^{ns}	-25.0^{ns}
50x109-5	-12.7^{ns}	-30.5*	-15^{ns}	-18^{ns}	32.7**	46.5^{*}	-20.9*	-21.6*	-27.1^{ns}	-35.2*	0.6^{ns}	-5.0^{ns}	-3.7^{ns}	-13.8^{ns}	-32.6^{ns}	-33.9^{ns}
50x109-7	-6.7^{ns}	-25.6^{ns}	-19*	-21*	18.1*	30.4*	-17.6*	-18.3*	-26.3^{ns}	-34.4*	0.4^{ns}	-5.3^{ns}	-0.7^{ns}	-11.1^{ns}	-21.5^{ns}	-23.0^{ns}
50x109-8	-6.9^{ns}	-25.9^{ns}	-15^{ns}	-18^{ns}	9.0^{ns}	20.4^{ns}	-10.8^{ns}	-11.5^{ns}	-2.3^{ns}	-13.1^{ns}	11.3^{ns}	5.0^{ns}	14.2^{ns}	2.2^{ns}	-17.9^{ns}	-19.4^{ns}
50x109-9	11.7^{ns}	-11.0^{ns}	-15^{ns}	-18^{ns}	11.7^{ns}	23.3*	-9.1^{ns}	-9.8^{ns}	-6.5^{ns}	-16.8^{ns}	7.4^{ns}	1.3^{ns}	6.8^{ns}	-4.4^{ns}	-4.5^{ns}	-6.3^{ns}

***Significant at P<0.05; **Significant at P<0.01; ^{ns}Not significant at P<0.05**

Table 7.23 Performance of CIP 442850 and Beauregard, and their F_1 hybrids

Genotype	β-carotene (mg/100g)DW	Dry matter (%)	Total sugars (%)	Starch (%)	Protein (%)	Iron (mg/100g)DW	Zinc (mg/100g)DW	Root yield (t/ha)
CIP 442850 (109)	24.12	25	38.22	49.41	3.17	2.04	1.20	35.33
Beauregard (82)	26.24	30	26.49	59.87	3.99	2.03	1.11	26.59
109x82-4	30.76	27	32.10	53.06	2.92	1.89	1.02	34.28
109x82-3	17.99	25	29.96	57.73	2.47	1.77	0.90	27.00
109x82-2	9.45	31	20.26	64.58	2.09	1.62	0.87	34.19
109x82-1	5.42	28	18.40	67.68	2.34	1.59	0.86	26.89
SED (5%)	7.96	4	4.00	3.75	0.78	0.18	0.12	6.27
Grand mean	20.5	27	28.40	58.00	2.82	1.83	0.99	28.00
Range	5.42 - 30.76	25 – 31	18.40- 38.22	49.41 - 67.68	2.09 - 3.99	1.59 - 2.04	0.86 - 1.20	26.59 - 35.33
CV (%)	47.4	19.8	17.2	7.9	33.7	11.7	14.9	27.7

Table 7.24 Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for the F_1 hybrids of CIP 442850 (109) and Beauregard (82)

Genotype	β-carotene		Dry matter		Total sugars		Starch		Protein		Iron		Zinc		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
109x82-4	22.2^{ns}	17.2^{ns}	-4^{ns}	-10^{ns}	-0.8^{ns}	0.2^{ns}	-2.9^{ns}	-11.4^{ns}	-18.6^{ns}	-26.9^{ns}	-7.3^{ns}	-7.3^{ns}	-11.3^{ns}	-15.0^{ns}	10.7^{ns}	-3.0^{ns}
109x82-3	-28.6^{ns}	-31.4^{ns}	-11^{ns}	-17^{ns}	-7.4^{ns}	0.1^{ns}	5.7^{ns}	-3.6^{ns}	-30.9^{ns}	-38.0^{ns}	-13.2^{ns}	-13.2^{ns}	-21.7*	-24.9*	-12.8^{ns}	-23.6^{ns}
109x82-2	-62.5*	-64.0^{ns}	11^{ns}	3^{ns}	-37.4**	-0.2^{ns}	18.2*	7.9*	-41.5^{ns}	-47.5*	-20.8*	-20.8*	-24.6*	-27.8*	10.4^{ns}	-3.2^{ns}
109x82-1	-78.5*	-79.3*	0.0^{ns}	-7^{ns}	-43.1**	-0.3^{ns}	23.9**	13.0**	-34.6^{ns}	-41.3^{ns}	-22.1*	-22.1*	-25.2*	-28.4*	-13.2^{ns}	-23.9^{ns}

***Significant at P<0.05; **Significant at P<0.01; ^{ns}Not significant at P<0.05**

Table 7.25 Performance of Resisto and CIP 443035, and their F_1 hybrids

Genotype	β-carotene (mg/100g)DW	Dry matter (%)	Total sugars (%)	Starch (%)	Protein (%)	Iron (mg/100g)DW	Zinc (mg/100g)DW	Root yield (t/ha)
Resisto (21)	27.53	38	18.53	65.43	5.62	2.34	1.22	3.25
CIP 443035 (79)	22.66	30	24.39	58.91	3.44	2.00	1.17	3.56
79x21-2	26.88	36	22.07	66.05	2.65	1.63	0.96	19.11
79x21-1	17.38	36	16.43	66.81	3.18	1.81	1.09	37.60
LSD (5%)	4.16	6	6.18	6.14	0.38	0.18	0.04	5.38
Grand mean	22.31	34	21.00	63.90	3.09	1.81	1.07	20.10
Range	17.38 - 27.53	30 – 38	16.43 - 24.39	58.91 - 66.81	2.65 - 5.62	1.63 - 2.34	0.96 - 1.22	3.25 - 37.60
CV (%)	11.4	10.6	18.0	5.9	7.5	6.4	2.8	16.4

Table 7.26 Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for the F_1 hybrids of Resisto (21) and CIP 443035 (79)

Genotype	β-carotene		Dry matter		Total sugars		Starch		Protein		Iron		Zinc		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
79x21-2	7.1^{ns}	-2.4^{ns}	6^{ns}	-5^{ns}	2.8^{ns}	19.1*	6.2**	0.9^{ns}	-41.6**	-52.9**	-24.8**	-30.3**	-20.4**	-21.7**	460.4**	436.8**
79x21-1	-30.8**	-36.9**	6^{ns}	-5^{ns}	-23.4^{ns}	-11.3^{ns}	7.5**	2.1^{ns}	-29.9**	-43.5**	-16.8**	-22.9**	-9.4**	-10.9**	1002.6**	956.2**

***Significant at P<0.05; **Significant at P<0.01; ^{ns}Not significant at P<0.05**

7.4. Discussion

The coefficient of variation (CV) for the traits were all less or equal to 30% except for beta-carotene content of the high beta-carotene population and in some cases for root yield. The high CV for the root yield is because of the variability in size and shape of the storage roots. That of the beta-carotene content could also be attributed to the high variation observed for the trait which varied from 2.72 mg/100gDW to 44.05 mg/100gDW for the high beta-carotene population. The high CV indicates high genotypic coefficient of variation which may suggest useful genetic variation for beta-carotene and storage root yield improvement.

Lack of seeds and fewer numbers of seedlings from some crosses may largely be attributed to poor flowering and incompatibility. According to (Martin, 1967) and (Martin and Cabanillas, 1968), the improvement of sweetpotato through conventional breeding is hindered by poor flowering and incompatibility. Among the parents used for the low sugar population, AAT-03-025 and CIP 442264 were very low in flower prolificacy that is why fewer crosses were made between them and subsequently fewer seeds were obtained. Among the high beta-carotene parents, Resisto was the most prolific in flower production but was the poorest parent in terms of cross ability. This is because most of the crosses in which it was involved were not successful and in few cases where successful crosses were achieved less viable seeds were obtained. This poor crossing ability could be as a results of genetic incompatibility. Cross-incompatibility is presumed to result from pollination between parental clones with the same self-incompatibility phenotype (Kowyama *et al.*, 2008). Cross-incompatibility among different varieties hinders targeted breeding especially when the parents with desirable traits of interest belong to the same incompatibility group (Charles *et al.*, 1973; Vimala, 1989).

The range of values obtained for this study were comparable to those reported by Grüneberg *et al.* (2009), and other studies in this thesis (Chapters Four and Six). Values for dry matter content were also comparable to those reported by Shumbusha *et al.* (2014).

There were both significant positive and negative heterosis for the two populations studied. The significant negative heterosis observed for sugar content is an important finding for sweetpotato improvement in Ghana. This is because the main trait preferred for sweetpotato to assume an increased staple food status in Ghana is non-sweetness (bland taste) (Missah and Kissiedu, 1994; Sam and Dapaah, 2009). This has made breeding for non-sweetness the most important breeding objective of the crop currently in Ghana. For the high beta-carotene population, the negative heterosis observed for dry matter and starch content were expected because of the negative relationship existing between these two traits and beta-carotene content (Grüneberg *et al.*, 2009). This association was also found in Chapter Four of this thesis. This suggests that many cycles of selection and hybridization may be required to develop sweetpotato varieties with high dry matter and high beta-carotene contents.

The sugar contents of the genotypes evaluated agrees with Kays *et al.* (2005). The authors classified sweetpotatoes based on sugar content as very high ≥38; high 29-37; moderate 21-28; low 12-20; and non-sweet ≤12. Based upon this classification, 15% of the F_1 hybrids of the low sugar population had sugar content of ≤12 whilst the remaining hybrids (85%) had 12 – 20%. This therefore means that 15% of the F_1 hybrids of the low sugar population were non-sweet and these will meet the staple food needs of Ghanaians. The beta-carotene population also had 14% of the F_1 hybrids having sugar content of 12 – 20%, 35% having 21 – 28%, 39% having 29 – 37% and 12% having ≥38%. This also means that 14% of the F_1

hybrids of the high beta-carotene population had low sugar content which is good considering the positive association between beta-carotene content and sugar content.

Based upon sugar content (mainly), dry matter content and root yield, the following genotypes were selected as non-sweet. They were Ogyefo x Histarch-11, Histarch x Ogyefo-13, Histarch x Ogyefo-52, Histarch x Ogyefo-37, Histarch x Ogyefo-65, Histarch x Ogyefo-88, Histarch x Ogyefo-39, Histarch x Ogyefo-16, and Histarch x Ogyefo-13. These genotypes have high dry matter content range of 42 – 46%, low sugar content range of 9 -12%, and root yield range of 12 – 31 t/ha as compared to the two low sugar released varieties Histarch (46% dry matter, 16.33% sugar content and 20.7 1t/ha root yield) and Ogyefo (41% dry matter, 13.62% sugar content and 13.61 t/ha root yield). These released varieties were the parents of these hybrids. In addition, 26 hybrids among the remaining hybrids of the low sugar population were selected for other purpose such as source of sugar flour for sweetening porridge and *aboolo*. Similarly, 16 F_1 hybrids with comparable beta-carotene content as Apomuden (the only released high beta-carotene variety in Ghana to date), and have higher dry matter content and relatively lower sugar content, and higher root yield were also selected. These genotypes had 16 – 33 mg/100gDW beta-carotene content, 29 – 38% dry matter content, up to 28% sugar content, and root yield range of 17 – 42 t/ha. Apomuden had beta-carotene content of 40.67 mg/100gDW, dry matter content of 28%, sugar content of 31.63% and root yield of 34 t/ha. The genotypes were CIP 443035 x Apomude-10, Apomuden x CIP 443035-2, CIP 443035 x Apomuden-4, CIP 443035 x Resisto-4, CIP 443035 x Resisto-2, Beauregard x CIP 443035-1, CIP 443035 x Apomuden-6, Beauregard x Apomuden-20, CIP 443035 x Apomuden-12, Resisto x Apomuden-1, Beauregard x Apomuden-21, CIP 443035 x Apomuden-9, CIP 443035 x Resisto-1, CIP 443035 x Apomuden-8, and Beauregard x Apomuden-32 and CIP 443035 x Beauregard-3.

7.5. Conclusion

Genetic variability existed for the traits studied. Significant heterosis was found which is useful for the improvement of the two populations. Negative heterosis observed for sugar content is very important because breeding for non-sweetness will raise sweetpotato to an increase staple food status in Ghana. Combining high beta-carotene content and high dry matter content into a common genetic background will be considered in a future study. The selected superior hybrids will be further tested multi-locationally for potential release to farmers. These selected genotypes together with their complementary parents used in this study will be used as the breeding population for sweetpotato improvement programme in my institute CSIR-CRI, at Fumesua, Ghana.

CHAPTER EIGHT

GENERAL DISCUSSION

Sweetpotato has great potential for food security and income generation, as well as, raw material for industry. In Ghana, the crop has proven to be useful in various food preparations in place of rice, cassava, yam, plantain and other well-integrated staples (Adu-Kwarteng *et al.*, 2001; Ellis *et al.*, 2001; Meludu *et al.*, 2003; Zuraida, 2003). In spite of its great potential to alleviate food insecurity, malnutrition and poverty, it is not well integrated into the average Ghanaian diet as its level of utilization is very low as compared to the other root and tuber crops. The aim of this study was to identify the constraints to sweetpotato utilization in Ghana and to develop end-user preferred varieties to increase its staple food status in Ghana and beyond.

To identify the constraints to sweetpotato utilization in Ghana and incorporate the preferred traits into the breeding programme, a survey was conducted using Focus Group Discussion (FGD) followed by administration of semi-structured questionnaire in some selected communities of Ghana where the crop is popular. These communities span all the five agroecological zones of Ghana. The potential of sweetpotato as a food security and an income generation crop was confirmed by this survey. Stakeholders' preferred sweetpotatoes with high storage root dry matter content. This is because such varieties suit their food preparation needs. Sweetpotatoes are consumed mainly after frying and boiling in the form of *ampesi* (coking in boiling water). The method of cooking and the form of utilization have critical influence on taste and consumptive quality (Sugri *et al.*, 2012). Cooking leads to changes in physical, sensory and chemical characteristics of the final product (Vitrac *et al.*, 2000; Fontes *et al.*, 2011). The storage root flesh of sweetpotato is mainly starch, which swells upon water absorption, and hydrolyses the weak bonds making it more easily

digestible. Low dry matter varieties lose their cooking quality (mealiness) when cooked, affecting textural characteristics preference. Frying enhances sensorial characteristics such as smell, flavour, colour, texture as well as overall palatability (Sugri *et al.*, 2012). It involves drying, cooking or fast dehydration in which the water is removed from the food by means of immersion into oil at temperatures of 120 – 180^0C (Vitrac *et al.*, 2000). The frying oil is incorporated into the food, occupies part of the space left by the water and thereby increases palatability, flavour, calorie supply and shelf-life (Vitrac *et al.*, 2000; Fontes *et al.*, 2011). Because the oil occupies spaces left by water, low dry matter sweetpotatoes absorbs more oil which is not economical to processors and to consumer in terms of health.

The survey revealed sweetness as the major constraint that causes people to turn away from the crop as staple food. This affirms earlier reports that locally available clones have very sweet taste, which limits their consumption as a staple food (Missah and Kissiedu, 1994; Opare-Obisaw *et al.*, 2000). The high levels of sweetness and strong flavour associated with many cultivars of sweetpotatoes may have reduced its popularity as a staple food (Woolfe, 1992). This could explain why it is uncommon to find sweetpotato served in most public places such as restaurants, workers canteens and schools in Ghana unlike the other roots and tubers which are widely consumed in a variety of preparations (Sam and Dapaah, 2009). Preference for varieties was also skewed towards low- and moderate beta-carotene sweetpotatoes (white- and yellow-flesh varieties). Orange-flesh sweetpotatoes are not popular in Ghana even though it has been shown that small amounts of these varieties as a regular part of the diet will eliminate vitamin A deficiency in adults and children. According to Thottappilly (2009), African countries have traditionally grown white-flesh sweetpotatoes which are low in vitamin A. The reason is that orange-flesh cultivars are very sweet and also have low dry matter content. Non-sweet, high root dry matter sweetpotatoes are preferred by

Ghanaians and this is the reason for consumers' lack of preference for the orange–flesh types. However, considering their health benefits, it is important to incorporate non-sweetness and high dry matter into the high beta-carotene genetic background. Preference for non-sweet, high dry matter sweetpotatoes was not influenced by socio-economic factors such as age, sex, and educational background. Therefore, developing non-sweet, high dry matter sweetpotatoes will increase the crop's preference and utilization in Ghana and beyond.

To develop non-sweet, high dry matter sweetpotato varieties, a total of 115 sweetpotato accessions were collected and evaluated. Applying agro-morphological, physico-chemical and SSR markers, a high degree of agro-morphological and physicochemical variation was observed among the accessions. Similar observation has been reported (Ravindran *et al.*, 1995; Aina *et al.*, 2009; Yada *et al.*, 2010b; Waramboi *et al.*, 2011; Somé *et al.*, 2014). Similarly, a high level of SSR marker diversity was observed and this confirms an earlier report of the discriminatory capacity of the SSR markers on sweetpotato (Gichuru *et al.*, 2006; Tumwegamire *et al.*, 2011). The AMOVA and ANOVA results also indicated a wide variation between the sweetpotato accessions studied. This agrees with what is reported in the literature (Zhang *et al.*, 2000; Zhang *et al.*, 2001; Gichuki *et al.*, 2003; Gichuru *et al.*, 2006; Abdelhameed *et al.*, 2007; Grüneberg *et al.*, 2009; Tumwegamire *et al.*, 2011), and demonstrates significant genetic diversity in the sweetpotato germplasm used for this study. It also indicates that selection and improvement on the traits studied is probable (Mohammed *et al.*, 2012; Nwangburuka and Denton, 2012). The variation observed also indicates that it is possible to select contrasting parents from these populations for genetic studies on beta-carotene content, sugar content and dry matter content in sweetpotatoes. The predicted improvement over the means from the base population developed here was very good, ranging from 10% to 105% for all the traits except starch (7.13%). Miller *et al.* (1958),

observed 13 – 15% for lint yield of upland cotton and reported that this was particularly encouraging. This suggests that sufficient useful genetic variation exists in this population which could be utilized to provide for substantial improvement through the selection of superior genotypes.

A general model for estimating genetic effects proposed by Gardner (1965), Eberhart and Gardner (1966), and Gardner and Eberhart (1966), which can be applied to both inbred parents and non-inbred parents (varieties and/or populations) was used for this study. Differences were found between the results for the crosses and their reciprocals. For instance, genotype (entry) x environment interactions (G x E) were not significant for any of the traits for the crosses except zinc content, but, G x E was significant for all the traits for the reciprocal except dry matter and starch contents. Overall heterosis was significant for all the traits for both the crosses and their reciprocals except zinc content for crosses. Similarly, average heterosis was also significant ($P<0.05$) for all the traits except dry matter content and sugar content for the crosses and only dry matter content for the reciprocal crosses. Variety heterosis on the other hand was significant ($P<0.05$) for all the traits in both the crosses and the reciprocals except iron and zinc contents for the crosses. Specific combining ability (SCA) was also significant ($P<0.01$) for only beta-carotene content for the crosses and beta-carotene content, sugar content and starch content for the reciprocal crosses. These differences between the crosses and their reciprocals may be attributed to maternal effects. Maternal effects are influences of parents on offspring phenotype occurring through pathways other than inherited DNA (Adkins-Regan *et al.*, 2013). Phenotypes that are controlled by cytoplasmic factors of the female parent are said to express a maternal effect.

Variety effect (vj) and variety heterosis (hj) were significant for the traits studied. Variety effects are calculated from the performance of parents (Harold *et al.*, 2001). It is the difference between the mean of a parent and the mean of all parents. Gardner (1967), defines variety heterosis (hj) as the contribution of heterosis by variety j in its crosses measured as a deviation from average heterosis. Although specific combining ability (SCA) and specific heterosis (sij,) were significant for some traits, the SCA accounted for a less sizeable portion of the total sum of squares compared to the variety heterosis for all the traits. This suggests that even though both additive and non-additive effects are involved in the expression of some of the traits, additive effects were more important than non-additive effects for all the traits studied. This agrees with Oduro (2013) and Shumbusha *et al.* (2014) findings on these traits in sweetpotato. The majority of the total sum of squares of the traits due to the differences among generation means could be explained by variety effects (vj) and variety heterosis (Crossa *et al.*, 1987; Adam *et al.*, 2001; Harold *et al.*, 2001). This means that variety effects for the parents are important predictors of hybrid performance and suggests that these traits could be improved by pedigree method. The negative values obtained for variety heterosis (h_{ij}) may be attributed to the unrealized performance expectation of the parents in the crosses. According to Harold *et al.* (2001), negative values of variety heterosis for a breeding population appear to represent an unfulfilling performance expectation arising from high variety effects (v_j) and their high average heterosis effect (h).

In this study, a genetic association between the traits was established. Genetic relationships between traits may result from pleotropic gene effects, linkage of two genes, linkage disequilibrium and epistatic effects of different genes or environmental influences (Falconer and Mackay, 1996). Except for the very high values (>1) observed for the association between dry matter and beta-carotene content (-1.2), sucrose and total sugar content (1.09),

sucrose and iron content (1.07), and sucrose and zinc content (1.15), the values for the genetic correlation coefficient were all in agreement with those reported by Grüneberg *et al.* (2009). Denton and Nwangburuka (2011), and Nwangburuka and Denton (2012), have also reported genotypic correlation coefficients greater than one in a study on *Solanum anguivi* and character associations in leaf *Corchorous olitorius*. The strong positive association observed between dry matter and starch, and the strong negative relationship found for sugars and dry matter and starch indicates that it is possible to develop non-sweet high dry matter sweetpotatoes. Similar observation was made by Gruneberg *et al*., (2009). Developing a non-sweet, high dry matter and high beta-carotene sweetpotatoes could be challenging due to the strong negative association between dry matter content and beta-carotene content and the positive association between beta-carotene content and the sugar content. Breeding for such cultivars, therefore, may require many cycles of selection and hybridization to break genetic linkages associated with the traits. Both significant positive and negative heterosis was observed for both the low sugar and the high beta-carotene populations developed. For the low sugar population, the negative heterosis found for sugar content is important for sweetpotato improvement in Ghana and beyond. This is because the major trait required for sweetpotato to assume an increased staple food status in Ghana is non-sweetness (bland taste) (Missah and Kissiedu, 1994; Sam and Dapaah, 2009). The results from the PRA affirmed this. These have made breeding for non-sweetness the most important breeding objective of the crop in Ghana currently.

Improvement of sweetpotato through conventional breeding is hindered by poor flowering and incompatibility (Martin, 1967; Martin and Cabanillas, 1968). Lack of flowering in sweetpotato breeding is a severe impediment to understanding its genetics and making gains in selection. Poor flowering may impede the use of a preferred clone selected as parent for

hybridization. This makes it prudent to verify sweetpotato flowering ability at the start of an improvement programme. In this work, 70% of the sweetpotato parents did not flower when the hybridization blocks were first established in the screen house, and those that did (30%) only produced a few flowers. Grafting the parents onto *I. setosa*, enhanced flowering but hybridization was not successful due to wilting and death of the *I. setosa* because of its virus detection attributes. This suggests that laboratory certified virus-free scion (parent) must be grafted onto *I. setosa* to have enhanced flowering and successful crosses. This necessitated the re-establishment of the crossing blocks in the field. In spite of this, the sweetpotato parents still varied in flowering prolificacy and the differences may be attributed to genetics. According to Fekadu *et al.* (2013), flowering prolificacy in sweetpotato is variety dependent. Whilst some varieties may not flower at all, others produce very few flowers. In addition, many sweetpotato genotypes rarely flower under normal conditions as a result of differential response to seasonal variation. Most genotypes are day length sensitive. Thus whilst some genotypes flower readily at any season, flower promotion in others occurs during short days (Martin, 1988b). Seasonal observations in North-Western Argentina for instance showed that sweetpotatoes flower best with daily maximum temperatures of 23 – 24^0C and minimum temperatures of 13 – 19^0C (Folquer, 1974). Night temperatures of 16 – 17^0C and day temperatures of 24 – 30^0C appeared to be optimum (Edmond and Martin, 1946). The best season for pollination in Taiwan, in the Northern hemisphere, is from the beginning of November to the middle of December, when the average daily temperature is between 20^0C and 25^0C with a maximum seed set occurring when the mean daily temperature is about 23.9^0C (Wang, 1982).

In this study, whilst the daily minimum temperature range for the hybridization blocks established in the field (15.68 – 20.51^{0}C) is in agreement with what is reported to favour flowering that of the screen house (21.28 – 22.47^{0}C) was higher. Maximum daily temperature range of 28.42 – 32.63^{0}C, and 33.65 – 37.34^{0}C were observed for the screen house and the field, respectively, and they were higher than the values reported by other authors. The data suggest that, in addition to day length, minimum temperatures may be important in promoting flowering in sweetpotato. Greenhouse crosses are best done at days of 12 hours and temperatures not excessively high (Jones, 1980), and 24^{0}C is the optimum temperature (Montelaro and Miller, 1951). Similar observation was made in Puerto Rico (Campbell *et al.*, 1963), where flowering in the greenhouse did not occur above 27^{0}C. In this study, the hybridization blocks in the screen house were established in the major cropping season when day lengths are longer whilst that established in the field was in the minor cropping season when day lengths are shorter. This may have resulted in the varying flowering prolificacy between the two hybridization blocks established. Establishing sweetpotato crossing blocks in the minor cropping season in the forest ecozone of Ghana where this work was done is better than in the major cropping season. Furthermore, sweetpotato seed matures in about a month, a little sooner under hot, summer temperatures and later in cool, fall temperature (Jones, 1980). This also gives minor season crosses an advantage since capsules will mature earlier and therefore, less resource (money and time) will be used. However, seed abortion may be higher due to dry spells, but this can be managed through supplementary irrigation as done in this work. Both self- and cross-incompatibility were observed in this study. Only the self of Apomuden produced a seed, which was sterile and failed to germinate. Self-fertilization in sweetpotato is rare (Jill *et al.*, 1989). Even though sweetpotato is almost always self-incompatible (Martin, 1967), self-compatible genotypes may be observed (Tumana and Kesavan, 1987). Some of the crosses also did not produce seeds. Similar

observation was made by Vimala and Hariprakash (2011). Higher success rate was attained in this study than the other reports. The 54% mean success rate observed exceeds the 1 – 48% reported (Jones, 1980; Jill *et al.*, 1989). The higher germination rates of the seeds and the seedling vigour observed here may also suggest no or lower sterility among the genotypes used for this study.

CHAPTER NINE

9.0 CONCLUSIONS AND RECOMMENDATIONS

9.1. Conclusions

The participatory rural appraisal (PRA) revealed that consumers in Ghana desire non-sweet, high dry matter sweetpotatoes with low or moderate beta-carotene content. There is justification to adjust breeding objectives to develop high dry matter, non-sweet sweetpotato types to boost utilization in Ghana. The diversity study provided estimates of the level of genetic variation among the sweetpotato accessions and their utilization in breeding in Ghana. This can be useful in sweetpotato germplasm management and improvement in Ghana and beyond. Non-sweet, high dry matter sweetpotato hybrids were identified. However, combining high beta-carotene content to these types may require many cycles of selection unless molecular marker technology is used. The study confirmed the discriminatory capacity of agro-morphological, physico-chemical and SSR markers for sweetpotato characterization. Lack of or poor flowering was a problem in this study. The best period to establish sweetpotato hybridization blocks in the forest ecozone is the minor cropping season. Hybrids were produced among four genotypes Histarch, Apomuden, Beauregard, and Ogyefo and the F_1 progenies were used to determine the gene action influencing beta-carotene content, dry matter content, sugar content and other important root quality traits. Genetic variability was significant for the traits studied and much of this genetic variation was additive in nature. Therefore, the high heritability coupled with the high expected genetic gain indicates high breeding value for the traits. There was significant heterosis in crosses among low sugar parents and among high beta-carotene parents. The significant negative heterosis observed for sugar content is very important in breeding for

non-sweetness which would help sweetpotato to assume an increased staple food status in Ghana and beyond.

9.2. Recommendations

Based upon sugar content (mainly), dry matter content and root yield, the following hybrids selected as promising non-sweet varieties should be tested multi-locational on-farm for potential release to farmers. These were all hybrids between Ogyefo and Histarch. The superior hybrids were Ogyefo x Histarch-11, Histarch x Ogyefo-13, Histarch x Ogyefo-52, Histarch x Ogyefo-37, Histarch x Ogyefo-65, Histarch x Ogyefo-88, Histarch x Ogyefo-39, Histarch x Ogyefo-16, and Ogyefo x Histarch-13. These genotypes had high dry matter content of 42 – 46%, sugar content of 9 -12%, and root yield of 12 – 31 t/ha as compared to the two released low sugar varieties Histarch (46% dry matter, 16.33% sugar content and 20.71 t/ha root yield) and Ogyefo (41% dry matter, 13.62% sugar content and 13.61 t/ha root yield). In addition, the 26 F_1 hybrids in the low sugar population identified for their high yielding and high dry matter content should also be further tested multi-location on-farm for potential release for other purpose such as source of sugar flour for sweetening porridge and *aboolo*. All hybrids identified to have comparable beta-carotene content as Apomuden (the only released high beta-carotene variety in Ghana to date), with higher dry matter content and relatively lower sugar content, and higher root yield should also be for further testing for potential release to farmers. These hybrids had 16 – 33 mg/100gDW beta-carotene content, 29 – 38% dry matter content, up to 28% sugar content, and root yield of 17 – 42 t/ha. Apomuden had beta-carotene content of 40.67 mg/100gDW, dry matter content of 28%, sugar content of 31.63% and root yield of 34 t/ha. The hybrids were CIP 443035 x Apomuden-10, Apomuden x CIP 443035-2, CIP 443035 x Apomuden-4, CIP 443035 x Resisto-4, CIP 443035 x Resisto-2, Beauregard x CIP 443035-1, CIP 443035 x Apomuden-6,

Beauregard x Apomuden-20, CIP 443035 x Apomuden-12, Resisto x Apomuden-1, Beauregard x Apomuden-21, CIP 443035 x Apomuden-9, CIP 443035 x Resisto-1, CIP 443035 x Resisto-8, Beauregard x Apomuden-32 and CIP 443035 x Beaurgard-3.

Also hybrids selected from the inheritance study based upon their sugar content which fell into the low-sugar content category (sugar content ranged from 12.93 – 14.88%) will be further tested. Among these, seven hybrids Histarch x Apomuden-11, Ogyefo x Histarch-3, Histarch x Apomuden-1, Histarch x Ogyefo-4, Ogyefo x Apomuden-16, Ogyefo x Histarch-9, and Histarch x Beauregard-2 stood out in terms of dry matter content and storage root yield. These hybrids were selected because their sugar content and dry matter content were comparable to the low sugar parents, but they out yielded these parents (except two that gave comparable yield). Three hybrids also from this study Apomuden x Histarch-15, Beauregard x Histarch-5 and Beauregard x Histarch-4 are also proposed for further testing since they haver moderate beta-carotene content, low sugar content and high dry matter content compared to Apomuden, the only released orange-flesh sweetpotato variety in Ghana. Their sugar content ranged from 18.03 – 22.78% whilst Apomuden had sugar content of 36.71%. They also out yielded Apomuden. These hybrids apparently break the positive relationships between beta-carotene content and sugar content and the negative association with dry matter content and could be significant in future breeding programmes. Some important uses of sweetpotato discovered through the PRA were the use of sweetpotato flour as a substitute for the normal sugars in porridge and other local dishes such as the *aboolo*. Because of this, hybrids with higher yields and high sugar content are also recommended for further testing for potential release for such purposes. In all 18 of such F_1 hybrids were identified (Table 6.12).

The selected hybrids for the low sugar and the high beta-carotene contents together with their respective parents will be selected to form the breeding populations for the sweetpotato improvement programme in my institute CSIR-CRI at Fumesua, Ghana. Some sweetpotato genotypes lack completely or have only traces of α-amylase and β-amylase in their storage roots. Such genotypes do not increase in sweetness during cooking, frying or processing. Without sufficient amount of the enzymes, the normal hydrolysis of starch to maltose does not occur. The F_1 hybrids of the low sugar population and the other low sugar hybrids identified from the other studies should be screen for this null α-amylase and β-amylase trait. Since sweetpotato breeding involves screening of large genotypes, phenotypic evaluation for the null α-amylase and β-amylase trait will be laborious and time consuming unless genetic marker screening techniques are employed. This will go a long way to support sweetpotato breeding for non-sweetness in Ghana and beyond.

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APPENDICES

Appendix 3.1. OPEN-STRUCTURED QUESTIONAIRE FOR FOCUS GROUP DISCUSSION

Date: **Region:** **District/Locality:**

1. Names and characteristics of participants.

2. Crop/produce enterprise (What type of crops do you cultivate? List and rank them)**.**

3. Crop/produce calendars and labour demand

4. Source of planting material?

5. Varieties currently grown/used and why?

List and rank them on their qualities (eg. yield, early/late maturing, mealiness, high starch, sweetness, flesh colour, skin colour, disease resistant etc.)

6. Average root yield?

7. Major constraints to production/marketing/processing (physical and biological)?

8. Period sweetpotato is commonly eaten/marketed/processed?

9. Source of sweetpotatoes commonly eaten/marketed/processed?

10. Ways in which you eat/market/processed sweetpotatoes?

11. Food consumption/produced used (Rank food crops in order of importance and their consumption patterns)

12. Perception of sweetpotato consumption on health?

13. Constraints to sweetpotato consumption/marketing/processing?

14What needs to be done to improve on sweetpotato consumption/marketing/processing?

15. Who needs to act to improve on sweetpotato consumption/marketing/processing?

16. Proportion of sweetpotato harvest sold?

17. Who buys the sweetpotatoes?

18. What do they use it for and why?

19. General description of the group dynamics (level of participation, presence of a dominant participant, level of interest).

20. Emotional aspects of participants (e.g., reluctance, strong feelings attached to certain opinions).

Appendix 3.2. SEMI-STRUCTURED QUESTIONAIRE USED FOR THE INTERVIEW

NB: Please Tick the appropriate box.

Date: **Region:** **District/Locality:**

1. **Name and characteristics of participant.**
2. **Occupation and source of income?**

☐ Full-time farming ☐ Part-time farming ☐ Off-farm income

3. **Crop/produce enterprise** (What type of crops do you cultivate? List and rank them)**.**
4. **Farm size and proportion of sweetpotato?**
5. **a. Cropping system of sweetpotato?** ☐ **Sole cropping** ☐ **intercropping**

   b. if intercropping, which crops?

6. **Crop/produce calendars and labour demand?**
7. **Source of planting material/produce?**
8. **Seedbed management and propagation**

☐ Mound ☐ Ridge ☐ Mound/Ridge ☐ Flat

9. **Method of vine storage?**

☐ Seedbed ☐ Hole ☐ Under tree ☐ Near home ☐ House ☐ Other

10. **Varieties currently grown/marketed/processed and why?**

List and rank them on their qualities (eg. yield, early/late maturing, mealiness, high starch, sweetness, flesh colour, skin colour, disease resistant etc.)

11. **Average root yield?**
12. **Major constraints to production/marketing/processing (physical and biological)?**
13. **Harvesting method?**

☐ Piecemeal ☐ All at once ☐ Both

14. Root storage method?

15. Period sweetpotato is commonly eaten/marketed/processed?

16. Source of sweetpotatoes commonly eaten/marketed/processed?

17. Ways in which you eat /marketed/processed sweetpotatoes?

18. Food consumption/produced marketed/processed (Rank food crops in order of importance and their consumption patterns)

19. Perception of sweetpotato consumption on health?

20. Constraints to sweetpotato consumption/marketing/processing?

21. What needs to be done to improve on sweetpotato consumption/marketing?

22. What type of sweetpotato do you prefer?

a. **Dry matter content** ☐ low ☐ moderate ☐ High

b. **Sweetness** ☐ less ☐ Sweet ☐ very sweet

c. **Beta-carotene** ☐ low ☐ moderate ☐ High

7. Who needs to act to improve on sweetpotato consumption/marketing/processing?

8. Proportion of sweetpotato harvest sold?

☐ Whole ☐ Half ☐ one-quarter

9. Who buys the sweetpotatoes?

Local mkt ☐ Trader ☐ other farmers ☐ Institutions ☐ Other

10. What do they use it for and why?

11. General description of participant dynamics

a. **level of participation** ☐ high ☐ moderate ☐ low

b. **level of interest** ☐ high ☐ reluctance ☐ strong feelings attached to certain issues

c. **Emotional aspects of participants (e.g., reluctance, strong feelings attached to certain opinions).**

Appendix 6.1. Performance of the four sweetpotato parents and their F1's

Clone	Beta-carotene (mg/100g) DW	Dry Matter (%)	Total Sugars (%)	Starch (%)	Iron (mg/100g) DW	Zinc (mg/100g) DW	Mean storage root weight (kg)	Storage Root yield (t/ha)
61X87-11	4.68	44	10.26	75.99	1.33	0.88	0.24	40.86
87X82-15	2.12	45	11.16	75.81	1.36	0.80	0.11	20.71
87X50-11	2.39	44	12.93	75.57	1.29	0.77	0.22	21.20
61X87-14	4.82	46	13.01	74.48	1.30	0.90	-	-
61X87-13	3.15	43	13.36	73.17	1.49	0.93	0.18	24.47
87X82-14	3.93	42	13.45	71.37	1.53	0.93	0.09	15.34
87X82-10	2.93	40	13.66	72.81	1.44	0.85	0.19	18.15
61X87-3	4.02	42	13.78	73.58	1.23	0.84	-	-
87X61-34	4.76	43	13.83	72.77	1.41	0.82	0.10	18.40
87X61-24	1.99	41	13.86	72.57	1.42	0.90	-	-
87X50-1	4.75	40	14.10	73.96	1.43	0.79	0.26	33.73
87X61-4	3.26	42	14.28	72.59	1.36	0.89	0.22	29.44
50X61-35	3.76	35	14.32	71.41	1.59	1.06	0.11	17.02
61X50-16	5.01	40	14.36	72.91	1.51	1.07	0.19	23.50
Ogyefo (61)	5.95	39	14.36	71.37	1.69	1.01	0.22	15.35
61X87-9	4.54	45	14.39	72.24	1.64	0.98	0.22	39.20
61X87-2	4.44	33	14.52	71.62	1.47	0.91	-	-
61X87-4	1.99	41	14.59	71.65	1.51	0.92	-	-
61X87-20	4.75	41	14.67	72.45	1.47	0.93	-	-
61X87-8	2.15	42	14.69	72.17	1.49	0.87	0.15	19.33
87X82-2	1.60	41	14.73	71.43	1.69	0.99	0.13	24.08
61X50-15	3.30	36	14.84	70.29	1.44	1.08	0.17	17.90
87X61-30	4.57	41	14.88	72.31	1.42	0.88	0.19	17.69
87X82-13	4.10	38	15.02	71.26	1.48	0.85	0.11	18.91
87X82-4	5.17	40	15.06	71.23	1.36	0.92	0.39	19.67
50X61-29	6.33	36	15.15	70.20	1.52	0.99	0.15	22.02
Histarch (87)	3.67	43	15.17	72.70	1.49	0.86	0.20	24.39
87X50-14	6.22	41	15.22	72.47	1.41	0.83	0.21	14.82
50X61-17	4.32	34	15.53	69.90	1.36	0.99	0.19	23.96
87X61-3	5.99	41	15.76	71.55	1.47	0.93	0.12	19.29
87X61-36	2.61	40	15.87	70.98	1.53	0.94	0.13	18.03
61X87-10	3.76	40	15.92	69.86	1.58	1.00	0.22	54.69
87X50-18	5.35	42	15.93	71.88	1.45	0.87	0.06	8.50
87X50-3	4.99	43	16.06	72.03	1.49	0.89	0.04	3.22
61X50-14	2.56	35	16.09	69.79	1.72	1.06	0.17	15.37
87X82-9	3.22	42	16.14	70.83	1.45	0.88	0.22	30.20
87X61-27	6.15	38	16.19	69.73	1.49	0.97	-	-

Appendix 6.1 cont'd. Performance of the four sweetpotato parents and their F_1's

Clone	Beta-carotene (mg/100g) DW	Dry Matter (%)	Total Sugars (%)	Starch (%)	Iron (mg/100g) DW	Zinc (mg/100g) DW	Mean storage root weight (kg)	Storage Root yield (t/ha)
87X61-37	3.71	39	16.20	70.69	1.57	1.00	0.22	27.32
50X87-8	6.46	41	16.22	70.07	1.58	1.00	-	-
87X50-31	5.74	40	16.23	70.32	1.37	0.89	0.11	12.33
87X61-38	5.65	41	16.35	68.51	1.75	1.02	0.21	24.74
87X82-12	2.96	44	16.51	70.32	1.43	0.91	0.13	16.14
50X61-6	6.06	34	16.52	69.91	1.58	1.03	0.42	18.17
87X82-5	6.91	39	16.61	70.54	1.45	0.89	0.17	24.10
87X50-19	7.52	36	16.62	69.52	1.68	0.88	0.09	11.91
87X50-23	9.04	37	16.66	70.31	1.57	0.88	0.18	18.47
87X50-22	14.70	40	16.69	71.99	1.40	0.82	0.12	9.87
50X61-11	13.78	34	16.73	68.42	1.66	1.04	-	-
50X61-1	4.25	35	16.84	68.88	1.69	1.02	0.23	23.57
61X87-7	1.78	38	16.87	69.23	1.55	0.99	-	-
87X82-8	6.15	40	17.02	68.92	1.62	0.99	0.23	21.99
50X61-34	5.76	36	17.07	69.23	1.36	1.08	0.17	18.08
61X87-15	6.21	42	17.09	69.98	1.56	0.94	0.20	38.79
87X61-39	4.25	40	17.16	67.14	1.75	1.07	-	-
87X50-33	8.24	41	17.25	69.62	1.45	0.89	0.08	5.92
61X50-20	2.93	36	17.31	67.76	1.69	1.10	0.15	16.70
87X82-18	4.90	38	17.44	70.73	1.34	0.80	0.14	14.49
87X61-32	7.82	37	17.47	69.39	1.37	0.96	0.14	31.35
61X50-10	4.12	29	17.53	68.97	1.61	1.03	0.16	22.45
87X82-21	19.55	35	17.62	68.50	1.71	0.90	0.16	17.30
87X50-17	17.18	39	17.63	68.60	1.69	0.95	0.10	10.26
61X50-9	8.64	37	17.66	67.83	1.68	1.05	0.14	28.47
87X50-30	3.32	42	17.78	70.38	1.41	0.93	0.13	12.66
61X82-6	3.55	29	17.85	67.88	1.65	1.01	0.16	22.75
50X61-16	11.20	32	17.94	66.26	1.67	1.07	0.17	24.97
50X61-8	3.06	35	18.01	68.35	1.49	1.03	0.12	17.89
82X87-5	24.98	36	18.03	67.83	1.59	0.89	0.16	22.14
50X61-27	7.14	34	18.14	66.93	1.70	1.03	0.25	22.33
87X50-4	3.66	37	18.17	69.08	1.55	0.96	-	-
61X50-5	2.94	35	18.19	68.74	1.55	0.98	0.14	16.94
87X50-7	15.17	37	18.37	67.94	1.59	0.88	0.16	13.93
50X61-14	3.68	32	18.45	67.67	1.54	1.02	0.16	33.06
50X87-3	3.57	43	18.65	74.05	1.35	0.85	-	-
82X87-13	3.40	35	18.66	67.40	1.86	1.04	0.38	47.90

Appendix 6.1 cont'd. Performance of the four sweetpotato parents and their F_1's

Clone	Beta-carotene (mg/100g) DW	Dry Matter (%)	Total Sugars (%)	Starch (%)	Iron (mg/100g) DW	Zinc (mg/100g) DW	Mean storage root weight (kg)	Storage Root yield (t/ha)
50X61-7	3.48	34	20.11	64.88	1.65	1.03	0.17	41.95
50X61-10	2.84	32	20.24	65.41	1.48	0.99	0.18	18.99
82X50-29	2.20	33	20.36	65.79	1.56	0.94	0.34	38.21
61X82-4	6.37	30	20.50	64.84	2.05	1.29	0.17	38.11
50X61-26	6.66	33	20.64	65.01	1.78	1.15	0.20	34.08
50X87-15	25.65	33	20.66	62.62	1.77	0.99	0.17	24.19
87X82-22	24.61	34	20.78	65.04	1.74	0.88	0.15	18.52
87X50-34	13.99	37	18.81	69.29	1.30	0.90	0.08	6.98
87X50-9	19.03	39	19.04	68.49	1.44	0.82	0.18	15.47
50X61-20	6.95	37	19.15	66.73	1.66	1.06	-	-
50X61-32	2.62	33	19.21	65.74	1.70	1.11	0.04	6.65
61X87-6	6.21	38	19.22	69.68	1.43	0.86	0.21	18.89
82X50-11	13.55	36	19.34	65.97	1.60	0.97	0.18	29.12
87X50-5	19.49	36	19.35	68.59	1.48	0.84	0.10	12.53
61X82-2	2.11	33	19.44	67.30	1.64	1.00	0.16	29.44
61X82-5	3.87	33	19.49	66.28	1.73	1.01	-	-
87X82-3	4.45	40	19.62	68.15	1.51	0.93	0.21	21.71
50X61-23	4.94	33	19.63	66.10	1.68	1.01	-	-
50X87-10	6.66	36	19.67	66.48	1.62	0.94	-	-
50X87-12	7.72	35	19.67	68.20	1.38	0.88	0.23	18.25
87X50-37	7.24	38	19.74	67.72	1.52	0.90	0.06	6.69
82X61-4	2.23	33	19.80	64.71	1.72	1.05	0.17	33.93
50X61-12	3.11	32	19.81	65.82	1.53	1.07	0.18	23.12
50X82-13	16.30	33	19.81	65.90	1.69	0.97	0.13	22.70
50X61-28	7.30	34	20.81	64.33	1.61	1.12	0.17	24.13
61X50-24	4.26	33	20.87	66.19	1.70	1.10	0.16	25.06
87X50-32	16.73	38	20.90	65.86	1.62	0.99	0.06	8.71
61X50-6	6.53	32	21.09	66.43	1.48	0.92	0.13	24.73
61X50-17	19.05	34	21.46	62.88	2.03	1.22	0.16	22.81
BC82	25.64	31	21.51	63.27	2.12	1.13	0.32	37.53
61X50-25	13.15	28	21.61	62.83	2.15	1.19	0.22	16.63
82X61-3	11.42	29	21.78	61.24	2.09	1.21	0.15	33.00
61X50-8	15.10	29	21.81	62.35	1.86	1.07	0.29	25.75
50X61-30	5.13	31	21.87	64.96	1.61	1.06	0.18	20.53
82X87-11	11.47	35	21.93	67.73	1.56	0.87	0.27	30.95
82X50-18	22.30	32	22.04	62.11	1.86	1.07	0.18	17.61
87X50-38	8.74	36	22.23	66.62	1.43	0.87	0.19	4.63
82X61-1	10.34	32	22.27	62.37	1.81	1.05	-	-
61X50-4	11.33	31	22.33	62.82	2.14	1.31	0.10	19.78

Appendix 6.1 cont'd. Performance of the four sweetpotato parents and their F_1's

Clone	Beta-carotene (mg/100g) DW	Dry Matter (%)	Total Sugars (%)	Starch (%)	Iron (mg/100g) DW	Zinc (mg/100g) DW	Mean storage root weight (kg)	Storage Root yield (t/ha)
50X61-7	3.48	34	20.11	64.88	1.65	1.03	0.17	41.95
50X61-10	2.84	32	20.24	65.41	1.48	0.99	0.18	18.99
82X50-29	2.20	33	20.36	65.79	1.56	0.94	0.34	38.21
61X82-4	6.37	30	20.50	64.84	2.05	1.29	0.17	38.11
50X61-26	6.66	33	20.64	65.01	1.78	1.15	0.20	34.08
50X87-15	25.65	33	20.66	62.62	1.77	0.99	0.17	24.19
87X82-22	24.61	34	20.78	65.04	1.74	0.88	0.15	18.52
50X61-28	7.30	34	20.81	64.33	1.61	1.12	0.17	24.13
61X50-24	4.26	33	20.87	66.19	1.70	1.10	0.16	25.06
87X50-32	16.73	38	20.90	65.86	1.62	0.99	0.06	8.71
61X50-6	6.53	32	21.09	66.43	1.48	0.92	0.13	24.73
61X50-17	19.05	34	21.46	62.88	2.03	1.22	0.16	22.81
Beauregard (82)	25.64	31	21.51	63.27	2.12	1.13	0.32	37.53
61X50-25	13.15	28	21.61	62.83	2.15	1.19	0.22	16.63
82X61-3	11.42	29	21.78	61.24	2.09	1.21	0.15	33.00
61X50-8	15.10	29	21.81	62.35	1.86	1.07	0.29	25.75
50X61-30	5.13	31	21.87	64.96	1.61	1.06	0.18	20.53
82X87-11	11.47	35	21.93	67.73	1.56	0.87	0.27	30.95
82X50-18	22.30	32	22.04	62.11	1.86	1.07	0.18	17.61
87X50-38	8.74	36	22.23	66.62	1.43	0.87	0.19	4.63
82X61-1	10.34	32	22.27	62.37	1.81	1.05	-	-
61X50-4	11.33	31	22.33	62.82	2.14	1.31	0.10	19.78
50X61-24	16.31	32	22.43	61.59	1.99	1.16	0.21	27.86
82X50-10	1.38	31	22.48	63.54	1.47	0.91	0.24	29.81
61X50-11	7.66	32	22.60	64.45	1.87	1.28	0.15	22.12
82X87-4	23.00	32	22.78	62.90	1.67	0.91	0.41	29.89
87X50-29	23.91	35	22.83	62.56	1.78	1.00	0.06	7.91
82X50-6	17.78	30	22.94	63.12	1.68	0.89	0.23	26.04
50X61-31	15.23	31	23.08	61.68	1.83	1.05	0.15	14.95
61X50-12	7.10	30	23.15	63.53	1.77	1.03	0.13	18.71
50X87-11	10.90	35	23.51	63.04	1.56	0.94	-	-
50X87-14	18.16	32	23.72	63.47	1.72	0.95	0.21	21.99
87X50-35	20.77	35	23.81	63.13	1.72	1.04	0.07	6.57
82X87-6	14.86	35	24.04	63.28	1.48	0.86	0.18	35.85
50X61-18	25.72	28	24.10	60.75	2.03	1.21	0.13	32.04
82X50-9	4.99	30	24.20	61.99	1.63	0.98	-	-
87X82-7	29.28	33	24.29	63.95	1.48	0.79	0.27	24.12
82X50-15	16.72	30	24.36	61.41	1.81	1.02	0.32	14.78
82X50-8	12.91	26	24.82	60.91	1.76	1.00	0.20	31.79

Appendix 6.1 cont'd. Performance of the four sweetpotato parents and their F_1's

Clone	Beta-carotene (mg/100g) DW	Dry Matter (%)	Total Sugars (%)	Starch (%)	Iron (mg/100g) DW	Zinc (mg/100g) DW	Mean storage root weight (kg)	Storage Root yield (t/ha)
50X87-13	27.18	30	25.00	60.03	1.86	1.02	0.14	21.24
50X82-9	10.33	30	25.26	60.72	1.79	0.99	-	-
82X50-23	33.73	29	25.71	58.81	2.01	1.12	0.16	35.69
61X50-19	18.62	30	26.05	58.83	1.96	1.14	0.16	20.48
82X50-24	2.67	30	26.81	61.26	1.63	0.89	-	-
82X50-3	25.20	29	26.89	58.25	1.94	1.04	0.18	26.99
82X50-30	22.49	30	27.35	58.27	1.90	1.06	0.25	59.57
82X50-7	28.79	29	27.38	58.02	1.88	1.00	-	-
50X61-19	19.32	31	27.39	60.08	1.78	1.00	0.13	17.30
82X61-2	22.20	29	27.57	54.62	2.21	1.32	-	-
87X50-36	28.16	32	27.63	59.42	1.79	1.05	0.09	8.07
50X82-8	9.44	29	27.65	60.44	1.53	0.82	-	-
82X87-3	19.46	29	27.66	59.87	1.73	0.99	0.20	33.44
50X82-2	16.58	28	27.77	55.57	2.03	1.24	-	-
82x50-17	25.47	27	28.85	56.75	1.85	0.96	0.22	26.76
50X82-10	36.05	28	29.53	54.61	1.97	1.05	0.14	25.51
82X50-27	37.58	26	29.72	56.03	1.87	1.07	0.12	29.28
61X50-13	17.07	28	29.74	54.92	2.04	1.17	0.15	26.78
82X87-7	23.20	29	31.80	55.36	1.82	1.07	0.22	32.31
82X50-12	28.08	25	31.84	52.55	2.03	1.07	0.21	36.55
82X87-9	32.49	26	32.67	51.20	2.07	1.09	0.35	22.28
82X50-19	25.97	26	32.80	52.36	1.96	1.13	0.23	26.95
82X50-4	33.47	26	32.88	51.62	2.12	1.26	0.21	35.28
82X50-13	33.62	25	33.32	48.95	2.27	1.23	0.20	26.50
82X50-26	38.76	26	34.29	51.35	1.89	1.02	0.13	14.63
82X50-5	27.23	25	36.19	43.47	2.86	1.71	0.24	14.08
50X82-4	41.71	23	36.35	47.04	2.09	1.20	0.14	22.78
Apomuden 50	37.19	26	36.71	45.44	2.56	1.53	0.13	19.72
50X82-5	39.42	26	37.82	49.86	2.17	1.38	-	-
82X50-16	41.48	21	41.78	42.03	2.43	1.40	0.29	28.83
SE (P<0.05)	3.94	3.00	2.68	3.04	0.16	0.10	0.07	9.36
Mean	11.81	350	20.56	65.54	1.67	1.00	0.18	22.78
CV (%)	41.1	8.7	15.9	5.7	11.1	11.5	47.2	49.8

Appendix 7.1. Performance of the four low sugar sweetpotato parents and their F_1 hybrids

Genotype	Dry Matter (%)	Total Sugars (%)	Starch (%)	Protein (%)	β-carotene (mg/100g) DW	Iron (mg/100g) DW	Zinc (mg/100g) DW	Harvest index	mean root weight (kg)	Total root yield (t/ha)
61X87-11	45	9.01	75.14	3.51	5.66	1.36	0.98	0.30	0.15	16.03
87X61-26	38	9.13	70.22	5.16	6.82	1.82	1.08	-	-	-
87X61-13	45	9.50	76.25	2.97	2.27	1.52	0.92	0.37	0.14	16.53
87X61-21	44	9.94	72.92	3.92	2.72	1.64	1.05	0.22	0.11	12.08
87x61-52	42	10.33	70.45	3.37	8.23	1.65	1.08	-	-	-
87X61-37	43	10.79	72.56	2.85	5.09	1.40	0.98	0.47	0.37	28.26
CIP 442264 (64)	42	10.80	68.27	3.82	6.37	1.77	1.00	0.22	0.14	5.07
87x61-65	45	11.18	74.13	2.89	3.40	1.40	0.94	0.34	0.26	14.94
87x61-87	42	11.72	72.05	3.97	6.46	1.65	1.04	0.21	0.25	7.57
87X61-88	44	11.76	74.27	2.95	3.33	1.37	0.98	0.37	0.16	14.54
87X61-39	43	11.77	72.89	3.00	3.48	1.50	0.88	0.49	0.26	31.61
87X61-16	46	11.80	75.11	3.71	2.20	1.47	0.97	0.40	0.10	15.97
61X87-13	43	11.82	72.79	3.07	1.64	1.52	0.96	0.36	0.20	20.16
87X61-15	43	11.98	70.99	4.50	2.77	1.74	1.17	0.27	0.11	2.80
87x61-86	42	12.07	71.35	3.46	2.69	1.60	0.98	0.23	0.12	5.33
61X87-2	40	12.07	72.54	2.46	4.81	1.46	0.92	0.32	0.13	12.14
87x61-92	45	12.09	73.32	2.77	4.63	1.69	1.03	0.47	0.10	18.75
87x61-68	48	12.13	74.39	3.29	2.44	1.37	0.98	0.32	0.13	14.00
87X61-32	36	12.19	71.91	3.10	5.37	1.43	0.97	0.45	0.21	22.54
87X61-93	45	12.25	72.49	2.82	4.94	1.38	0.93	0.30	0.08	11.03
64X87-3	46	12.25	72.94	3.27	7.90	1.40	0.91	-	-	-
SED (5%)	2	2.28	1.75	0.52	1.92	0.14	0.08	0.1	0.08	6.13
Grand mean	43	13.45	72.64	3.02	4.24	1.45	0.95	0.33	0.17	16.04

Appendix 7.1 cont'd. Performance of the four low sugar sweetpotato parents and their F_1 hybrids

Genotype	Dry Matter (%)	Total Sugars (%)	Starch (%)	Protein (%)	β-carotene (mg/100g) DW	Iron (mg/100g) DW	Zinc (mg/100g) DW	Harvest index	mean root weight (kg)	Total root yield (t/ha)
87X61-76	43	12.38	73.74	3.19	4.91	1.26	0.93	0.52	0.17	11.93
87x61-94	42	12.40	71.08	3.07	3.00	1.49	0.97	0.43	0.12	9.65
87x61-75	42	12.46	72.61	3.41	4.23	1.60	0.98	0.35	0.32	18.67
87x61-69	44	12.47	74.69	2.63	4.40	1.45	0.92	0.38	0.16	17.11
AAT-03-025 (72)	43	12.47	72.32	2.27	2.41	1.31	0.82	0.55	0.27	19.87
87x61-63	47	12.51	73.84	3.38	4.14	1.54	0.95	0.32	0.16	14.83
87X61-56	44	12.53	74.43	2.27	2.54	1.21	0.90	0.41	0.25	15.72
64X87-2	48	12.59	72.96	4.01	4.97	1.69	1.06	0.33	0.07	12.04
87X61-19	45	12.62	73.99	3.09	4.00	1.63	1.05	0.25	0.12	7.76
61X87-18	43	12.64	73.64	2.86	4.70	1.31	0.92	0.34	0.19	11.21
87X61-24	42	12.66	73.13	3.06	3.94	1.43	0.87	0.40	0.35	19.17
87X61-36	41	12.69	73.48	3.17	3.90	1.47	0.98	0.33	0.13	13.13
87X61-40	41	12.69	72.08	2.52	3.88	1.30	0.88	0.38	0.19	25.49
61X87-10	42	12.74	73.72	3.14	1.78	1.42	0.96	0.44	0.19	22.97
61X87-20	44	12.77	73.65	3.29	3.05	1.44	0.95	0.39	0.11	14.33
61X87-19	44	12.77	74.41	3.10	2.52	1.40	0.92	0.28	0.13	15.99
87X61-78	41	12.87	72.85	2.80	3.16	1.40	0.98	0.27	0.27	18.67
87x61-80	45	12.91	74.88	3.19	2.24	1.39	0.93	0.45	0.16	26.33
87X61-3	43	12.94	73.91	3.43	6.83	1.34	0.95	0.39	0.19	26.01
87X61-31	41	12.96	70.97	1.99	2.96	1.28	0.91	0.23	0.12	14.02
87X61-50	41	13.01	74.10	2.77	4.24	1.27	0.94	0.45	0.20	16.64
SED (5%)	2	2.28	1.75	0.52	1.92	0.14	0.08	0.1	0.08	6.13
Grand mean	43	13.45	72.64	3.02	4.24	1.45	0.95	0.33	0.17	16.04

Appendix 7.1 cont'd. Performance of the four low sugar sweetpotato parents and their F_1 hybrids

Genotype	Dry Matter (%)	Total Sugars (%)	Starch (%)	Protein (%)	β-carotene (mg/100g) DW	Iron (mg/100g) DW	Zinc (mg/100g) DW	Harvest index	mean root weight (kg)	Total root yield (t/ha)
61X87-14	44	13.03	74.36	2.48	2.87	1.38	0.88	0.34	0.12	14.79
61X87-9	43	13.04	72.90	3.24	4.63	1.46	0.93	0.31	0.12	12.86
87X61-8	45	13.16	74.18	2.85	6.12	1.43	0.98	0.22	0.06	8.92
87x61-64	44	13.20	73.93	3.27	2.79	1.38	0.92	0.34	0.18	23.53
87X61-28	42	13.28	73.91	2.46	5.05	1.39	0.91	0.19	0.09	12.53
87x61-71	43	13.44	72.93	4.25	3.82	1.63	1.09	0.28	0.12	13.03
61X87-7	42	13.49	73.32	3.05	5.10	1.34	0.90	0.29	0.24	13.53
87X61-41	44	13.50	74.19	2.54	3.19	1.34	0.92	0.30	0.13	18.72
61X87-3	41	13.58	73.50	2.57	2.53	1.34	0.85	0.38	0.25	26.33
Ogyefo (61)	41	13.62	72.92	2.86	3.75	1.481	0.94	0.17	0.22	13.61
87X61-38	43	13.62	72.29	3.83	4.11	1.53	0.97	0.36	0.30	27.17
87X61-58	42	13.70	72.91	3.14	5.74	1.42	0.97	0.47	0.28	36.31
87x61-49	42	13.73	70.04	2.59	3.69	1.42	0.96	0.10	0.17	6.96
87X61-1	44	13.85	74.79	2.73	3.22	1.45	0.83	0.27	0.16	11.46
87X61-29	43	13.95	74.74	2.68	3.27	1.45	0.88	0.31	0.18	22.58
87X61-45	45	14.03	74.63	2.52	4.44	1.45	0.88	0.25	0.12	11.41
87X61-67	40	14.09	72.58	2.26	2.83	1.37	0.90	0.34	0.16	13.68
87X61-66	42	14.09	72.12	3.03	3.29	1.43	0.93	0.32	0.19	16.80
87X61-6	43	14.10	72.49	2.61	4.21	1.38	0.94	0.34	0.15	24.25
87X64-2	48	14.14	72.59	3.33	7.00	1.72	0.97	0.26	0.12	15.93
87X61-4	41	14.16	72.22	3.10	3.60	1.48	0.95	0.35	0.22	22.68
SED (5%)	2	2.28	1.75	0.52	1.92	0.14	0.08	0.1	0.08	6.13
Grand mean	43	13.45	72.64	3.02	4.24	1.45	0.95	0.33	0.17	16.04

Appendix 7.1 cont'd. Performance of the four low sugar sweetpotato parents and their F_1 hybrids

Genotype	Dry Matter (%)	Total Sugars (%)	Starch (%)	Protein (%)	β-carotene (mg/100g) DW	Iron (mg/100g) DW	Zinc (mg/100g) DW	Harvest index	mean root weight (kg)	Total root yield (t/ha)
87x61-74	44	14.18	72.78	3.61	4.39	1.62	1.06	0.39	0.15	13.42
87X61-82	41	14.23	73.11	2.24	3.37	1.33	0.90	0.21	0.07	8.81
87X61-62	45	14.26	74.12	2.70	3.12	1.32	0.88	0.29	0.12	15.61
64X87-1	48	14.29	72.06	3.93	5.96	1.79	1.02	0.22	0.10	13.31
87X61-73	39	14.34	72.20	2.84	4.62	1.30	0.92	0.39	0.17	20.44
87X61-27	40	14.38	72.05	3.15	6.05	1.46	0.98	0.45	0.24	30.88
87X61-53	40	14.39	72.94	2.48	1.63	1.26	0.88	0.30	0.20	10.83
87x61-44	41	14.42	71.75	2.52	3.48	1.37	0.94	0.20	0.49	13.69
61X87-17	42	14.44	71.14	2.74	5.77	1.38	0.92	0.38	0.21	10.14
87x61-70	42	14.46	72.26	3.24	7.16	1.51	1.03	0.21	0.09	9.54
87X61-30	41	14.51	72.51	2.44	2.74	1.30	0.85	0.33	0.16	22.36
61X87-8	42	14.56	72.31	3.65	2.64	1.52	0.96	0.23	0.21	13.64
87X61-72	40	14.70	70.38	3.06	4.04	1.49	0.97	0.29	0.10	11.13
61X87-16	41	14.86	71.84	2.51	4.70	1.50	0.91	0.31	0.16	11.68
61X87-1	42	14.90	72.56	2.84	3.67	1.39	0.84	0.38	0.17	28.96
87X61-51	43	14.91	73.83	2.86	3.85	1.51	0.94	0.37	0.15	20.47
87X61-54	40	14.93	72.71	2.51	2.73	1.41	0.95	0.42	0.17	16.95
87X61-83	41	14.98	69.97	2.41	8.16	1.46	0.94	0.33	0.14	20.88
87X61-89	43	15.02	72.04	2.86	2.01	1.36	0.93	0.41	0.15	15.09
87X61-23	43	15.19	72.50	3.41	6.83	1.50	0.95	0.37	0.21	15.50
87X61-20	42	15.32	72.38	3.40	6.44	1.35	0.96	0.41	0.19	15.22
SED (5%)	2	2.28	1.75	0.52	1.92	0.14	0.08	0.1	0.08	6.13
Grand mean	43	13.45	72.64	3.02	4.24	1.45	0.95	0.33	0.17	16.04

Appendix 7.1 cont'd. Performance of the four low sugar sweetpotato parents and their F_1 hybrids

Genotype	Dry Matter (%)	Total Sugars (%)	Starch (%)	Protein (%)	β-carotene (mg/100g) DW	Iron (mg/100g) DW	Zinc (mg/100g) DW	Harvest index	mean root weight (kg)	Total root yield (t/ha)
61X87-15	42	15.33	71.75	2.55	4.86	1.38	0.89	0.28	0.09	8.21
87X64-1	46	15.44	69.74	3.78	7.44	1.65	1.09	0.29	0.13	13.57
61X87-6	39	15.63	68.34	2.56	4.45	1.46	0.92	0.21	0.10	9.64
87X61-77	38	15.64	72.20	3.59	5.49	1.35	1.00	0.33	0.30	21.97
87x61-42	41	15.95	70.54	2.22	3.90	1.30	0.85	0.23	0.16	11.53
87X72-2	40	16.16	70.36	2.72	5.59	1.47	0.85	0.23	0.22	6.89
61X87-4	40	16.26	72.23	2.51	3.17	1.43	0.86	0.39	0.18	22.47
87X61-47	40	16.29	71.37	2.77	3.92	1.42	0.93	0.38	0.18	19.17
Histarch (87)	46	16.33	72.82	2.68	4.74	1.56	0.87	0.26	0.20	20.71
87X72-1	43	16.90	71.25	2.96	7.31	1.43	0.96	0.36	0.26	17.36
87X61-46	40	17.18	70.30	2.31	6.43	1.32	0.88	0.13	0.11	3.56
87x61-57	39	17.53	69.78	3.15	2.56	1.48	1.00	0.32	0.18	20.19
SED (5%)	2	2.28	1.75	0.52	1.92	0.14	0.08	0.1	0.08	6.13
Grand mean	43	13.45	72.64	3.02	4.24	1.45	0.95	0.33	0.17	16.04
Range	36 - 48	9.01 - 17.53	68.27 - 76.25	1.99 - 5.16	1.63 - 8.23	1.21 - 1.82	0.82 - 1.17	nil - 0.55	nil - 0.49	nil - 36.31
CV (%)	6.3	20.7	2.9	20	55.3	12	9.3	35.60	59.2	46.90

Appendix 7.2. Performance of the five high beta-carotene sweetpotato parents and their F_1 hybrids

Genotype	β-carotene (mg/100g) DW	Dry matter (%)	Total sugars (%)	Starch (%)	Protein (%)	Iron (mg/100g) DW	Zinc (mg/100g) DW	Harvest index	Mean root weight (Kg)	Total root yield (t/ha)
82X50-13	44.05	23	41.32	43.38	3.20	2.17	1.23	0.63	0.16	38.41
50X79-4	42.50	25	36.93	47.36	4.05	2.47	1.57	0.51	0.09	22.37
50X82-1	41.91	22	34.33	40.37	6.07	2.81	1.77	0.47	0.11	19.00
82X50-27	41.66	25	39.21	50.51	3.03	2.01	1.16	0.68	0.16	48.35
50X82-4	41.00	24	44.75	43.63	2.72	2.08	1.21	0.46	0.18	18.00
Apomuden (50)	40.67	28	31.63	49.35	4.06	2.30	1.52	0.63	0.16	34.00
50X109-3	40.00	23	41.56	42.53	2.91	2.07	1.17	0.52	0.15	31.20
50X82-12	39.65	28	34.21	48.81	4.11	2.50	1.57	0.52	0.10	19.22
82X50-14	39.10	22	32.66	46.53	2.68	1.99	1.09	0.72	0.27	69.52
82X50-4	38.70	25	38.45	47.05	3.43	2.23	1.38	0.61	0.35	44.11
82X50-17	37.92	24	30.95	51.06	3.13	2.06	1.12	0.65	0.18	42.52
79X50-13	36.70	27	39.03	47.49	3.54	2.12	1.29	0.54	0.11	27.07
50X82-11	36.62	27	34.57	54.57	3.24	1.96	1.16	0.46	0.11	26.68
82X50-22	36.39	28	31.10	56.06	3.44	1.98	1.11	0.46	0.12	24.44
50X109-9	36.19	23	39.00	44.87	3.38	2.33	1.45	0.39	0.13	33.11
82X50-26	35.36	26	31.80	53.41	3.00	1.86	1.00	0.72	0.13	52.55
50X109-12	34.86	24	39.62	45.47	2.56	2.06	1.25	0.39	0.15	24.74
50X82-5	34.81	25	36.82	45.40	3.25	2.11	1.29	0.56	0.16	47.11
50X109-1	34.45	24	39.48	48.17	2.60	1.92	1.02	0.63	0.19	47.26
79X50-14	34.43	27	31.73	51.02	3.72	2.17	1.36	0.46	0.22	9.44
50X109-13	33.57	24	35.19	51.51	3.41	2.20	1.37	0.42	0.14	18.52
SED (5%)	8.18	3.00	4.05	4.65	0.57	0.20	0.14	0.08	0.06	8.14
CV (%)	42.2	12.5	17.2	10.3	22.0	12.9	15.3	17.9	48.6	31.6

Appendix 7.2 cont'd. Performance of the five high beta-carotene sweetpotato parents and their F_1 hybrids

Genotype	β-carotene (mg/100g)DW	Dry matter (%)	Total sugars (%)	Starch (%)	Protein (%)	Iron (mg/100g) DW	Zinc (mg/100g) DW	Harvest index	Mean root weight (Kg)	Total root yield (t/ha)
21X50-2	33.17	29	32.96	55.62	2.98	1.95	1.08	0.52	0.13	34.41
79X50-10	33.07	31	37.61	48.92	3.52	2.32	1.47	0.53	0.08	35.89
82X50-3	32.37	27	33.06	53.26	2.83	1.96	1.10	0.53	0.13	24.63
82X50-16	31.90	24	33.90	48.30	3.18	2.07	1.26	0.56	0.11	47.30
50X21-1	31.18	26	42.50	47.16	3.20	2.13	1.30	0.60	0.13	36.67
50X79-2	31.01	30	27.99	57.98	3.64	2.09	1.22	0.64	0.16	29.89
79X50-1	30.96	28	32.32	54.30	3.21	1.93	1.19	0.50	0.16	32.26
109X82-4	30.76	27	32.10	53.06	2.92	1.89	1.02	0.71	0.18	34.28
50X109-7	30.24	22	41.25	40.68	2.66	2.18	1.35	0.44	0.10	27.22
50X109-8	30.15	23	38.07	44.05	3.53	2.42	1.55	0.35	0.15	28.48
82X109	29.82	25	33.36	53.47	2.76	1.90	0.97	0.52	0.19	31.59
50X109-4	29.19	22	30.74	48.71	2.52	1.97	1.10	0.50	0.16	26.50
82X79-4	28.95	27	29.74	57.44	2.59	1.77	1.00	0.46	0.11	18.28
79X82-2	28.85	31	23.42	60.88	2.60	1.81	1.01	0.42	0.12	28.64
82X50-5	28.84	25	34.04	46.30	4.29	2.41	1.47	0.46	0.07	18.74
82X50-24	28.63	28	31.75	54.65	3.24	1.87	1.06	0.76	0.16	35.11
79X50-4	28.39	31	22.30	60.16	3.23	1.93	1.13	0.48	0.10	32.44
79X82-4	28.35	30	23.34	61.39	2.64	1.81	0.98	0.57	0.20	30.04
50X109-5	28.28	23	46.34	39.05	2.63	2.18	1.31	0.44	0.17	23.37
50X82-6	28.17	26	33.56	54.27	3.03	1.92	1.04	0.70	0.17	37.97
50X82-10	27.97	28	37.28	52.30	3.14	1.92	1.11	0.58	0.18	30.00
Resisto (21)	27.53	38	18.53	65.43	5.62	2.34	1.22	0.50	0.12	3.25
SED (5%)	8.18	3.00	4.05	4.65	0.57	0.20	0.14	0.08	0.06	8.14
CV (%)	42.2	12.5	17.2	10.3	22.0	12.9	15.3	17.9	48.6	31.6

Appendix 7.2 cont'd. Performance of the five high beta-carotene sweetpotato parents and their F_1 hybrids

Genotype	β-carotene (mg/100g)DW	Dry matter (%)	Total sugars (%)	Starch (%)	Protein (%)	Iron (mg/100g) DW	Zinc (mg/100g) DW	Harvest index	Mean root weight (Kg)	Total root yield (t/ha)
79X21-2	26.88	36	22.07	66.05	2.65	1.63	0.96	0.48	0.11	19.11
79X82-3	26.63	31	22.53	62.34	2.92	1.73	0.96	0.51	0.18	30.70
82X50-12	26.42	25	27.80	56.03	3.05	1.80	0.96	0.66	0.18	35.09
79X109-1	26.33	28	31.37	53.60	4.27	2.12	1.17	0.63	0.09	23.31
82X50-7	26.29	29	24.85	59.99	2.84	1.71	0.97	0.63	0.11	33.11
Beauregard (82)	26.24	30	26.49	59.87	3.99	2.03	1.11	0.49	0.26	26.59
82X50-18	25.92	27	32.27	58.74	4.01	1.97	1.13	0.65	0.23	30.11
82X79-1	25.38	30	20.32	59.66	3.12	1.81	1.09	0.45	0.15	30.94
82X50-28	24.72	28	31.22	55.60	3.44	1.90	1.17	0.69	0.13	50.02
CIP 442850 (109)	24.12	25	38.22	49.41	3.17	2.04	1.20	0.66	0.40	35.33
82X50-19	23.23	31	25.34	57.78	2.87	1.80	1.09	0.61	0.11	24.09
CIP 443035 (79)	22.66	30	24.39	58.91	3.44	2.00	1.17	0.62	0.15	3.56
79X50-6	22.63	35	20.82	63.60	3.20	1.89	1.12	0.59	0.22	26.41
50X82-7	22.37	34	30.27	55.20	2.90	2.00	1.06	0.32	0.10	12.74
79X50-2	22.09	30	21.06	59.86	2.98	1.82	1.12	0.49	0.14	18.50
82X50-20	22.08	31	28.76	61.00	3.03	1.74	1.04	0.55	0.23	37.28
79X50-12	21.87	31	33.88	57.93	2.81	1.70	0.99	0.51	0.18	30.11
82X50-23	21.87	27	30.45	57.19	3.66	1.94	1.13	0.66	0.16	40.06
79X50-5	21.84	33	24.21	61.01	3.30	1.97	1.14	0.48	0.15	32.15
79X82-8	21.73	29	23.85	60.13	3.28	1.89	1.14	0.51	0.15	27.45
79X109-3	21.66	30	25.36	57.10	3.40	2.09	1.17	0.52	0.11	26.07
82X50-30	21.54	29	27.68	57.89	3.10	1.83	1.04	0.55	0.18	23.67
SED (5%)	8.18	3.00	4.05	4.65	0.57	0.20	0.14	0.08	0.06	8.14
CV (%)	42.2	12.5	17.2	10.3	22.0	12.9	15.3	17.9	48.6	31.6

Appendix 7.2 cont'd. Performance of the five high beta-carotene sweetpotato parents and their F_1 hybrids

Genotype	β-carotene (mg/100g)DW	Dry matter (%)	Total sugars (%)	Starch (%)	Protein (%)	Iron (mg/100g) DW	Zinc (mg/100g) DW	Harvest index	Mean root weight (Kg)	Total root yield (t/ha)
21X50-1	21.18	32	22.45	62.45	3.07	1.94	1.17	0.51	0.20	35.89
82X50-6	20.94	29	33.22	57.62	3.20	1.96	1.13	0.55	0.11	41.48
82X50-21	20.32	31	22.69	62.08	2.81	1.69	0.98	0.56	0.16	38.44
82X50-15	19.97	28	37.45	56.78	2.91	1.77	1.01	0.64	0.26	56.15
79X109-2	19.95	31	33.45	51.64	4.32	2.24	1.27	0.26	0.08	13.00
82X50-29	18.21	27	30.45	57.72	3.42	1.91	1.13	0.54	0.12	22.17
109X82-3	17.99	25	29.96	57.73	2.47	1.77	0.90	0.65	0.17	27.00
79X50-9	17.55	36	22.65	63.68	3.39	1.78	1.08	0.56	0.12	17.07
79X21-1	17.38	36	16.43	66.81	3.18	1.81	1.09	0.49	0.11	37.60
50X109-14	17.13	29	28.10	58.25	2.23	1.71	0.97	0.52	0.19	45.17
109X50-2	16.84	33	24.72	59.52	3.53	1.93	1.15	0.53	0.18	39.50
50X82-13	16.71	32	25.98	61.12	2.84	1.81	0.99	0.46	0.20	25.55
82X50-2	16.39	28	27.96	58.06	2.75	1.75	1.03	0.57	0.14	33.00
79X50-8	16.37	38	18.09	65.60	3.74	1.86	1.14	0.67	0.14	42.09
82X50-32	16.37	33	31.97	60.28	2.38	1.63	0.94	0.56	0.26	43.26
79X82-5	15.50	33	19.92	64.89	2.98	1.65	0.99	0.48	0.13	21.00
79X82-10	14.76	32	22.83	62.00	3.15	1.71	1.01	0.45	0.17	17.71
79X82-9	14.21	32	27.12	62.32	2.12	1.48	0.83	0.35	0.11	18.22
79X50-3	14.16	32	21.87	65.58	2.85	1.77	1.05	0.44	0.12	31.00
50X82-9	12.96	28	30.92	58.60	3.16	1.86	0.99	0.56	0.15	31.96
79X50-7	12.68	38	26.56	66.49	3.32	1.59	0.92	0.52	0.15	29.07
79X82-6	12.44	34	20.34	63.78	2.92	1.67	0.97	0.42	0.12	19.96
SED (5%)	8.18	3.00	4.05	4.65	0.57	0.20	0.14	0.08	0.06	8.14
CV (%)	42.2	12.5	17.2	10.3	22.0	12.9	15.3	17.9	48.6	31.6

Appendix 7.2 cont'd. Performance of the five high beta-carotene sweetpotato parents and their F_1 hybrids

Genotype	β-carotene (mg/100g)DW	Dry matter (%)	Total sugars (%)	Starch (%)	Protein (%)	Iron (mg/100g) DW	Zinc (mg/100g) DW	Harvest index	Mean root weight (Kg)	Total root yield (t/ha)
79X82-7	12.36	34	21.64	65.26	3.28	1.67	0.98	0.49	0.12	21.78
50X82-8	11.65	23	28.11	57.90	1.89	1.51	0.79	0.47	0.19	34.07
82X50-9	11.06	32	23.73	64.48	2.40	1.57	0.85	0.59	0.21	41.19
82X50-11	10.62	32	27.83	63.56	2.51	1.50	0.88	0.48	0.07	27.49
50X109-11	10.15	35	23.25	66.06	1.96	1.54	0.95	0.46	0.19	30.30
109X50-1	10.06	27	29.22	58.48	2.63	1.76	0.94	0.61	0.21	45.65
82X50-8	10.00	29	26.38	61.79	2.90	1.61	0.90	0.67	0.20	43.94
109X82-2	9.45	31	20.26	64.58	2.09	1.62	0.87	0.56	0.18	34.19
82X50-1	8.89	28	28.05	59.79	3.20	1.82	1.06	0.60	0.13	35.66
82X50-10	8.26	29	25.21	60.20	2.71	1.61	0.97	0.62	0.14	41.09
82X79-3	7.70	33	22.30	64.67	2.97	1.52	0.94	0.48	0.16	21.13
79x82-1	7.24	35	19.74	68.96	2.54	1.34	0.78	0.52	0.13	19.52
50X21-5	6.32	33	17.44	63.35	3.42	1.84	1.11	0.52	0.36	31.85
109X82-1	5.42	28	18.40	67.68	2.34	1.59	0.86	0.46	0.13	26.89
82X79-2	3.90	32	18.32	66.68	2.70	1.51	0.95	0.50	0.13	20.78
50X21-4	2.72	32	19.42	66.16	3.22	1.65	1.08	0.67	0.12	19.70
SED (5%)	8.18	3.00	4.05	4.65	0.57	0.20	0.14	0.08	0.06	8.14
Grand mean	24.13	29	29.41	56.39	3.11	1.90	1.11	0.54	0.16	30.67
Range	2.72 - 44.05	22 - 38	16.43 – 46.34	39.05 – 68.96	1.89 - 6.07	1.34 – 2.81	0.78 - 1.77	0.26 - 0.76	0.07 - 0.40	3.65 - 69.52
CV (%)	42.2	12.5	17.2	10.3	22.0	12.9	15.3	17.9	48.6	31.6