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# GENETIC CONTROL OF SUGARS, DRY MATTER AND BETA-CAROTENE IN SWEETPOTATO (*Ipomoea batatas* [L.] Lam)

**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

Sweetpotato has immense potential for food and nutrition security in Ghana. It is however, infrequently used in local cuisines. Breeders have attributed this low utilization to the fact that sweetpotato lacks quality characteristics that make it amenable to local food preparation. The present study was carried out to develop varieties that combine high dry matter, low sugar and high β-carotene traits, to meet the needs of Ghanaian consumers. A Participatory Rural Appraisal (PRA) and a survey were conducted to assess farmers' production constraints and quality characteristics that would enhance utilization of sweetpotato. Subsequently, 130 accessions were assembled and evaluated to assess variation and identify parental genotypes. Ten of these clones with good yield potential and desirable quality attributes were evaluated with a local check variety in four environments to assess genotype x environment interaction effect on expression of the quality traits under study. Eleven parental genotypes were identified as cross compatible and were used in a North Carolina mating design II for development of populations and to estimate genetic parameters for the desired traits. The production constraints listed by farmers during the PRA included, drought, pests and diseases, labour cost, declining soil fertility, low utilization, cost of vines, low market prices and lack of ready markets. Drought was ranked highest among the constraints. Farmer preferred quality attributes included low-sugar, high dry matter, and poundable varieties, with 70% of respondents indicating that the high sugar levels is a limiting factor to regular usage. The PRA also revealed farmers' willingness to use orange-fleshed sweetpotato with the desired quality attributes. A high diversity index of 0.85 was obtained for morphological traits using Rogers Tanimoto index while an index of 7.41 was obtained for quality traits using mean Euclidean dissimilarity index, indicating the presence of high diversity among the 130 genotypes. The G x E study revealed that genotype and

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environmental main effects and their interactions were significant for most traits. Regarding yield traits, G x E was more important while genotype main effects were more important than G x E for quality traits. The AMMI biplot and regression analysis revealed stable and specific adaptation for yield, dry matter, sugars, and β-carotene. Low broad sense heritability ($H^2$) of 27% was recorded for yield but high estimates between 70% and 86% were obtained for quality traits. Narrow sense heritability ($h^2$) estimates for yield was 27% and 51% using parent-offspring analysis and variance components respectively. Parent-offspring regression gave moderate estimates of 0.38, 0.40, 0.39, 0.24 and 0.36 respectively, for dry matter, starch, fructose maltose and total sugars respectively while relatively high estimates of 0.56, 0.53, 0.45, 0.59, and 0.48 respectively were obtained with variance component method. Very high $h^2$ estimate of 0.80 was observed for β-carotene using variance method, while a moderate estimate of 0.40 was obtained using regression of offspring values on mid-parent values. The moderate $h^2$ estimates for yield was associated with a moderate genetic advance implying that progress can be made through selection. With the exception of dry matter, starch sucrose and glucose were associated with low $h^2$ and low genetic advance. All other quality traits including total sugars and β-carotene, had moderate to high $h^2$ that also associated with moderate genetic advance indicating that progress could be made through selection. General combining ability (GCA) for males and females were highly significant ($P < 0.001$) for most agronomic and quality traits. The presence of more significant GCA than Specific Combining Ability (SCA) effects and the substantially greater GCA than SCA ($\sigma_{gca}^2 / \sigma_{sca}^2$; between 2.7 – 21.8) confirm the preponderance of additive over non-additive gene action in the expression of the traits. Twenty-eight $F_1$ clones with desired characteristics have been selected for further evaluation.

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## DEDICATION

**To God be the glory for His mercies and protection throughout my studies. To my husband Patrick and daughter Abby, for their support, understanding and sacrifice, without which I would have lacked the strength to continue. To my beloved late father whose tireless efforts and encouragement spurred me on. To my mother, a pillar of strength and a friend. Thank you all so much.**

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# LIST OF ABBREVIATIONS

| | |
|---|---|
| **AMMI** | Additive Main effect and Multiplicative Interactions |
| **BC** | β-carotene |
| **CIP** | International Potato Center |
| **Comyld** | Commercial root yield |
| **CV** | Coefficient of Variation |
| **BNARI** | Biotechnology and Nuclear Agriculture Institute |
| **DM** | Dry Matter |
| **F1** | First filial generation |
| **FAO** | Food and Agriculture Organization of United Nations |
| **FAOSTAT** | Food and Agriculture Organization of United Nations, Statistics Department |
| **GAEC** | Ghana Atomic Energy Commission |
| GCA | General Combining Ability |
| **GPS** | Global Positioning System |
| **GxE** | Genotype by Environment Interaction |
| **$H^2$** | Broad sense heritability |
| **$h^2$** | Narrow sense heritability |
| **ha** | Hectare |
| **HI** | Harvest Index |
| **HPLC** | High Performance Liquid Chromatography |
| **IITA** | International Institute for Tropical Agriculture |
| **IRWT** | Individual root weight |
| NIRS | Near Infrared Spectrophotometer |

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| | |
|---|---|
| **NOCR** | Number of commercial roots |
| **N:P:K** | Nitrogen – Phosphorous – Potassium |
| **OFSP** | Orange-Fleshed Sweetpotato |
| **PCA** | Principal Component Analysis |
| **PPB** | Participatory Plant Breeding |
| **PRA** | Participatory Rural Appraisal |
| **PVS** | Participatory Varietal Selection |
| **QTL** | Quantitative Trait Loci |
| **REML** | Restricted (or Residual) Maximum Likelihood |
| **RY** | Root Yield |
| **SSA** | Sub-Saharan Africa |
| **SCA** | Specific Combining Ability |
| **UPGMA** | Unweighted Pair Group Method using arithmetic Average |
| **WED** | Weevil damage |

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# CHAPTER ONE

## 1.0 GENERAL INTRODUCTION

Sweetpotato (*Ipomoea batatas* (L.) Lam.) is the seventh most important food crop in the world (FAOSTAT, 2012). In developing countries it ranks fifth in terms of economic value of production (Thottappilly and Loebenstein, 2009). Among the tropical root crops it is the second most important after cassava (Srinivas, 2009; FAOSTAT, 2012). In sub-Saharan Africa, where the crop is grown on some 13.37 million hectares of land (FAOSTAT, 2012), it is the third most important root crop after cassava (*Manihot esculenta* Crantz) and yam (*Dioscorea* spp.).

Sweetpotato is mainly grown in developing countries where over 95 % of the world's production occurs (Loebenstein, 2009). Asia is the world's largest producing region while China, being the largest producing country, (FAOSTAT, 2012) accounts for over 70 % of the world's production (Loebenstein, 2009). Most of the crop produced in China (70 %) and other parts of Asia are used to feed animals, particularly pigs. Sweetpotato therefore plays an important role in many rural economies in Asia (Loebenstein, 2009).

Africa produces about 15 % of the world's sweetpotato (Loebenstein, 2009). The largest producer in Africa is Tanzania, followed closely by Nigeria with production figures of about 3.6 and 3.3 million tons respectively (FAOSTAT, 2011). Unlike Asia where most of the crop is used in the animal industry, the crop is a major staple in countries surrounding the Great Lakes in Eastern and Central Africa; Malawi, Angola, Mozambique, Uganda, and Madagascar in Southern Africa, and Nigeria in West Africa. In Ghana and parts of West Africa it is referred to

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as a secondary crop because it complements the major root crops - cassava and yam (Akoroda, 2009)

Sweetpotato has many positive attributes. It produces more carbohydrate per unit area per unit time than other root crops, has short production cycle, grows well in many agroecologies, requires low inputs, and is fairly tolerant to production stresses such as high temperature, water deficits, insects, diseases and low soil fertility (Woolfe, 1992). Nutritionally, its high levels of proteins, minerals and dietary fibre, make it superior to most staples (Woofe, 1992; Jaarsveld *et al., 2005;* Low *et al.*, 2007). The orange-fleshed varieties are rich in provitamin A. It is reported that regular intake of one hundred grams of orange-fleshed varieties containing about 3 mg/100 g β-carotene on a fresh weight basis is adequate to meet the recommended daily allowance of vitamin A, and prevent vitamin A deficiency in pregnant mothers, and also prevent blindness in children (Woofe, 1992; Low *et al.*, 2007; Mcharo and La Bonte, 2007). Sweetpotato is also a good source of dietary fiber and provides a feeling of satiation that helps to control food intake and promote a healthy digestive tract. Thus, consumption of sweetpotato helps to lower the risk of constipation, diverticulosis, colon and rectal cancer and obesity (Willcox *et al.*, 2009). The orange and purple-fleshed varieties are known to have antioxidant properties which give protection from the formation of free radicals and therefore, prevent cancers (Willcox *et al.*, 2009). Sweetpotato is known to have low glycemic index, in that, the slow rate of digestion of its complex carbohydrate, lowers the rate of absorption of sugars into the blood stream. It is therefore, a suitable source of food for the diabetics (Willcox *et al.*, 2009).

Sweetpotato has many industrial applications (Lin *et al.*, 2007). It is an industrial source of starch and alcohol (Rahman *et al.*, 2003), yielding 30–50 % more starch than rice, corn and wheat sources measured under the same conditions (Wang, 1984). Its high grade starch is suitable for

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food and pharmaceutical industries, and has been used in textile, paper, cosmetics, insulating and adhesive industries (Rahman *et al.*, 2003; Veeraragavathatham *et al.*, 2007) and has great potential for biofuel production (Mays *et al.*, 1990).

Sweetpotato has a long history as a lifesaver and a food security crop. In Japan it saved lives after the second world war, and when typhoons demolished rice fields (Anonymous, 2000), millions were kept from starvation in famine-plagued China in the early 1960s and Rwanda in 1999 (Jayasinghe *et al.*, 2003). In Uganda, rural communities depended on sweetpotato when cassava crops were devastated by virus in the 1990s (Taylor, 2007). Sweetpotato therefore, has immense potential and has a major role to play in human nutrition, health, food security, industry, and poverty alleviation.

In Ghana, sweetpotato is particularly important in the Northern and Coastal belts where it is both food and cash crop (Otoo *et al.*, 2000; Otoo *et al.*, 2001; MOFA-SRID, 2012). It is produced mostly by subsistence farmers on small acreages without inputs such as fertilizer. It is the third most important root and tuber crop after cassava and yam. Yields in Ghana are, however, very low hovering around 2.0 tons/ha (FAOSTAT, 2012). Production levels are also low compared to countries like Burkina Faso (Some, 2013) and Nigeria (Tewe *et al.*, 2003; FAOSTAT, 2012) in the sub region and has more or less stagnated over a decade (Appendix 1) with annual average production figures of about 117,000 tons (FAOSTAT, 2012).

A number of factors are responsible for this trend in production. Among these are abiotic and biotic constraints such as viral infection, weevil infestation, lack of quality planting materials and lack of improved cultivars with high and stable yields. In addition to these common constraints to sweetpotato production worldwide, sweetpotato production in Ghana is further limited by the lack of diversified usage and infrequent utilization in traditional food preparations (Sam and

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Dapaah, 2009). Low utilization decreases demand which in turn constrains production. Another factor responsible for both low production levels and utilization is the relatively low level of investment in sweetpotato research as compared to major staples like cassava or yam.

### 1.1 Justification of research

Sweetpotato has been cultivated in Ghana for many years; however until recent efforts at the Crops Research Institute (CRI) to develop breeding populations, research into its improvement had remained at its infancy (Otoo *et al.*, 2001; Akoroda, 2009). As a result current varieties are unable to meet the varietal needs of farmers and consumers. Utilization of the crop is thus very low, when compared to cassava, yam and cocoyam, which have been the principal root and tuber crops over the years. When compared to sweetpotato, these starchy staples are non-sweet, high in dry matter, and mealy. These quality attributes make them very suitable for use in many local cuisines. Sweetpotato varieties in Ghana are, however, deficient in these quality traits that make a starchy staple amenable to local cuisines. As such, while cassava for example, is used in about thirteen different local preparations, sweetpotato is prepared in only three ways (fried, boiled or roasted), principally as snack. It is hypothesized among breeders that low utilization is due to the sweetness of the crop (Sam and Dapaah, 2009).

Indeed, most staples of the world such as rice, wheat, maize, Irish potatoes, cassava and yam are non-sweet. Sugar content of most staples have been described as low, example, rice and Irish potato have 1 % and 2 % sugar compared to sweetpotato with 8 – 40 % sugar (Villareal, 1982). Even though sweetpotato is consumed as a staple in many countries it is thus rarely preferred (Kay *et al.*, 1999; Kays *et al.*, 2005). The sweetness in sweetpotato is mainly due to presence of sugars in raw roots and high levels of maltose formation during cooking. High sugar content in

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sweetpotato intensifies flavor impact (Kays *et al.*, 1999; Kays, 2006), making frequent consumption overly tiresome and limits usage as a staple in places where non-sweet staples are preferred. Low-sugar cultivars have the potential to increase the acceptability of sweetpotato as a staple and improve utilization in Ghana. The evidence gathered through a survey of sweetpotato germplasm worldwide indicates that there is sufficient variation in sweetpotato flavors (sugars and aroma), to allow significant increases or decreases in sweetness (Kays, 2005; Kays *et al.*, 2005a). Exotic varieties low in sugars could be evaluated and exploited through breeding to reduce sugar levels in locally adapted varieties. However, information on Ghanaian germplasm diversity as well as farmer production constraints and preferences is limiting and must be assessed to obtain a more holistic approach towards improvement of the crop.

Apart from sugars, dry matter content is another determinant of consumer acceptability of sweetpotato in Ghana (Sam and Dapaah, 2009). Large genetic variation and high heritability have been reported for dry matter (Zhang *et al.*, 2004; Tsegaye *et al.*, 2007; Lebot, 2008; Tumwegamire, 2011). Rapid genetic gain can therefore be made when selecting for dry matter.

Ghana is among the countries in Sub-Saharan Africa where vitamin A deficiency is a serious health concern (Akoroda, 2009). Orange-fleshed sweetpotato (OFSP) varieties that have high levels of β-carotene have the potential to alleviate vitamin A deficiency (VAD) in children and lactating mothers (Low *et al.*, 2007). Increased consumption of OFSP will therefore help to improve both food and nutrition security. Increased consumption of OFSP in Ghana will however be difficult, because the often high levels of sugar and low dry matter that characterize these clones do not appeal to the Ghanaian palate. This difficulty can be circumvented if high β-carotene is introduced into the genetic background of clones with the preferred culinary attributes (Cervantes-Flores *et al.*, 2011). Large variability in β-carotene exists within the gene

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pool of sweetpotato, making such an effort feasible (Kapinga *et al.*, 2003; Van-Jaarsveld *et al.*, 2005; Andrade *et al.*, 2009; Chiona, 2009 ). Estimation of genetic parameters such as heritability and combining ability of parents will help breeders make informed choices on selection methods that will increase gain in selection. Determination of the magnitude of genotype x environment effects will also help in the identification of stable genotypes for use as parents for hybridization or as potential clones for release after further evaluation.

**The main objective of this study was:**

To develop sweetpotato varieties with the desired combination of quality traits, namely, low-sweet, high dry matter and high β-carotene content.

**The specific objectives were** to;

1. assess production constraints and farmer varietal preferences for sweetpotato in Ghana
2. assess available diversity within sweetpotato germplasm and select superior clones as parents for crosses.
3. estimate the heritability of sugars, dry matter and β-carotene and determine general and specific combining ability of selected parents
4. estimate the magnitude of G x E effect on the expression of above named traits and identify stable genotypes.

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# CHAPTER TWO

## 2.0 LITERATURE REVIEW

### 2.1 Origin and distribution of sweetpotato

Sweetpotato (*Ipomoea batatas* (L.) Lam.) is a dicotyledonous plant, classified along with its closely related wild species into the morning-glory family Convolvulaceae, genus *Ipomoea*, subgenus *Eriospermum*, section *Eriospermum* (formerly *Batatas)* and series *Batatas* (Austin, 1988). The genus *Ipomoea* contains 600 to 700 species, most of which are concentrated in the Americas (Austin, 1988; Huaman, 1999). The sweetpotato is, therefore believed to originate from the Americas (Nishiyama, 1961; Huaman, 1999). Studies on diversity assessment using molecular markers, found the highest diversity in Central America, suggesting that this region is the primary center of diversity and most likely the center of origin of sweetpotato (Huang and Sun, 2000; Zhang *et al.*, 2000).

Peru-Ecuador, Papua New Guinea and the South Pacific are among the secondary centers of origin (Yen, 1974). In Papua New Guinea and in other parts of Asia, many types of sweetpotato can be found that are genetically distinct from those found in their area of origin (Zhang *et al.*, 2000). In sub-Saharan Africa (SSA), East Africa may be a secondary center of genetic diversity due to the large genetically distinct types that exist there (IBPGR, 1981; Huaman and Zhang, 1997; Tumwegamire, 2011). Sweetpotato may have spread from the Americas via slave traders into tropical Africa (Low *et al.*, 2009).

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## 2.2 Cytology and Genetics

Sweetpotato is a hexaploid species (2n=6x=90) with a base chromosome number of 15 (Jones, 1965) but the nature of its polyploidy remains uncertain. A number of hypotheses have been made with supportive cytological data in efforts to elucidate the origin of sweetpotato and both allopolyploidy and autopolyploidy have been proposed. Earlier theories suggested an allohexaploid origin (Gustafson and Gadd, 1965; Jones, 1965; Magoon *et al.*, 1970). An autopolyploid origin with two functionally homologous basic genomes, B1 and B2 have also been proposed (Nishiyama *et al.*, 1975; Shiotani and Kawase, 1989). Nishiyama *et al*. (1975) suggested that the related species, *Ipomoea leucantha* (2*x*), *Ipomoea littoralis* (4*x*) and *Ipomoea trifida* (6x) may be the progenitors of the sweetpotato (6x), in an autopolyploid series with doubling of the *I. leucantha* B genome. Also, using molecular technology, autopolyploid features have been suggested (Kriegner *et al.*, 2003; Cervantes-Flores, 2006).

Sweetpotato is cross pollinated and highly heterozygous (Jones, 1980; Jones *et al.*, 1986a). It has very large numbers of small chromosomes which pose difficulties for plant breeders (Cervantes-Flores *et al.*, 2011). However, because it is a hexaploid, there is extensive variability within the species, available for exploitation by plant breeders (Tsegaye *et al.*, 2007). Most of its economically important traits like yield show quantitative mode of inheritance (Tsegaye *et al.*, 2007). According to Jones, (1980), every trait studied from wide genetic backgrounds has varied over an extensive range.

Commonly, sweetpotato is vegetatively propagated, but can also be propagated through seed. Recombination through sexual reproduction can generate new types with desirable combination of economically important traits. A single seed therefore can give rise to a potentially

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commercial variety. This is because after identifying this genotype it is maintained through vegetative propagation without further recombination (Jones, 1980; Saladaga, 1989).

Sexual reproduction in sweetpotato is challenged by the existence of self- and cross-incompatibilities (Reynoso *et al.*, 1999) which can prevent quick introgression of desirable traits from landraces (La Bonte, 2002). Self-incompatibility in flowering plants is an elaborate genetic system that prevents self-fertilization and therefore promotes out-crossing so as to maintain genetic diversity within a species (Tomita *et al.*, 2004). Sweetpotato exhibits sporophytic self-incompatibility (SI) controlled by a single multi-allelic SI locus (Tomita *et al.*, 2004) that constitutes the main barrier to seed production. Thirteen causes of cross-incompatibility have also been identified (Martin, 1982). Among these are chemical barriers, short life span of pollen, incompatible stigma and abortion of embryos. Abnormalities in meiosis due to the hexaploid nature of this species and hybrid sterility have also been associated with limited fertility (Martin and Ortíz, 1966).

Even when a cross is compatible, post-pollen germination barriers to fertility, often impede seed production (Martin and Cabanillas, 1966; Murata and Matsuda, 2003). Compatibility may also be unilateral, that is seed set takes place in one direction only (Vimala, 1989). Crosses between compatible parents often produce one to two seeds per capsule (Jones, 1980; Reynoso *et al.*, 1999) instead of the 4 seeds expected from an ovary with two carpels and two locules. According to Reynoso *et al*. (1999), different sources of accessions can be classified into incompatibility groups. Clones within one group are incompatible but compatible with those from different groups. Clones within the different incompatibility groups have been identified. These are referred to as ‘incompatibility testers’ (Reynoso *et al.*, 1999).

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## 2.3 Methods for sweetpotato improvement

Breeding is the strategy for improvement in yields and for introducing quality traits such as higher micronutrient content, dry matter, sugar and flavor into the variety developed. Improvement in quality traits might not contribute to yield improvement *per se* but are essential for achieving other goals, such as consumer acceptance and improvement in diet (Low *et al.*, 2009). A number of methods have been employed towards sweetpotato improvement. This section discusses a few of these strategies.

### 2.3.1 Polycross method

To overcome the barriers associated with sweetpotato hybridization, genotypes are allowed to cross to each other in a nursery by natural pollinators, in a mating system known as polycross (Jones, 1980). Stuber (1980) defined the term polycross as a mating arrangement for interpollinating a group of genotypes using natural hybridization in an isolated crossing block. Polycross mating has been used extensively in sweetpotato improvement (Jones, 1980; Wang, 1982; Martin, 1988; Wilson *et al.*, 1989). The strategies for providing equal chances for each parent to pollinate others include synchronizing flowering (Ahn *et al.*, 2004) and the use of large numbers of replications (10 or more) of single randomized plants (Stuber, 1980). Usually a limited number of parents (30 or less) are randomly crossed in isolation for the purpose of deriving new cultivars or advanced breeding lines. When too many parents are used the average effect of each parent is diluted and the hard decisions of which lines to drop are avoided, resulting in reduced selection progress (Stuber, 1980).

Seeds harvested from a polycross nursery are used in the next cycle of selection. (Stuber, 1980). The high level of genetic variation in polycross breeding lines are useful for selecting elite

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materials (Hwang *et al.*, 2002). Selections made in the first year are tested in the second year seedling trials and in advanced line trials. The final genotypes are then multiplied exclusively and indefinitely by vegetative means (Jones *et al.*, 1986a).

In a polycross the male parent of any one progeny may have come from any of the entries in the polycross and remains unknown unless molecular methods are used to determine parentage. The polycross mating design therefore, generates half-sibs. The mean performance of the progeny of any one female parent is frequently used in seed propagated crops for evaluating general combining ability of that female parent (Tysdal and Crandal, 1948; Stuber, 1980) but is also applicable to clonally propagated crops (Lebot, 2008). The general combining ability reflects the additive genetic component of variance (Falconer and Mackay, 1996). According to Jones *et al*. (1986a) the use of polycross and mass selection techniques appears to be the most efficient way to breed sweetpotato. The use of controlled crosses to improve the crop has also been reported (Mwanga *et al.*, 2002; Lin *et al.*, 2007; Grüneberg *et al.*, 2009a; Cervantes-Flores *et al.*, 2011; Todd, 2013).

### 2.3.2 Controlled mating strategies

Unlike the polycross, both parents are predetermined for controlled hybridization and crosses can be in one direction or in a reciprocal fashion. Controlled mating designs commonly used in sweetpotato breeding lately, are the North Carolina design two (NCII) and the diallel cross (Mwanga *et al.*, 2002; Lin *et al.*, 2007; Chiona, 2009 ; Some, 2013). In NCII, the same group of females are mated to each of the males while in the diallel, mating occurs in all possible combinations among a set of parents (Griffing, 1956). Both NCII and diallel mating designs are generally used to obtain estimates of general combining ability (GCA) specific combining ability (SCA) and gene action (Griffing, 1956).

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In Uganda, a North Carolina II mating design involving 7 female and 6 male elite cultivars, resulted in wide variability in $F_1$s for important traits such as β-carotene (Gasura *et al.*, 2008). In this study the authors reported heterosis in some traits such as storage root size and storage root number per plant. In Burkina Faso, NCII design followed by parent-offspring regression analysis was used to estimate heritability of yield and carotene in sweetpotato (Some, 2013). Lin *et al*. (2007), conducted reciprocal crosses to obtain information on maternal effects on yield and quality traits of sweetpotato. Mwanga *et al*. (2002) used a diallel design to analyze resistance to sweetpotato virus diseases in Uganda, while Chiona (2009) employed the same design to improve yield and β-carotene content in high dry matter sweetpotato genotypes in Zambia (Chiona, 2009 ).

Not only are these mating strategies used in direct improvement studies but also in genetic marker studies as tools for complementing and improving breeding success. For example, Kriegner *et al*. (2003) used seeds of an $F_1$ mapping population that originated from a two-way bi-parental mating between two African sweetpotato landraces, to develop genetic linkage map of sweetpotato. From a mapping population of 240 progenies, derived from a bi-parental mating, quantitative trait loci associated with root knot nematode resistance in sweetpotato was detected (Cervantes-Flores *et al.*, 2008a). A pseudo-test cross mapping population consisting of two parents and 87 $F_1$ progeny between the two parents were used to study the inheritance, segregation and linkage of ISSR markers (Hu *et al.*, 2003).

### 2.3.3 Mass selection

After progenies are raised, a critical step to ensure overall success of breeding is selection (Jones *et al.*, 1986a). Mass selection in sweetpotato has been shown to be an effective way of combining favorable characters in parental types (Jones *et al.*, 1976) to produce new types and

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ensure a wide genetic base needed for continuous selection advance in future years (Jones *et al.*, 1986a)

In mass selection procedure, true seeds from selected plants/parents are advanced each year by bulking them to begin subsequent cycles of selection with low selection pressure in the early generations (Jones *et al.*, 1986b). This results in rapid accumulation of major dominant genes, and slower accumulation of minor and recessive genes (Martin, 1988). Jones (1976) suggested that selection for simply inherited characters should be avoided until after four to five generations of intermating. This would avoid chromosome segment fixation that reduces the frequency of effective recombination. Selections made from mass selection populations can be tested directly for cultivar potential but are more likely to provide a source of parental material for a more restricted polycross nursery (Jones *et al.*, 1986a).

Grüneberg *et al*. (2009) have modified the general mass selection scheme into what is now referred to as Accelerated Sweetpotato Breeding (ASPB). Just like the traditional mass selection method, ASPB is used for population improvement (pre-breeding) and the release of new varieties. The advantage of ASPB is that the breeding cycle is reduced to 3-4 years instead of the 6-8 years in the formal method. This is achieved through the use of multiple selection sites from the initial stage of selection, with no replication or minimized replication. In this way information on stability of genotypes being tested is obtained while conserving resources (Grüneberg *et al.*, 2010). Another essential feature of ASPB is farmer participation (Abidin *et al.*, 2002; Laurie and Magoro, 2008) which further accelerates the breeding and cultivar selection process.

ASPB is in two stages, early and later breeding stages. In the early breeding stages, also known as the observational trial (OT), large numbers of plants are raised from true seeds and evaluated

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on small plots with or without replication, in more than one environment with locations treated as replications for the purpose of statistical analysis. At this stage selection is based on a few highly heritable traits such as susceptibility to pathogens, storage root quality characteristics such as dry matter, protein, starch, sugar(s) and pro-vitamin A concentrations (Jones *et al.*, 1986a; Anshebo *et al.*, 2004; Gasura *et al.*, 2008). Evaluation of genotypes across locations allows analysis of G x E interaction and information on stability of genotypes across locations to be obtained (Grüneberg *et al.*, 2005; Grüneberg *et al.*, 2010). Between 3-15% of clones is selected in OTs to advance to later breeding stages.

The later breeding stages consist of preliminary yield trials (PYTs) and advanced yield trials (AYTs) in multiple locations. Conducting PYTs across locations, with two or more replications, allows the separation of the effects due to genotype by environment interactions, and due to the plot error for each trait (Grüneberg *et al.*, 2005; Grüneberg *et al.*, 2010). Farmers are involved in the selection process during AYTs so as to eliminate the possibility of putting forward genotypes for official variety release that are not accepted by farmers. Re-evaluation of selected clones are conducted in the next growing season at the same locations and additionally in more than 10 on-farm trials linked with the process of official variety release (Grüneberg *et al.*, 2009b; Grüneberg *et al.*, 2010).

### 2.3.4 Farmer participation in sweetpotato research

It is important to take into account farmers' needs and preferences when developing and selecting sweetpotato varieties so as to promote the rapid adoption of improved varieties (Abidin *et al.*, 2002). One way to do this is through farmer participatory approach (Gasura *et al.*, 2008). Farmer participation can begin from the early stages of breeding, involving germplasm collection

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(Abidin *et al.*, 2002) to the later stages involving variety release trials (Grüneberg *et al.*, 2009b; Grüneberg *et al.*, 2010).

Involvement of farmers in the identification of local germplasm with desirable traits has great impact on the success of breeders (Abidin *et al.*, 2002; Rees *et al.*, 2003). Local germplasm may sometimes be more desirable than exotic introductions since in most cases such accessions have better adaption to the local environment (Gasura *et al.*, 2008). In Uganda for example, improved varieties with high yield potential were introduced for adoption by farmers. These were however very susceptible to the devastating sweetpotato virus disease (Mwanga *et al*., 2002). Farmers abandoned these varieties and returned to their own varieties. This emphasizes the need for local breeding programs that exploit the potential of local germplasm (Gasura *et al.*, 2008) through farmer involvement.

Through farmer participation potentially useful cultivars were rapidly identified in Uganda Abidin *et al*., 2002; Mwanga *et al.*, 2003; Abidin *et al.*, 2005; Gibson *et al.*, 2008), several of which were farmers' varieties that showed good average yield and stability, while others displayed specific adaptation. Farmer participation in sweetpotato breeding efforts led to the rapid selection and dissemination of new varieties in Ethiopia (Anshebo *et al.*, 2000), Tanzania (Kapinga *et al.*, 2000) and Kenya (Ndolo, 2001). These results illustrate the potential that farmer participation can have in the improvement of sweetpotato.

### 2.4 Breeding sweetpotato for quality traits

In many countries in sub-Saharan Africa (SSA) the preferred types of sweetpotato are those that are higher in dry-matter content (28–30 %) and have little to no sweetness (Mwanga *et al.*, 2007a). The high dry matter and low sugar cultivars are not as nutritious as the orange-fleshed

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types because they tend to be low in carotenoid content (Low *et al.*, 2007). Therefore, much breeding work in SSA is focused on the development of higher dry-matter, semi-sweet OFSP while also improving yields (Low *et al.*, 2009; Cervantes-Flores *et al.*, 2011). This new direction is aimed at addressing vitamin A deficiency needs of women and children in order to prevent malnutrition and enhance nutrition and food security (Low *et al.*, 2007; Andrade *et al.*, 2009; Low *et al.*, 2009).

### 2.4.1 Breeding sweetpotato for low sugar content

The principal sugars in raw roots of sweetpotato are sucrose, glucose, and fructose (Picha, 1997; Morrison *et al.;* 1993; Kays, 2005). In cooked roots starch is hydrolyzed to produce maltose. It has been reported that about 42-95 % of the starch in several cultivars of sweetpotato was converted during baking and that most (72-99 %) of the converted starch accumulated as maltose (Walter *et al.*, 1975). Maltose production by ß-amylase activity elevated total sugar concentrations to 31.0 % in the baked product in four lines that exhibit distinct differences in sweetness after cooking (Morrison *et al.*, 1993)

The different sugars, at the same concentrations, have differing levels of perceived sweetness (Moskowitz, 1970; Shallenberger, 1993). Sucrose, the most abundant sugar in raw roots (Picha, 1987), is about three times sweeter than maltose while fructose and glucose are, respectively, 5-fold and 2-fold sweeter than maltose with maltose appearing to be the most preferred sugar by consumers (Koehler and Kays, 1991; Lewthwaite *et al.*, 1997). Since levels of sweetness of individual sugars vary, sweetness among clones may be compared by calculating their sucrose equivalents (SE). That is, the individual sugars are quantified and then adjusted for their relative sweetness by using the sweetness of sucrose as 1 (one). For example, if the relative level of sweetness of sucrose is 1.0, then fructose = 1.73, glucose = 0.74, and maltose = 0.33

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(Moskowitz, 1970). Hence, three molecules of maltose are needed to equal the sweetness of one molecule of sucrose. Therefore, the type of sugar has an effect on both sweetness and flavor of the sweetpotato. The quantitative and qualitative characterization of the preferred sugar status of sweetpotato would assist in defining flavor criteria and goals for breeding programs (Koehler and Kays, 1991).

Depending on the cultivar, sucrose, fructose, and glucose can account for as much as one-half of the perceived sweetness of a cooked sweetpotato (Walter, 1992). Higher sugar content in raw sweetpotato implies a sweeter cooked product. However, high sugar content in a raw sweetpotato does not necessarily result in higher sugar content in a cooked sweetpotato. For example in studies carried out by Picha (1987) and La Bonte and Picha (2000), one variety- 'Travis', recorded the highest level of total sugars when raw but had a lower level of total sugars than another variety- 'Jewel' when cooked. This was because starch availability for conversion to maltose by β-amylase in Travis was lower than in Jewel.

Genetically, two phenomena have been suggested as accounting for lack of sweetness in the staple-type sweetpotato. These are low background levels of sucrose, glucose and fructose; and/or low levels of ß-amylase mediated starch hydrolysis and maltose formation (Morrison *et al.*, 1993). A recessive allele of the gene, β-amy has been reported to be responsible for the low β-amylase activity in homozygous genotypes (Kumagai *et al.*, 1990). Lines that are low-sweet, have low enzyme activity, while sweet types have high enzyme activity (Morrison *et al.*, 1993). The recessive allele of β-amy, either fails to synthesize the protein or produces an inactive form of it. This recessive allele appears in a reasonably high frequency within sweetpotato clones (Kumagai *et al.*, 1990). In a study involving 272 sweetpotato clones in the USDA germplasm repository, Kays *et al*. (2005), found a wide variation in total endogenous sugars and maltose. In

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a spread sheet containing 410 genotypes from the USDA (Stan Kays, personal communication) β-amylase activity also varied widely from very low (2% of the population) to very high with majority of the lines (69%) falling into the medium range.

According to Kays *et al*. (2005), increasing or decreasing sweetness of clones involves altering the two groups of genes: i) genes controlling the formation of starch, which influence latent pools of mono- and disaccharides within the storage roots and ii) genes controlling starch hydrolysis and maltose formation. The evidence gathered in their survey of sweetpotato germplasm worldwide indicates that there is sufficient variation in both traits. The potential therefore exists for tailoring sugar levels to specific consumer preferences and product usage so as to increase utilization of the crop (Kays *et al.,* 2005; Kays, 2006). This potential however, remains to be exploited by breeders.

Most studies on root sugars have focused on physiological assessment and diversity studies in flavor and sugars (Picha, 1987; La Bonte and Picha, 2000; Wang *et al.*, 2006) with no breeding strategies explicitly aimed at decreasing sugar levels. A recent report documents heritability estimates for reducing sugars (fructose and glucose) and sucrose in raw roots (Todd, 2013) but no estimate was reported for maltose – the most abundant sugar in cooked roots. An earlier study using discriminant analysis selected a total of 8 markers for total sugars in raw roots but each of the markers accounted for just a small percentage of the variation for total sugar content (Mcharo, 2005). Todd (2003) found that 6 QTLs were associated with decreased starch and dry matter content and 8 QTLs were associated with increased sugar content in Beauregard, a US variety (Todd, 2013). In the same study 2 QTLs each were associated with increased starch and decreased starch in Tanzania, an East African variety. Sugar content has been found to negatively correlate with starch and dry matter content (Gasura *et al.*, 2008; Lebot, 2008).

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Selecting for high dry matter and starch content will, therefore, have direct impact on selection for low sugar lines. The negative correlation between sugars and β-carotene content may impede progress in combining all three traits, namely low- sugar, high dry matter and β-carotene in one cultivar. With recurrent mass selection it should be possible to accumulate favorable alleles so that progress can be made over time.

### 2.4.2 Breeding Sweetpotato for high dry matter content

The dry matter of sweetpotato is made up of about 80-90% carbohydrates (Palmer, 1982; Picha, 1987) and exists in the form of starch and sugars (Palmer, 1982; Mcharo and La Bonte, 2007). Starch represents the primary carbohydrate found in the sweetpotato roots and it is found in two general forms amylose and amylopectin The ratio of amylose and amylopectin is genetically controlled and varies between lines (Kays, 1992). Starch content is apparently determined mainly by the additive effect of polygenes. The accumulation of genes controlling high starch content is therefore, recommended (Lebot, 2008) for achieving high dry matter content. In Japan the strategy for accumulating genes for starch content has been via inbreeding in self-compatible clones and sib mating (Lebot, 2008).

A high starch content is a desired attribute of the staple, low sugar types which generally predominate in the tropics (Mok *et al.*, 1997; Mwanga *et al.*, 2007a). Staple sweetpotato types typically have a white to cream flesh with dry weight (DW) contents ranging from 30-35 % (Lewthwaite *et al.*, 1997; La Bonte and Picha, 2000). Dessert sweetpotato types generally have a cream colored to orange flesh and dry matter content ranging from 17.7 % to 26.3 % (Picha, 1987).

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High heritability estimates of 75-88 % (Zhang and Li, 2004), 64 % (Jones *et al.*, 1986a; Lebot *et al.*, 2009) and 69.84 % (Tsegaye *et al.*, 2007) have been reported for dry matter content. There is also high variation in the trait, ranging from 14 % to more than 44 % in sweetpotato germplasm (Lebot, 2008). With the availability of large genetic variation and high heritability estimates, rapid progress can be made when selecting for increased dry matter content (Mok *et al.*, 1997).

### 2.4.3 Breeding Sweetpotato for high beta-carotene content

Orange-fleshed sweetpotato are the most valuable sources when breeding for high β-carotene content. However, white-fleshed varieties with flecks of orange can also contribute to β-carotene production (Cervantes-Flores, 2006). High heritability estimates for beta-carotenes have been reported (Hernandez *et al.*, 1967; Jones *et al.*, 1986a; Tsegaye *et al.*, 2007), and total carotene content appears to be controlled by several additive genes (Hernandez *et al.*, 1967). Cervantes-Flores (2006) suggested that, the accumulation of favorable or loss of deleterious alleles in the progeny from sweetpotato crosses results in transgressive segregation for some desirable traits such as beta-carotene, dry matter and starch content (Cervantes-Flores *et al.*, 2008b). The authors attributed this to the high levels of heterozygosity of the parents that allowed complementation between favorable alleles. Cervantes-Flores *et al.* (2011) identified 8 QTLs involved in the variation of β-carotene content and suggested that, β-carotene, dry matter and starch exhibited quantitative mode of inheritance. They also suggested that qualitative genes controlling the trait may have been duplicated due to the hexaploid nature of the crop.

Beta-carotene and dry matter are however, negatively correlated (Cervantes-Flores J. C., 2006). This may constitute a major challenge to breeding orange fleshed sweetpotato with high dry matter content. Genotypes containing higher levels of β-carotene are more likely to have lower levels of starch and, therefore, lower levels of dry matter (Cervantes-Flores *et al.*, 2008a). With

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the use of recurrent mass selection however, successes have been attained in breeding varieties that combine both traits in that several high dry matter cultivars have been developed that have high levels of beta-carotene (Andrade *et al.*, 2009).

### 2.5 Methods for assessing quality traits in sweetpotato

#### 2.5.1 Methods for assessing sugars in sweetpotato

Selection is very simple for traits such as root color, shape and yield, in which superior progeny can be easily identified. With traits such as flavor (sugar and aroma), where a subjective analysis is required, accurate identification of superior progeny is much more difficult and serves as an obstacle to reliable selection (Katayama *et al.*, 1996; Lebot, 2008). Flavor analysis involves the measurement and evaluation of the sensory characteristics of the cooked product, typically using a descriptive test with trained panelists. This arduous assessment method generally results in sensory traits such as flavor being the last to be assessed (Katayama *et al.*, 1996; Wang and Kays, 2003). For many crops, more than 99 % of the original progeny and genetic variation is discarded prior to flavor assessment (Wang and Kays, 2003) essentially guaranteeing little or no improvement in flavor. An alternative approach is to rely on the public's acceptance or rejection of the new cultivar in the marketplace instead of screening for flavor (Wang and Kays, 2003).

Analytical techniques have been developed that are suitable for accurate assessment of large numbers of progeny for flavor and allow for the evaluation of flavor much earlier in the selection sequence, thereby, increasing the chances of developing truly superior cultivars (Wang and Kays, 2003).

Picha (1985) developed reliable high performance liquid chromatography (HPLC) procedures for quantitative analysis of sugars in raw and baked sweetpotatoes. HPLC has since been used for

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sweetpotato root quality analysis (Picha, 1987; Lin *et al.*, 2007; Mcharo and La Bonte, 2007). HPLC is, however, a tedious and expensive procedure (Takahata *et al.*, 1993). Other methods that have been used for sugar determination include refractive index (Walter, 1992) and near infrared reflectance spectroscopy (NIRS) (Lu and Sheng, 1990). NIRS is well adapted to the conditions in developing countries and can be used for the high-throughput screening of a great number of samples (Lebot *et al.*, 2009). It is a rapid, cost-effective, and non-destructive method, allowing the simultaneous determination of major constituents in a mixture by multivariate data analysis (Lebot *et al.*, 2009).

Many compounds can be quantified routinely using NIRS (Lebot, 2008; Lebot *et al.*, 2009). NIR analysis is widely used in cereal breeding programs by measuring the reflectance spectra in ground samples (Katayama *et al.*, 1996). In potato it has been used to measure tuber quality, starch and protein (Dijk van *et al.*, 2002; Haase, 2006). NIRS is an efficient method for crops with inherently low moisture content. However, root crops, like sweetpotato, with more than 60% moisture content can also be analyzed using NIRS, but samples need to be dried prior to NIRS (Katayama *et al.*, 1996). NIRS have been used in a number of studies using dry samples to measure proteins, sugars, starch, amylose and beta-carotene contents in sweetpotato (Lu and Sheng, 1990; Lu *et al.*, 2006; Lin *et al.*, 2007). NIRS can also be performed with fresh samples of sweetpotato. Katayama *et al*. (1996) used NIRS to adequately predict starch, moisture, and sugar content in fresh sweetpotato storage roots and investigated variation in these components across growing years.

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### 2.5.2 Dry matter quantification

The most commonly used method for quantifying dry matter in sweetpotato is as follows; the fresh weight (about 200 g) of thinly sliced roots are measured, followed by oven-drying at 60° or 70°C for 2–5 days. Dry-matter content is then calculated by determining initial and final weight, and estimating the percentage of dry weight (Cervantes-Flores *et al.*, 2011). An alternative to oven drying is to freeze dry fresh samples (King, 1971) before dry weight determination.

### 2.5.3 Quantification of beta-carotene content in sweetpotato

High performance liquid chromatography has been used to determine β-carotene contents in sweetpotato (Bushway, 1986; Simonne *et al.*, 1993). However this methodology is tedious and Takahata *et al*. (1993) have documented a quicker method that links beta-carotene content and the intensity of the orange flesh color of the sweetpotato. β-carotene content is significantly correlated with sweetpotato flesh color, with the orange fleshed varieties being highest in β-carotene (Takahata *et al.*, 1993; Wu *et al.*, 2008). β-carotene content can thus be assessed directly from the field using a color chart developed at CIP (Burgos *et al.*, 2009).

Near infrared (NIRS) analysis has been examined and recommended for improving the efficiency of breeding for crop quality (Starr *et al.*, 1981). Spectrophotometry over estimates the HPLC values for beta-carotene content because of the presence of minor carotenoids (Lebot, 2008). However, large samples can be first screened using cost effective spectrophotometer before accurate quantification of beta-carotene using HPLC (Lebot, 2008). The NIRS technique may represent an efficient method to assay the sugar, starch, dry matter and beta-carotene content simultaneously in sweetpotato. However, several factors may affect the accuracy of NIR predictions for a given genotype (Norris and C, 1984). Prediction errors vary greatly due to the environment, i.e., year and location effects and the assay temperature (Katayama *et al.*, 1996).

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## 2.6 Genotype by environment interaction in sweetpotato breeding

Assessment of wide and specific adaptation and stability play a central role in many breeding programs (Abidin *et al*., 2005). A variety is said to have specific adaptation if it ranks among the highest yielders at some locations, but not at others while widely adapted varieties have high mean yields across environments (Shukla, 1972). Sweetpotato is widely grown between latitudes 40°N to 40°S and at altitudes as high as 2500 meters above sea level (Hahn and Hozyo, 1984). In spite of the wide range of environments and its adaption to harsh growing conditions (Woolfe, 1992), its performance in terms of yield, quality attributes, resistance to biotic and abiotic stresses, are affected by environmental changes (Mcharo and La Bonte, 2007; Tsegaye *et al.*, 2007). A study to determine stability of root yield and the nature and magnitude of genotype x environment (G X E) interaction in sweetpotato, revealed a significant G X E interaction in which newly introduced varieties gave high root yield and were more responsive to high yielding environments than the local cultivars, while the local cultivars were better adapted to poor environments (Tekalign, 2007). G x E interactions must be considered when developing high yielding and stable genotypes but careful considerations must also be given to the choice of selection environments for an overall success.

### 2.6.1 Genotype environment interaction on quality traits

Sweetpotato quality traits are also affected by environmental factors. Studies related to sweetpotato nutritional traits indicate substantial variation for food quality in different genotypes across locations. For example, dry matter (Grüneberg *et al.*, 2005; Tumwegamire, 2011) and β-carotene (Manrique and Hermann, 2001; Mwanga *et al*., 2003) were all found to be significantly affected by environments. Knowledge of the magnitude of G x E effects on phenotypes improves the accuracy in characterizing genotypes and improves gain in selection by enabling the

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identification of locations and input systems to use (Grüneberg *et al.*, 2005). While selecting for wide and specific adaptations for yield, therefore, the magnitude of G x E interaction for quality traits must also be assessed.

The measures of G x E are important, for establishing breeding objectives, such as the choice of parents, identification of the ideal test conditions and recommendations for regional adapted cultivars (Yan *et al.*, 2000). Among the methods used to analyze G x E effects, the additive main effects and multiplicative interaction (AMMI) has been widely used. It is valuable among the statistical analysis, because of the large group of technical interpretation available (Balestre *et al.*, 2009), its ability to capture a large portion of the G x E sum of squares and its effectiveness to separate main and interaction effects (Ebdon and Gauch, 2002). AMMI has been shown to be a very effective tool for the analysis of sweetpotato multi environment (MET) data (Grüneberg *et al.*, 2005). Stability can also be measured by linear regression slopes and deviations from the regression (Finlay and Wilkinson, 1963). A stable variety is one that has high mean performance, a regression coefficient that is close to one and a deviation that is close to zero (Eberhart and Russell, 1966).

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# CHAPTER THREE

## 3.0 PRODUCTION CONSTRAINTS AND FARMER PREFERENCE FOR SWEETPOTATO IN GHANA

### 3.1 INTRODUCTION

Sweetpotato is an important food crop in many regions of sub-Saharan Africa, where the crop is grown on about 3.34 million hectares (FAOSTAT, 2011). When compared to other major staple foods like cassava, yam, cocoyam and maize, sweetpotato has superior agronomic and nutritional attributes. It produces more carbohydrate per unit area per time, has short production cycle, grows well in many agro-ecologies, requires low inputs, and is fairly tolerant to production stresses such as high temperature, water deficits, insects and diseases, and low soil fertility (Woolfe, 1992).

Nutritionally, the crop contains more protein, minerals and dietary fiber than most staples (Woolfe, 1992). Its most sterling nutritional value is the high levels of β-carotene, the precursor of vitamin A, found in the orange fleshed (Woolfe, 1992; Low *et al.*, 2007; Mcharo and La Bonte, 2007). Daily intake of just one hundred grams of orange fleshed sweetpotato is adequate to meet the recommended daily allowance of vitamin A and prevents blindness in children (Woolfe, 1992; Low *et al.*, 2007). It is therefore, an excellent source of food that is nutritionally superior to most staples (Kays and Kays, 1998). In addition, the crop has potential as an industrial crop for the production of alcohol, animal feed, and pharmaceutical applications (Mays, 1990; Rahman *et al.*, 2003; Umesh *et al.*, 2007).

In spite of all its natural endowments and the various uses of the crop, the potential of sweetpotato has not yet been achieved in much of Sub-Saharan Africa (Rees *et al.*, 2003).

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Relative to other crops sweetpotato research in Africa is still at its infancy. In Ghana for example, sweetpotato has been cultivated for many years and is of particular importance in the Northern and Coastal belts where it is both a food crop and a cash crop (Missah and Kissiedu, 1994; Missah *et al*., 1996; Otoo *et al*., 1998; Otoo *et al*., 2000). Being a vitamin A deficient country, consuming OFSP rich in carotene in Ghana could help fight vitamin A deficiency in children (Low *et al*, 2007; Akoroda, 2009). In spite of this, not much has been done in the area of sweetpotato research in Ghana. Until recent efforts to improve populations at the Crops Research Institute (CRI), there had been practically no actual breeding. Research in the past, focused mainly on multi-location adaptive trials (Missah *et al.*, 1996; Otoo *et al.*, 1998; Otoo *et al.*, 2000; Akoroda, 2009) of clones developed elsewhere (mainly from International Institute for Tropical Agriculture, IITA and the International Potato Center (CIP). From these trials varieties were officially released in 1998 and 2005 (Akoroda, 2009). An additional 4 varieties from IITA and CIP were released in December 2012 by Crops Research Institute (CRI). These are now being used as parents in a crossing block established in CRI. No formal adoption studies have been conducted of these officially released varieties, but they do not appear to predominate on Ghanaian sweetpotato farms.

It is hypothesized among breeders that preferred culinary attributes of sweetpotato in Ghana are low-sweetness and mealy texture, and that low integration of the crop in traditional food preparations could be due, among others, to the high levels of sugar in the crop. Indeed, Cassava and yam, non-sweet starchy staples in Ghana for example, can be used in about thirteen different traditional preparations while sweetpotato is mostly prepared in only three different ways (boiling, frying and roasting), predominantly as a snack. Nevertheless, the crop should have wider usage on account of its high nutritive value, its potential as a food security crop and its

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ability to alleviate Vitamin A deficiency Woolfe, 1992; Low *et al*, 2007). To understand the influence of sweetness on regular consumption and also to assess farmers' knowledge of sweetpotato production, it is important to interact with farmers themselves. One proven way to do this is through a Participatory Rural Appraisal (PRA).

Participatory Rural Appraisal (PRA) is a form of client-oriented procedure which allows researchers to elicit farmers' indigenous knowledge, needs, perceptions and preferences and incorporated in setting and implementing research agendas (Odendo *et al*., 2002; Witcombe *et al*., 2005). More often than not, technologies developed by researchers alone suffer low adoption, which confirms the need for client-orientation in research and development (Witcombe *et al*., 2005). PRA results in the development of appropriate technologies that meet farmers' needs and preferences, and are, therefore, likely to be adopted (Witcombe *et al*., 2005).

Other examples of client oriented development are Participatory Plant Breeding (PPB) and participatory varietal selection. In PVS scientists and farmers work together to identify preferred varieties while in PPB new clones from seedling populations are identified (Gibson *et al*., 2008). According to Laurie and Magoro (2008), PVS is a logical step before PPB, and PVS can rapidly provide farmers with improved germplasm. The selected germplasm can then flow into PPB for the development of new populations (Laurie and Magoro, 2008). The main thrust for success of PPB in Africa has been in addressing the diverse needs of resource-poor farmers (Sperling *et al*., 2001; Witcombe *et al*., 2005).

Participatory methods, whether PVS, PPB or PRA, all attempt to meet needs of resource-poor farmers and enhance the development and adoption of new and better technologies (Gibson *et al*., 2008). Through PRA potentially useful sweetpotato cultivars were rapidly identified in

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Uganda (Abidin *et al.,* 2002; Abidin *et al.,* 2005) several of which were farmers' varieties that showed good average yield and stability, while others displayed specific adaptations. Farmer participation in sweetpotato breeding efforts has led to the rapid selection and dissemination of new varieties in Ethiopia (Anshebo *et al*., 2000), Tanzania (Kapinga *et al*., 2000), Uganda (Mwanga *et al*., 2003; Gibson *et al*., 2008) and Kenya (Ndolo *et al*., 2001). These results illustrate the potential of farmer involvement in sweetpotato improvement.

In Ghana, there is a lack of information on farmers' varieties, germplasm diversity, production constraints, utilization, yield potential and preferred quality attributes. This lack of information impedes breeding progress because such knowledge cannot be exploited in the development of sweetpotato research goals.

**The aim of this work was therefore to identify;**

1. factors inhibiting sweetpotato production in Ghana, from farmers' perspectives
2. farmers' organoleptic preferences for sweetpotato and factors limiting utilization of the crop

## 3.2 MATERIALS AND METHODS

### 3.2.1 Survey sites

PRA was carried out in three regions of Ghana where sweetpotato is important as both food and cash crop. These are Central, Volta and Upper East regions. Central region lies within the dry equatorial and moist semi-equatorial zone. It has coastal savannah and grassland vegetation along the coast while semi-deciduous forest dominates inland areas. Rainfall is bimodal with annual rainfall of 1,000mm along the coast to about 2000 mm in the interior. Mean monthly temperature ranges from 24ºC - 30ºC. The Volta region is located along the Eastern border of

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Ghana. It has most of the vegetation zones found in Ghana, that is, the coastal grassland and mangrove swamps at the coastal portion, the guinea savannah and moist semi-deciduous forests in the central highland areas, and sahel-savannah and wooded savannah in the north. Rainfall pattern is bi-modal, the first from March to July and the second from mid-August to October. Annual average rainfall is between 513-1099 mm while temperature ranges from 21-32ºC. The Upper East region is located in the north-eastern corner of the Ghana. Its vegetation is that of savannah woodland characterized by short scattered drought-resistant trees and grass. It has one rainy season from June to September/October. The mean annual rainfall during this period is between 800 mm and 1,100 mm with temperatures that can be as low as 14ºC to more than 35ºC.

### 3.2.2 Districts and communities

With the help of extension agents, two districts were chosen in each region. Nine (9) or 10 representative farming communities were selected within each region, based on accessibility, cost considerations and production levels. In the Central and Volta regions, the study was carried out in July and August, 2010 respectively while in the Upper East region the study was conducted in January, 2011. Differences in periods of carrying out surveys in the different study areas were based on availability of farmers as advised by extension agents.

Figure 3.1 is a Map of Ghana showing the regions and communities where both PRA and structured surveys were conducted. A total of 641 farmers in 28 farming communities were involved in focus group discussion. Of these 145 were from nine communities in Central Region. Two hundred and sixty-two were from ten communities in Volta Region, and 234 were from 9 communities in the Upper East region.

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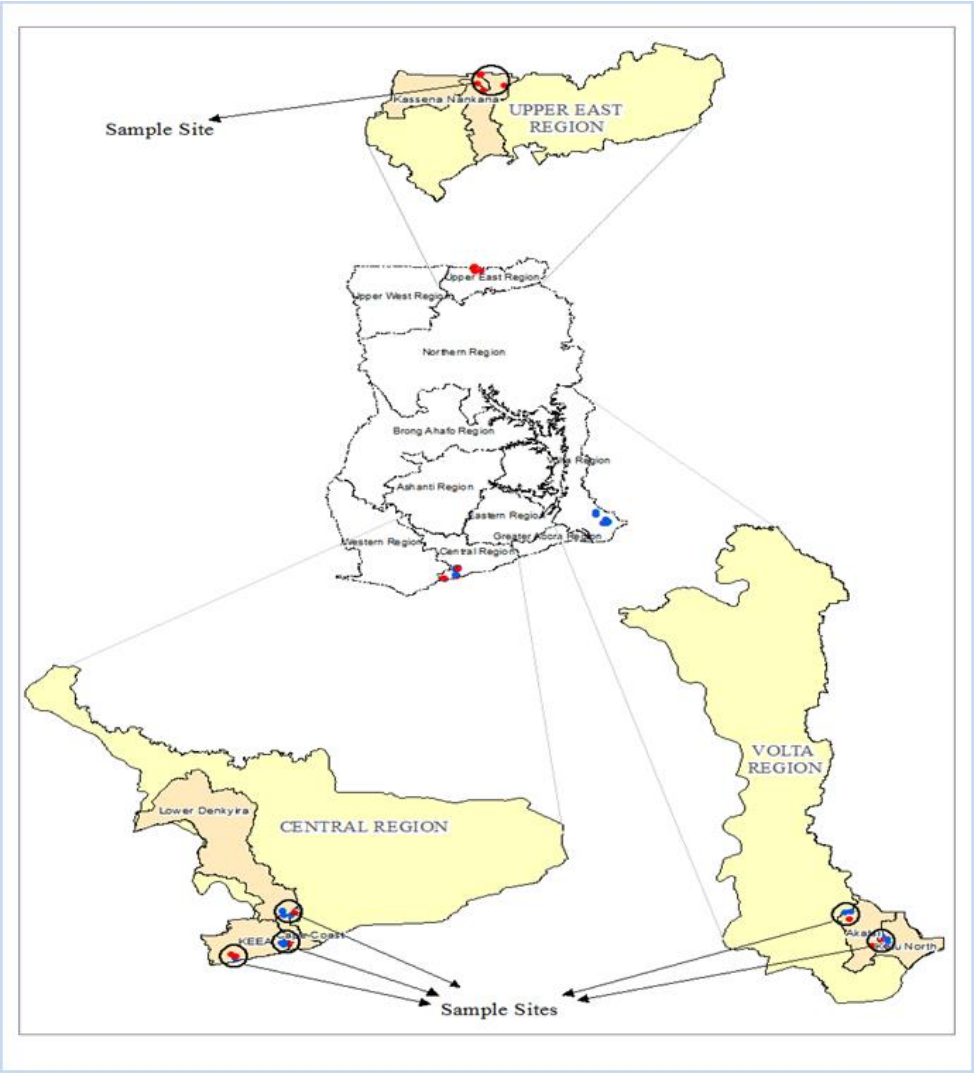


**Figure 3. 1: Map of Ghana showing sites of surveys of sweetpotato farmers conducted in 2010 and 2011.**

### 3.2.3 The PRA team

The PRA team included a breeder, two technicians, two extension agents and a translator (a member of the community who could speak and understand the local language). Opinion leaders in the communities were consulted to encouraged farmers to participate in the focus group discussions. The farmers that gathered therefore were a random sample of the members of the

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community. Interviews were held either under shaded trees at locations where the community often gathered for meetings (Figure 3.2a) or in a farmer's home (Figure 2b).


**Figure 3. 2: (a) A cross section of farmers gathered under shaded tree in Volta region; and Figure (b): A cross section of farmers gathered in a farmers home in the Central region during focus group discussions**

### 3.2.4 PRA methodology

PRA tools used included focus group discussions, seasonal and daily activity assessment, matrix and pairwise ranking and direct observations. In order to factor gender issues into the discussions, it was important to separate females from male farmers at points where gender issues were discussed. Open-ended questions were used in the focus group discussions in order to obtain views that otherwise would not be mentioned. The discussions were conducted with all the participants mixed except during the gender activity calendar analysis when men and women were separated. The language used was the local dialect with the help of a translator. In addition to the informal focus group discussions, questionnaires were also administered. Survey questions (appendix 3.1) included open and specific questions. In each region the survey lasted two weeks. Farmers who participated in the structured survey were a simple random sample of farmers in the 28 farming communities. One hundred and ten questionnaires each were administered in Central

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and Volta Region while 100 were administered in the Upper East Regions. A total of 320 questionnaires were administered. The structured survey captured the following parameters: educational status, off-farm employment, farm activities and labour, land size, cropping calendar, varieties under cultivation, most preferred cultivars, availability of resources, and importance of crops for food and income and production constraints among others. Based on farmers responses on the size of land allotted to sweetpotato cultivation, they were classified into 0.2-0.8, 1.2-1.6, 2.0-2.6, 3.2-4.1 and above 4.1ha.

### 3.2.5 Data analysis

Data collected were entered into the Statistical Package for Social Scientists (SPSS) version 17.0 and analyzed. Analysis was done for descriptive statistics, frequencies and percentages. Cross tabulations were also done. Comparisons were made between regions and between males and females. Tests for significant differences among categorical variables were done using chi-squared tests at 5 % significant level. Pie charts and histograms were also used to graphically display results.

## 3.3 RESULTS

### 3.3.1 Gender distribution within communities under study

Sixty-five per cent of the farmers involved in the focus group discussion were males and 34.8 % were females (Table 3.1). Central region had the least number of respondents with 22.6 % of the respondents followed by Upper East and Volta regions with 36.5 % and 40.9 % respectively. Also, in the structured survey similar distribution of 67 % males and 33 % female were obtained (Table 3.2).

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**Table 3. 1: Gender distribution of farmers' interviewed during focus group discussion and the districts and communities where interviews were held**

| REGIONS | District | Community | Male | Female | Total |
|---|---|---|---|---|---|
| CENTRAL | KEEA | Atonkwa | 12 | 2 | 14 |
| | KEEA | Ntranoa | 8 | 4 | 12 |
| | KEEA | Nkotrondo | 19 | 5 | 24 |
| | KEEA | Kuful farms | 13 | 6 | 19 |
| | Upper Denkyira | Danhia | 20 | 5 | 25 |
| | Upper Denkyira | Koforidua | 12 | 5 | 17 |
| | Lower Denkyira | Jukwa Abodo | 10 | 3 | 13 |
| | Lower Denkyira | Jukwa Zongo | 3 | 7 | 10 |
| | Komenda | Komenda Zongo | 10 | 1 | 11 |
| **TOTAL** | | **9** | **107** | **38** | **145 (22.6%)** |
| VOLTA | Ketu North | Kporkuve | 7 | 18 | 25 |
| | Ketu North | Tadzewu | 10 | 12 | 22 |
| | Ketu North | Devego | 22 | 9 | 31 |
| | Ketu North | Ohawu | 19 | 26 | 45 |
| | Ketu North | Vume | 11 | 11 | 22 |
| | Ketu North | Xantroli city | 7 | 8 | 15 |
| | Ketu North | Avevlime | 9 | 4 | 13 |
| | Ketu North | Xipe | 32 | 5 | 37 |
| | Akatsi | Have-Fiakpokope | 14 | 10 | 24 |
| | Akatsi | Wuxor | 18 | 10 | 28 |
| **Total** | | **10** | **149** | **113** | **262 (40.9%)** |
| UPPER EAST | KNW | Nyangua | 20 | 9 | 29 |
| | KNW | Bambisi | 15 | 6 | 21 |
| | KNE | Bonyano | 19 | 9 | 28 |
| | KNE | Boania | 19 | 8 | 27 |
| | KNE | Mancharo | 18 | 7 | 25 |
| | KNE | Tekuru | 17 | 9 | 26 |
| | KNE | Nimbasinia | 16 | 10 | 26 |
| | KNE | Punyoro | 20 | 8 | 28 |
| | KNE | Tekuru | 18 | 6 | 24 |
| **Total** | | **9** | **162** | **72** | **234 (36.5%)** |
| **Grand Total** | | **28** | **418 (65.2%)** | **223 (34.8%)** | **641** |

**KEEA= Komenda-Edina-Eguafo-Abrem, KNW= Kassina Nankana West, KNE= Kassina Nankana East**

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### 3.3.2 Characteristics of farmers' involved in the structured survey

The ages of the farmers captured in the structured survey ranged from 20-80 years with a mean value of 45 years. There was a significant difference ($\chi^2$ = 59.06, P< 0.05) among the gender categories with respect to number involved in the structured survey. The responses of the female and male surveyed farmers as regards their levels of education revealed a significant (P<0.05) difference between the two sexes for all categories of levels of education (Table 3.2). Thirty-seven per cent (37 %) of the respondents had no formal education, 20% were illiterate male while 17 % were illiterate females. Of the 44 % that had primary education, about 15 % were females while 30% were males. About 17 % and 2 % had secondary and tertiary education respectively. Only 2 % of farmers with secondary education were females while 14 % were males. No female farmer had tertiary education; however, about 2 % males had been educated to tertiary level. There were also significant differences (p<0.05) between males and female with respect to engagement in off-farm employment (Table 3.2). The majority of farmers (61 %) had no off-farm employment. The more educated farmers were, the more off-farm employment they had. Females who were the least educated (Table 3.2) had the least off-farm employment with 36 % respondents while males who were the most educated had the most off-farm employment with 41 % respondents.

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**Table 3. 2 Gender distribution and educational levels of all farmers' interviewed during structured surveys of sweetpotato farmers**

| Description | Male % | Female % | Total % | $\chi 2$ | p-value |
|---|---|---|---|---|---|
| **Number interviewed (%)** | 67 | 33 | 100 | | |
| **Not educated (%)** | 20.8 | 16.4 | 37.2 | 21.4 | < 0.05 |
| **Up to primary education (%)** | 29.7 | 14.8 | 44.5 | 75.9 | <0.05 |
| **Up to secondary education (%)** | 14.5 | 2.2 | 16.7 | 27.9 | <0.05 |
| **Tertiary education (%)** | 1.6 | 0.0 | 1.6 | 69.9 | <0.05 |
| **Have off-farm employment (%)** | 41.0 | 36.0 | 39.0 | 8.8 | <0.05 |
| **Have no off-farm employment (%)** | 59.0 | 64.0 | 61.0 | 8.8 | <0.05 |
| **Total (N)** | 212 | 105 | 317 | 36.1 | <0.05 |

**Note: $\chi 2$ value for off-farm employment was 16.8 and was significant at P<0.05 level**

### 3.3.3 Gender distribution and total land size under cultivation

Information gathered during focused discussions showed that farmers owned between 0.2 to 10.1 ha of land with a mean farm size of 0.8 ha, on which they assigned the various crops they cultivate. Some farmers however hired a few more acres to supplement what they owned. Results from formal survey indicated significant (P<0.05) differences between farm size owned by male and female farmers (Table 3.3) except for those cultivating 0.2 – 0.8 ha and 3.2 ha. Male farmers cultivated between 0.8 ha and above 4.1 ha while females planted mostly between 0.2 ha and 2.8 ha, with the majority planting between half and two hectares.

During the focus discussion females mentioned that home chores (such as fetching water, firewood, cleaning homes, child care etc.) and tasks they are required to take on their husbands'

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farms constraints their ability to grow large acreages. The number of female farmers decreased sharply as cultivated farm size increased. Apart from a few female farmers who owned land, the majority generally did not own land but planted whatever parcels of land was allotted them by their husbands.

**Table 3. 3 Gender distribution and land size under cultivation**

| Gender | Total land size | | | | | Total |
|---|---|---|---|---|---|---|
| | 0.2-0.8 ha | 1.2-1.6 ha | 2.0-2.8 ha | 3.2 ha | >4.5 ha | |
| male | 27 | 74 | 61 | 10 | 38 | 211 |
| female | 40 | 36 | 24 | 6 | 0 | 106 |
| Total (n) | 67 | 110 | 85 | 16 | 38 | 317 |
| **$\chi 2$** | **2.4** | **12.1*** | **16.1*** | **1.0** | **42.9*** | |

*** = Significant at P<0.05 and 1*df***

### 3.3.4 Crops cultivated by respondents

Farming was the main vocation for most farmers and crops grown were therefore for food and income generation. The three regions did not differ (P>0.05) with respect to their response to cultivation of sweetpotato as multiple or sole crop, however in each region, significant differences (P<0.05) were realized between the two categories of sweetpotato cultivation (Table 3.4). Ninety-nine percent of farmers cultivated other crops apart from sweetpotato and 1 % practiced sole cropping. The crops listed by farmers in the Central and Volta regions include cassava, sweetpotato, yam, cocoyam, maize, plantain, vegetables, fruits, legumes and oil palm. In addition to these, Volta region farmers also cultivated rice. Farmers in Upper East region grew all crops listed above in addition to sorghum, millet, Frafra potato and sesame seeds.

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**Table 3. 4 Number of respondents in structured survey that cultivate sweetpotato in multiple cropping system or as sole crop**

| Regions | Multiple cropping | Sole crop | Total | $\chi 2$ |
|---|---|---|---|---|
| **Central region** | 109 | 1 | 110 | **110.7*** |
| **Volta region** | 105 | 2 | 107 | **100.4*** |
| **Upper East region** | 100 | 0 | 100 | **95.0*** |
| **Total** | **314(99 %)** | **3(1 %)** | **317** | **308.1*** |
| **$\chi 2$** | **0.39** | **1.0** | | |

*** = significant at P<0.05, 1degree of freedom (*df*)**

### 3.3.5 Gender and size of land under sweetpotato cultivation

As shown in Table 3.5, there were significant (P<0.05) differences between the sexes for farmers growing 0.2 – 0.8 ha of sweetpotato in Upper East region and for farmers cultivating 0.9 – 1.8 ha in Central and Volta regions. Significant differences (P<0.05) were also observed among the three regions for all categories of sweetpotato farm sizes cultivated except for 3.1 -4.0 ha. Seventy-nine percent (79.2 %) of respondents cultivated between 0.2 – 0.9 ha of sweetpotato. This comprised 49.5 % of male respondents and 29.7 % of female respondents. About seventeen percent of farmers cultivated 0.9 – 1.8 ha, corresponding to 13.6 % of males and 3.2 % of females. Only one farmer out of the 317 farmers interviewed planted more than 4.0 ha of sweetpotato. The farmers attributed the low acreages of sweetpotato cultivation to labour intensive and high costs of mound making, low prices and lack of ready market among others. In contrast to the Upper East region where farmers cultivated only between 0.2 and 0.8 ha of sweetpotato, farmers in the Central and Volta Regions cultivated between 0.2 ha and more than 4.0 ha.

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**Table 3.5 Gender distribution and number of respondents for each category of farm size allotted to sweetpotato production in each region covered in formal survey**

| | | Gender | | | |
|---|---|---|---|---|---|
| **Size of Sweetpotato farm** | **Regions of survey** | **Male** | **Female** | **Total/category** | **χ2** |
| **0.2-0.8ha** | Central Region | 46 | 38 | 84 | **0.8** |
| | Volta Region | 28 | 39 | 67 | **1.8** |
| | Upper East Region | 83 | 17 | 100 | **43.5*** |
| | **Total** | **157(49.5 %)** | **94(29.7 %)** | **251(79.2 %)** | |
| | **χ2** | **30.1**** | **9.8**** | **6.5**** | |
| **0.9-1.8ha** | Central Region | 21 | 4 | 25 | **11.5*** |
| | Volta Region | 22 | 6 | 28 | **9.1*** |
| | **Total** | **43(13.6 %)** | **10(3.2 %)** | **53(16.8 %)** | |
| | **χ2** | **21.6**** | **5.6**** | **26.8**** | |
| **1.9-3.0ha** | Central Region | 1 | 0 | 1 | **1.0** |
| | Volta Region | 8 | 2 | 10 | **3.6** |
| | **Total** | **9(2.9 %)** | **2(0.6 %)** | **11(3.5 %)** | |
| | **χ2** | **12.7**** | **3.8** | **16.5**** | |
| **3.1->4** | Central Region | 1 | 0 | 1 | **1.0** |
| | **Total** | **1(0.3 %)** | **0(0 %)** | **1(0.3 %)** | |
| | **χ2** | **2.0** | | **2.0** | |

***= Significant at P<0.05, 1*df* and ** = Significant at P<0.05, 2 *df***

### 3.3.6 Cropping system and calendar of activities

Significant differences (P<0.05) were observed between the regions with respect to cropping calendar and between the categories of planting dates within each region. In the Central Region, the season begins in March with land preparation. Maize is usually planted in April, followed by sweetpotato and cassava. The main period for sweetpotato cultivation is between May and

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September (Table 3.6) either as a sole crop or intercropped with maize or cassava. Farmers who planted sweetpotato as a sole crop staggered planting within this period. Sweetpotato harvest begins in August and continues till December. Farmers in Kuful in the KEEA district of the Central region reported that wetland planting in the dry season (between December and January) was also practiced because the Kakum River creates marshy areas around their farms making water accessible. Vines were also preserved and multiplied in these wetlands for major season planting.

**Table 3. 6: Number of respondents in the different categories of cropping calendar for sweetpotato in the three regions**

| | Number of respondents and planting date | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **Regions** | Mid Mar-Apr | Mid May-Jun | Mid Jun - Jul | Mid Jul-Aug | Mid Aug.-Sep | Harvest | Total | **χ2** |
| **Central region** | 12 | 67 | 29 | 2 | 0 | Aug-Dec | 110 | 139*** |
| **Volta region** | 1 | 12 | 74 | 17 | 1 | Aug-Dec | 105 | 173.2*** |
| **Upper East region** | 0 | 5 | 93 | 2 | 0 | Mid-Jul-Sept | 100 | 333.9*** |
| **Total** | 13 | 84 | 196 | 21 | 1 | | 315 | 416.5*** |
| **Mean** | 4. | 26.7 | 62.2 | 6.7 | 0.003 | | | |
| | 19.2** | 82.4** | 35.2** | 22.4** | 331.3** | | | |

**** = Significant at P<0.05, 2*df*; *** = Significant at P<0.05, 4*df***

The chi-squared values show significant (P<0.05) differences among regions with respect to periods of planting sweetpotato. In the Volta Region, land preparation starts between February

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and March. If rains are early, maize is planted in March while sweetpotato is planted in May (Table 3.6) as a sole crop or intercropped with maize. Minor season crop may be grown in September and harvested in January if the rains continue until then. Some farmers undertook vine multiplication in March at the onset of the rains in this region. In the Upper East Region sweetpotato is the first crop to be planted in the major season before major crops like maize, millet and sorghum are planted. Due to the short production cycle of sweetpotato, farmers indicated that, they are able to harvest sweetpotato early for consumption while waiting for maturity of their major crops. Sweetpotato is therefore a major food security crop for farmers in this region.

### 3.3.7 Sources of water

Informal discussions revealed that all farmers relied on rainfall for their farm activities because irrigation cost was prohibitory. Other sources of water like streams, rivers, boreholes and pipe borne water were mostly for household uses. In the Upper East region a major dam that supplied water for many communities had dried up and was no longer useful for farming. Lack of pumps and irrigation facilities in these areas implies total crop failure if the rains fail.

### 3.3.8 Acquisition of sweetpotato planting material

During focus group discussion most farmers in all three regions, indicated that, they preserved and multiplied their own vines. Some multiplied vines on wetlands during the dry season. Others also grew vines around their homes where they are able to irrigate with waste water from household activities. Some farmers however bought vines from other farmers or got them free from neighbours. Others made use of re-growth from previous sweetpotato sites.

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### 3.3.9 Cost of production of sweetpotato

The main cost item in sweetpotato production as gathered in the informal discussion in the three regions was labour for mound making and weeding. None of the farmers interviewed used agrochemicals or heavy machinery. Due to labour requirements, sweetpotato cultivation is almost described as a youth activity. To offset labour cost, farmers either engage family members (wives and children) or practiced what is commonly known as the 'Nnoboa' system, where a group of farmers agree to work on each other's farms in turns. When children are involved they could be as young as eight years of age. Occasionally however, some farmers especially those cultivating over 2 ha, hire labour to augment their efforts. Another major cost is in the transportation of farm produce to market centers for sale.

### 3.3.10 Marketing sweetpotato

According to farmers involved in focus discussions, harvesting is staggered, based on demand. Farms are usually far away from market centres and roads to these farms are inaccessible, especially during the major rainy season. A lot of roots are therefore lost before they get to the market. Farmers in Central region had their main markets in Accra, Kumasi and in Cape Coast, while those in Volta region sell mainly to market women in Akatsi, Keta, Accra and sometimes Togo. Farmers revenue from sale of roots is higher in the minor season because demand out strips supply. Results obtained from the structured survey indicated however that, when there was bumper harvest in the major season, most farmers (93.4 %) were unable to store their crop after harvest for lack of storage facilities (Table 3.7). The 4 %, who did, used very old traditional methods which were ineffective. Significant differences were observed between farmers who store and do not store sweetpotato. As indicated by the chi-squared values, the regions varied

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significantly (P<0.05) in terms of storage of sweetpotato but did not vary with regard. Eleven respondents out of the 13 farmers who stored sweetpotato were in the Upper East Region while 2 respondents were in the Central region. Focus discussions revealed that the lack of storage facility causes market glut and loss of revenue to farmers. In the Upper East region, farmers complained about their inability to compete with sweetpotato imports from Burkina Faso as these were often perceived as much better quality than what the local farmers produced.

**Table 3.7: Number of farmers' in the three regions who store sweetpotato**

| | Farmers response | | | | $\chi 2$ |
|---|---|---|---|---|---|
| **Regions of Survey** | **Farmers storing sweetpotao** | **Farmers not storing sweetpotato** | **Farmers not responding** | **Total** | |
| **Central** | 2 | 104 | 4 | 110 | |
| **Volta** | 0 | 103 | 4 | 107 | |
| **Upper East** | 11 | 89 | 0 | 100 | |
| **Total (n)** | **13 (4.1%)** | **296 (93.4%)** | **8 (2.5%)** | **317** | **303.7*** |
| **$\chi 2$** | **16.0**** | **1.4** | | | |

*** = Significant at P<0.05, 1*df*; ** = Significant at P<0.05, 2*df***

### 3.3.11 Varieties of sweetpotato cultivated by farmers'

Farmers interviewed in the formal survey listed a number of varieties that they grew. Among these were Faara, Santom Pona, Jukwa Orange, Kadzie, Blue Blue, Worleworme and others. As shown in Figure 3.3 most farmers generally cultivated more than one variety. Almost 50 % of farmers interviewed cultivated between one and two different varieties while 35 % grew three to four varieties. Ten percent of farmers grew 5-6 varieties while only 6 % grew more than six varieties. The most popular varieties with high market value were Blue Blue in the Central

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region and Faara and Kadzie in the Volta region. Farmers in Upper East Region could not agree on their best variety.

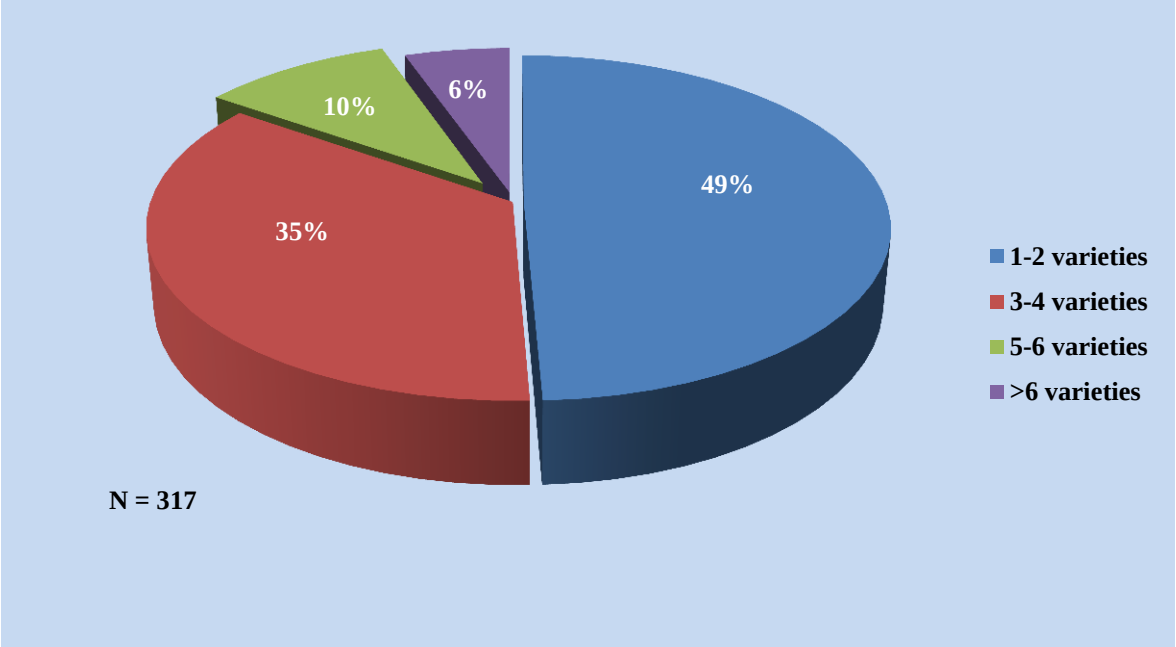


**Figure 3.3: Percentage of farmers' and the four categories of number of varieties grown**

Table 3.8 shows significant differences between farmers growing only local and farmers growing both improved and local varieties. Sixty-eight per cent of farmers grew both local and improved varieties, while 31 % had discarded their old varieties for new ones. Of the farmers who had discarded their old varieties, 72 % did so as a result of poor yields. Eleven per cent (11 %) said their varieties were too sweet while 16 % abandoned their varieties as a result of poor market value (Figure 4).

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**Table 3.8: Number of farmers' growing local and improved varieties in the three regions**

| | Varieties Grown by farmers | | | $\chi 2$ |
|---|---|---|---|---|
| **Regions** | **Local and improved** | **Only local** | **Total** | |
| **Central region** | 64 | 46 | 110 | |
| **Volta region** | 54 | 50 | 107 | |
| **Upper East region** | 98 | 2 | 100 | |
| **Total (N)** | **216(68 %)** | **98(31 %)** | **317** | **44.0*** |
| **$\chi 2$** | **14.8**** | **43.4**** | | |

*** = Significant at P<0.05, 1*df* and ** = Significant at P<0.05, 2*df***

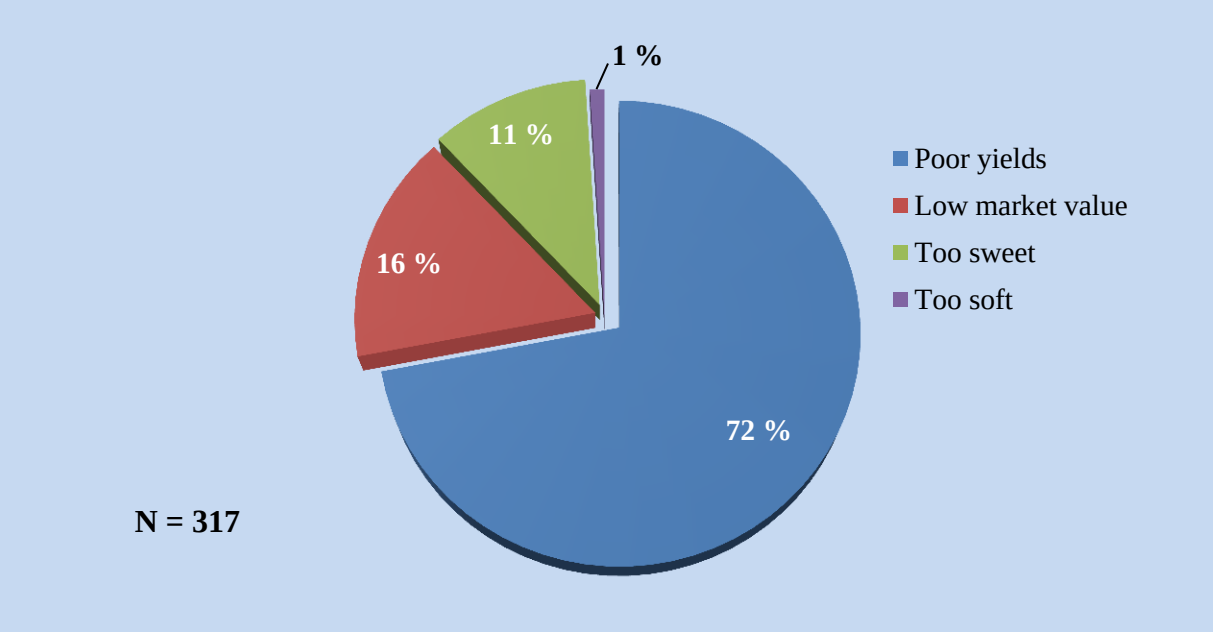


**Figure 3.4: Farmers' reasons for discarding their (local) varieties**

### 3.3.12 Relative importance of crops for food

During informal interviews a number of crops were listed as important in the diets of farmers. A pairwise comparison was performed to identify the most important crops for food. The most preferred food for Central region and Volta Region were Cassava and maize respectively. In

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Upper East, millet ranked highest for food. Results from the structured survey also gave a similar picture. Figure 3.5 shows the level of importance of crops for food as ranked by the respondents. Different crops were selected as most important food in the three regions. Cassava ranked highest with 91 % respondents, followed by maize with 8 % respondents in the central region. In the Volta Region, maize ranked highest with 98 % respondents, while in the Upper East Region millet ranked highest (68 %) followed by maize (18 % respondents) and sorghum (4 % respondents). Cassava was ranked highest in Central Region because; farmers' major local meal (fufu) has cassava as its main constituent and is eaten almost every day of the week. Akple, the main traditional food preparation in the Volta Region is made from maize. It is therefore understandable that maize ranked highest in that region.

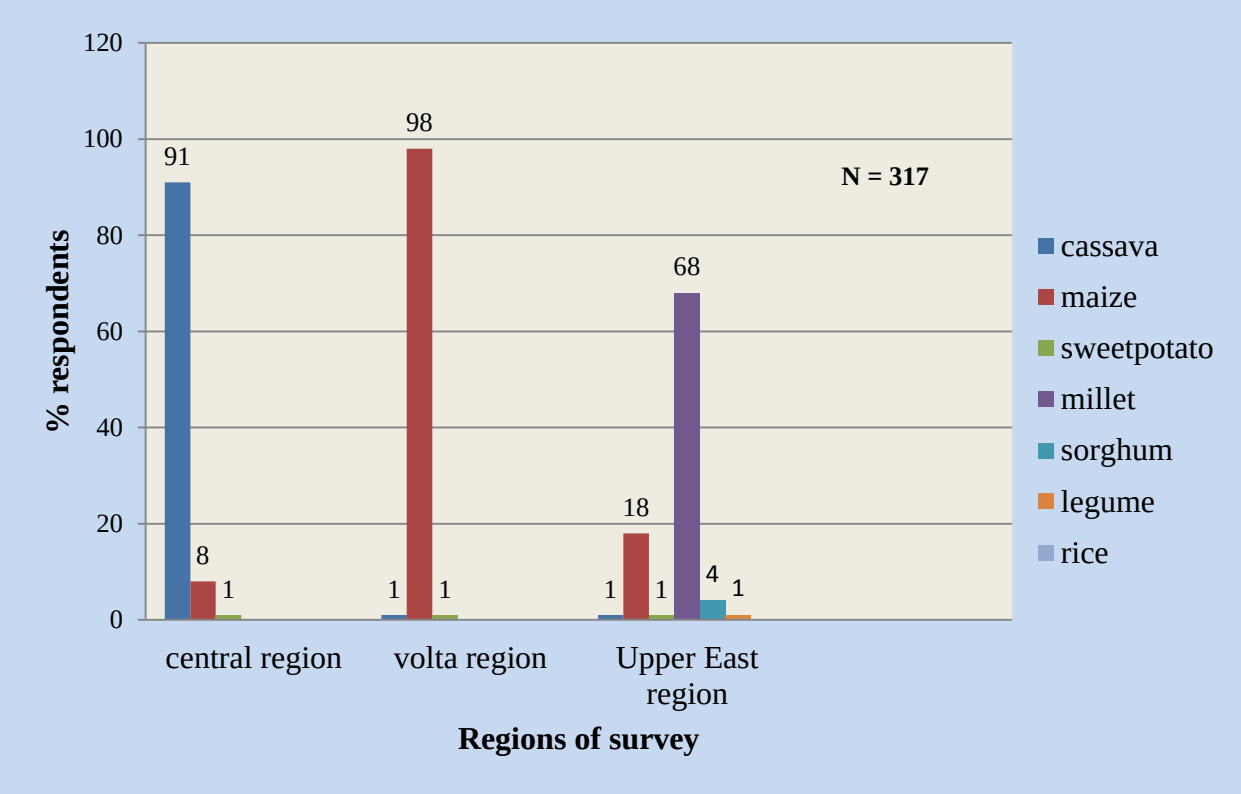


**Figure 3.5: Relative importance of crops for food in the three Regions of Ghana**

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Farmers ranked millet highest (68 % respondents) in the Upper East Region because of the numerous uses of the crop. Not only is millet important in their traditional cuisine 'tuo' but it is used for payment of dowry, donations at funerals and many other customary rites. The farmers in all three regions cited ignorance of other culinary uses of sweetpotato as one factor responsible for infrequent use of the crop in traditional cuisines. While cassava for example could be put into about thirteen different local preparations (fufu, banku, gari, agbelima akple, yakayake, tapioca, starch, konkonte, biscuit, kakro, agbozume and ampesi), sweetpotato is cooked mainly in about four ways (frying, boiling, roasting, and sometimes made into porridge (mpotompoto) for children. Figure 3.6, shows that 50 % of farmers knew only three traditional methods of cooking swetpotato while another 32 % and 16 % knew two and four ways respectively. Also the low dry matter and high sugar levels in the roots render then unsuitable for local preparations as sweetness made frequent usage tiresome. Some farmers believed that, frequent consumption of sweetpotato causes diarrhoea, malaria and impotence in men.

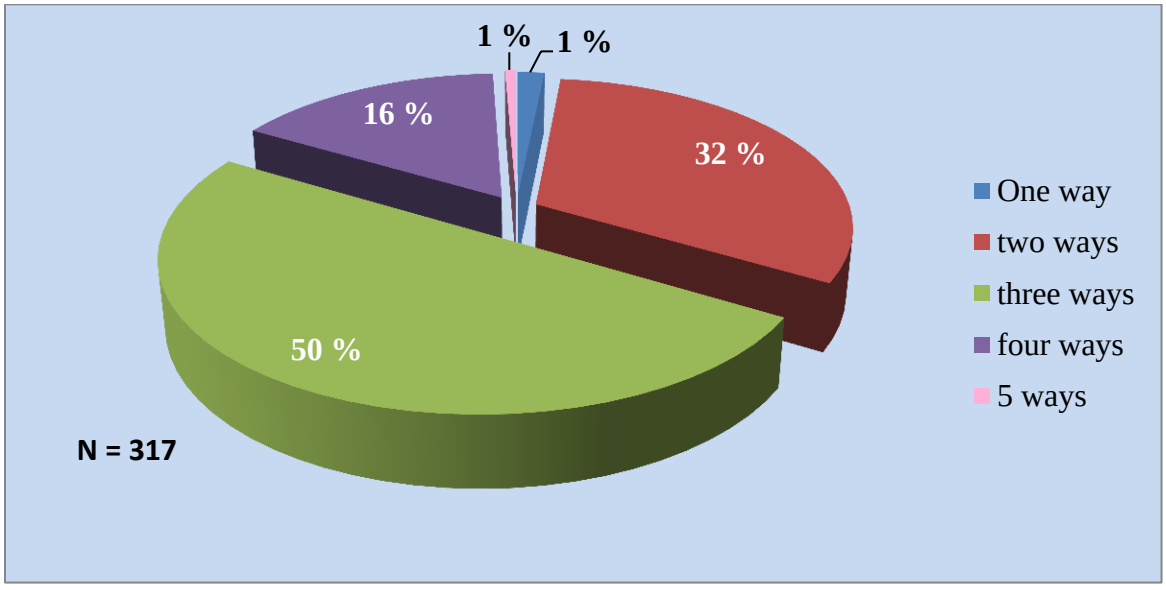


**Figure 3.6: Farmers' responses to the number of different ways that sweetpotato is prepared locally**

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Data was obtained on the percentage of farmers to whom sweetness of the crop was a hindrance to its frequent utilization in local cuisines. A significant ($P<0.05$) difference was observed between farmers who were indifferent about sweetness crop and those to whom sweetness limits frequent usage(Table 3.9). Sixty-nine per cent of respondents stated that the sweetness affected regular consumption while for 31 % were indifferent. Other reasons given for low utilization were low dry matter, and the seasonality of the crop relative to cassava, maize and millet which are available year round. Some farmers believed that due to the high sugar levels, frequent consumption of sweetpotato causes diarrhoea, malaria and impotence in men. In the focus group discussion, however, women farmers in the Upper East region emphasized the importance of sweetpotato as a hunger relief crop during the lean season and before maturity of major food crops. In Central region the difference between the two categories of scores was not significant ($P>0.05$) but significant ($P<0.05$) differences were observed between the two categories in Volta and Upper East regions.

**Table 3.9: Farmers' responses on impact of sweetness on regular consumption**

| Regions | Sweetness limits regular usage | Indifferent | No answer | Total | $\chi 2$ |
|---|---|---|---|---|---|
| **Central** | 63 | 47 | 0 | 110 | 2.3 |
| **Volta** | 70 | 34 | 3 | 107 | 12.2* |
| **Upper East** | 82 | 18 | 0 | 100 | 40.9* |
| **Total** | **215(69 %)** | **99(31 %)** | **3** | **317** | **22.5**** |

*** = P<0.05 at 1df and ** = P<0.05 at 2df**

### 3.3.13 Preferred sensory attributes for frequent consumption

Figure 3.7 shows sensory attributes that were listed by farmers as important. Of these low sweet ranked highest with 53.2 % respondents followed by poundability at 27.1 %. Firmness (a

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measure of dry matter content) ranked third at 12.4 %. These results were also supported by farmers during focus group discussion when farmers reiterated that sweetpotato was not used in traditional food preparations because it is deficient in the attributes necessary for such usage. These rankings demonstrated that high dry matter and low sugar varieties are important if the crop is to gain prominence as one of the major staples.

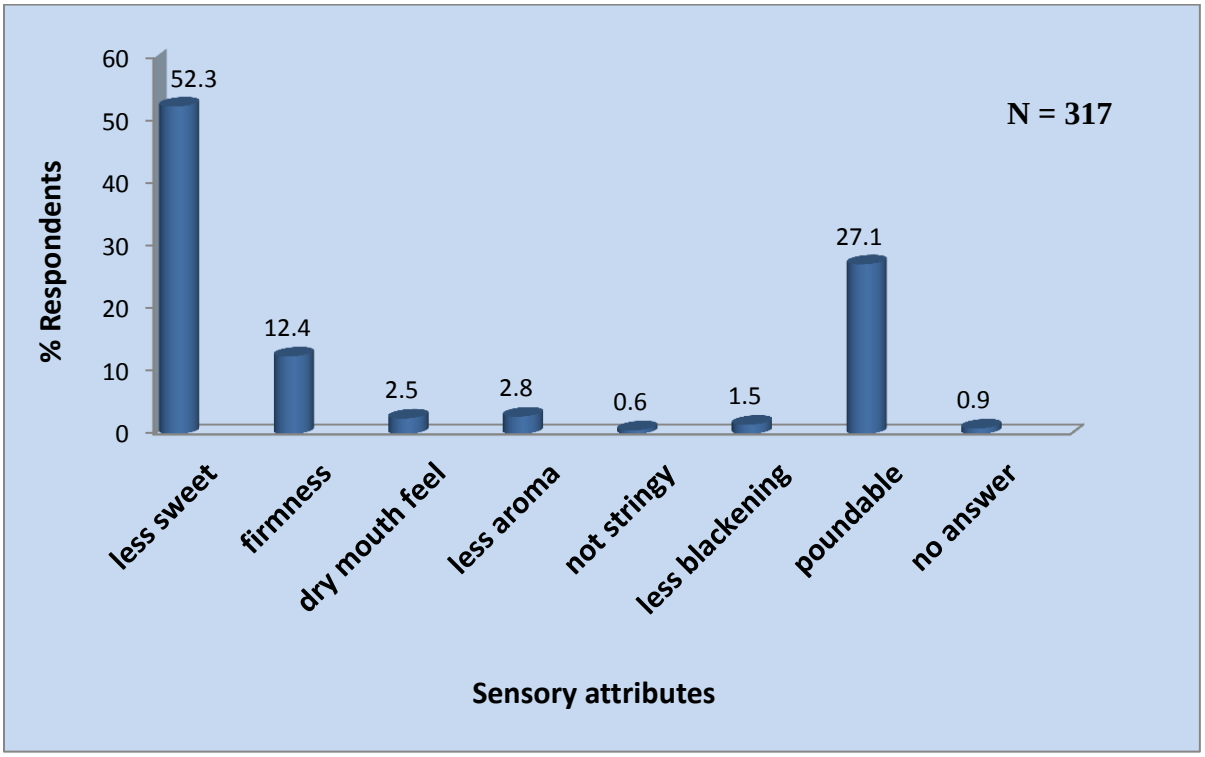


**Figure 3.7: Preferred sensory attributes for regular consumption of sweetpotato**

### 2.3.14 Farmers' willingness to grow low-sugar cultivars

On farmers willingness to grow and consume low-sugar cultivars as shown in Figure 3.8, 70 % of farmers expressed willingness while 30 % did not. The focus group interviews in the three regions supported this finding with farmers advocating for such cultivars to boost utilization and production of sweetpotato and thereby increase farmers' incomes.

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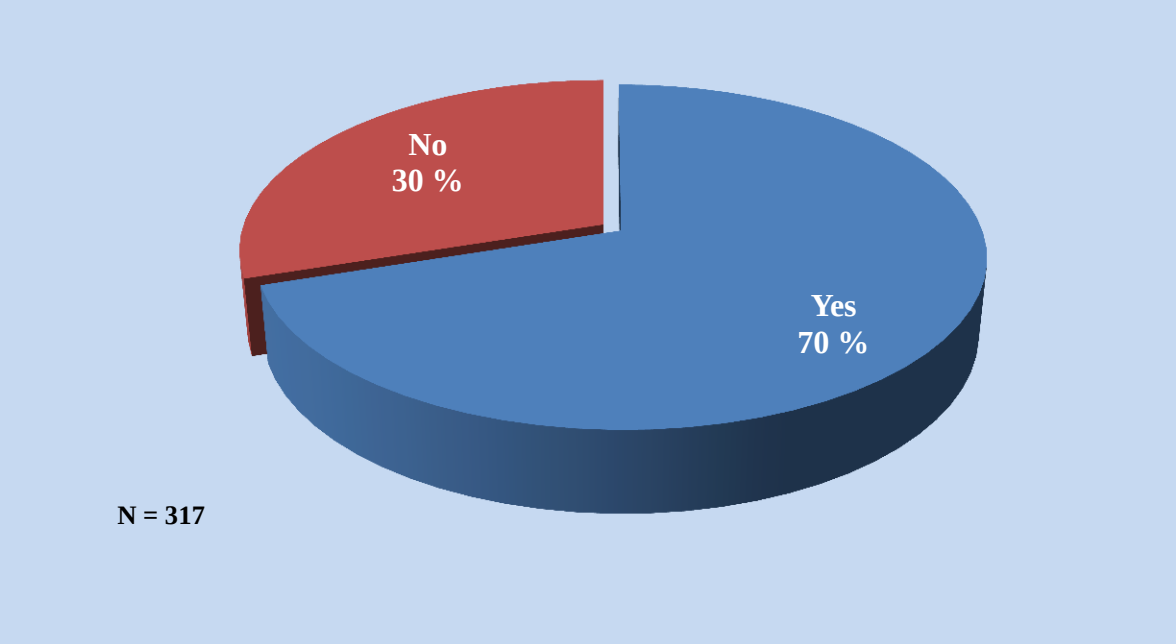


**Figure 3.8: Percentage of farmers' willing to grow low-sweet varieties**

### 3.3.15 Relative importance of crops for income on a per hectare basis

Regarding income generation from crops, sweetpotato ranked highest (55 %, 52% and 40 %) for Central, Volta and Upper East Regions respectively (Figure 3.9). Cassava was second for Central (39 %) and Volta regions (19 %) while vegetables and Legumes placed second (34 %) and third (14 %) respectively in the Upper East Region. The informal survey findings was in conformity with these results as farmers enumerated the following as contributory factors to the ranking of sweetpotato high for income generation; higher yield per acre, short production cycle and higher price per bag. The farmers recognize that sweetpotato has a higher commercial value i.e. yield and income per acre compared to the other crops. The lack of storage technology however, often resulted in market gluts and losses in revenue. Also, due to the low comparable consumer

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demand of sweetpotato, occasioned by deficiencies in consumer preferred traits, farmers prefer to focus more on the cultivation of the other staples.

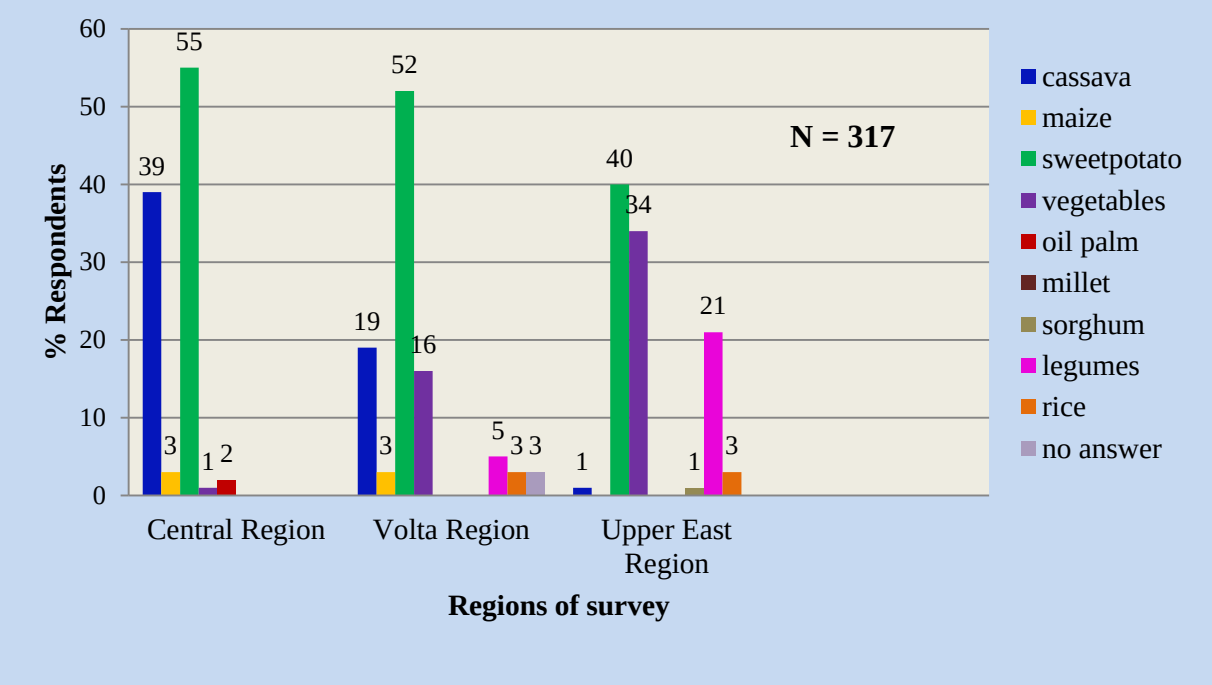


**Figure 3.9: Relative importance of crops for income on a per hectare basis**

### 3.3.16 Farmers knowledge on orange fleshed sweetpotato (OFSP)

Figure 3.10 shows proportion of farmers with or without prior knowledge on the existence and nutritional importance of OFSP. Unlike in the Central Region where 78 % of farmers were unaware of such varieties 74 % of farmers in the Volta and 56 % in Upper East Regions had seen or heard about these varieties. In all regions farmers who knew about OFSPs had also heard about its nutritional benefits and expressed interest in them. Some of the farmers had eaten OFSPs in the past, but complained about their overly sweet and watery characteristics.

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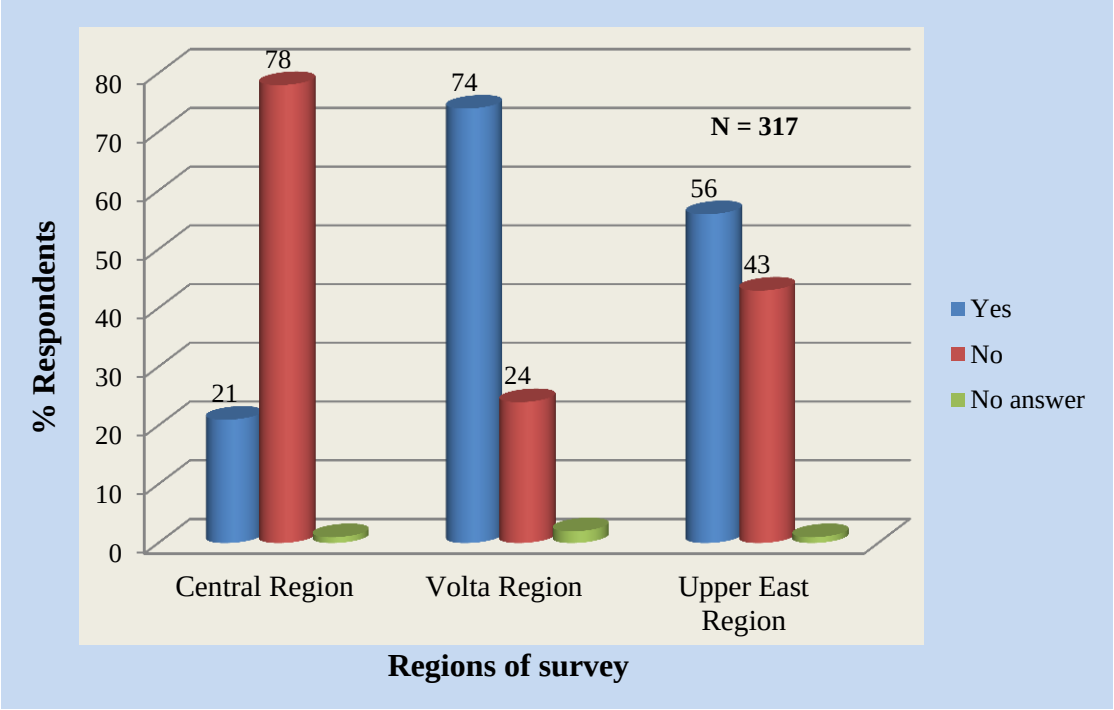


**Figure 3.10: Farmers' knowledge on orange-fleshed sweetpotato**

### 3.3.17 Production constraints

Production constraints can be grouped into two categories A and B (Figure 3.11). Category A consists of constraints that limit cultivation of the crop while category B constraints relate to demand and supply. Drought ranked highest among constraints in category A and was the most important production constraint identified by farmers in Central and Volta Regions with 55 % and 59 % respondents respectively. Low market price was identified as the most limiting category A constraint to production for Upper East farmers with 50 % respondents (Figure 3.11). However in the focus discussion farmers bemoaned the negative impact of demand on production. According to them, low utilization of the crop in local cuisines and lack of diversified usage result in lack of ready market and low prices. This is confirmed by the results

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depicted in figure 3.11. According to the farmer, increasing demand will result in increase in production levels

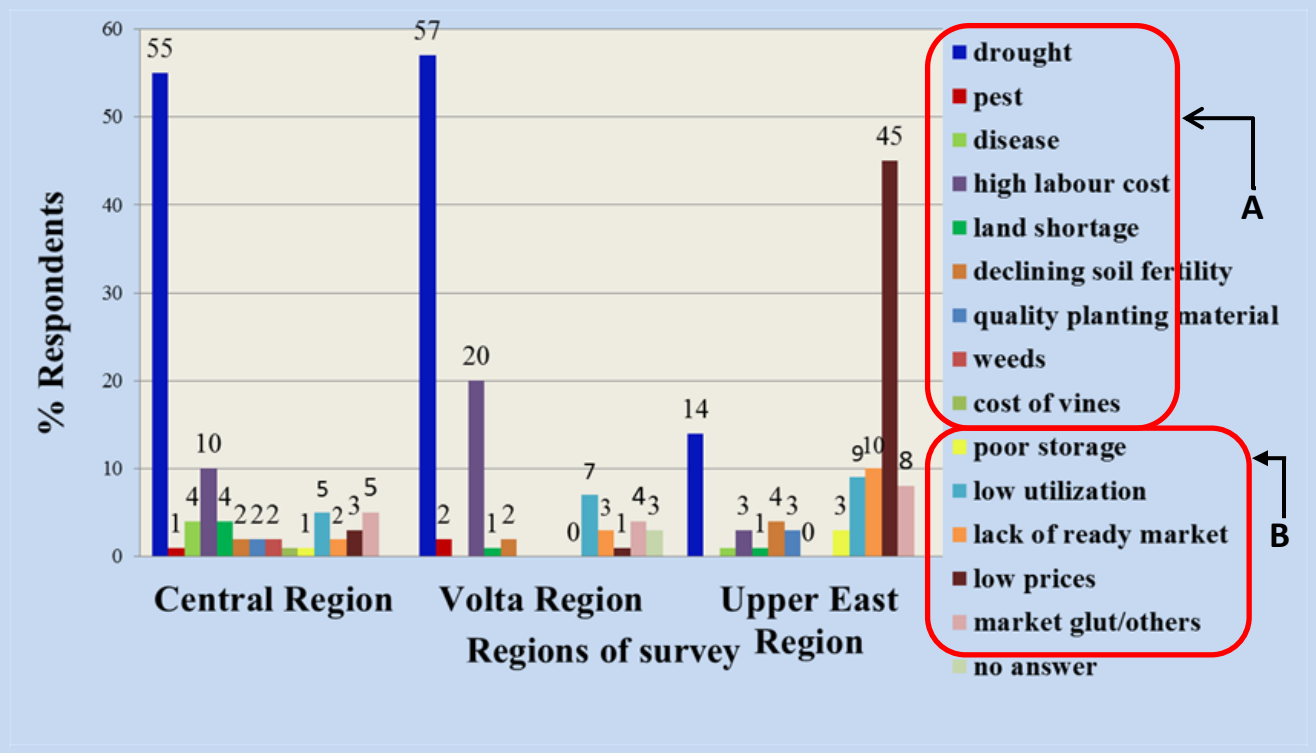


**Figure 3.11: Production constraints listed by farmers' in the three Regions of the survey in Ghana**

### 3.3.18 The five most important characters for choosing a variety to grow

During open interviews, farmers listed a number of characters in sweetpotato that determined their choice of a variety to grow. Information obtained in structured interviews on the five most important of these traits is presented in Figure 3.12. High market value ranked highest with approximately 50 % of respondents, followed by high yielding varieties with approximately 40 % respondents. Drought resistance and early maturity placed third with 4 % respondents each.

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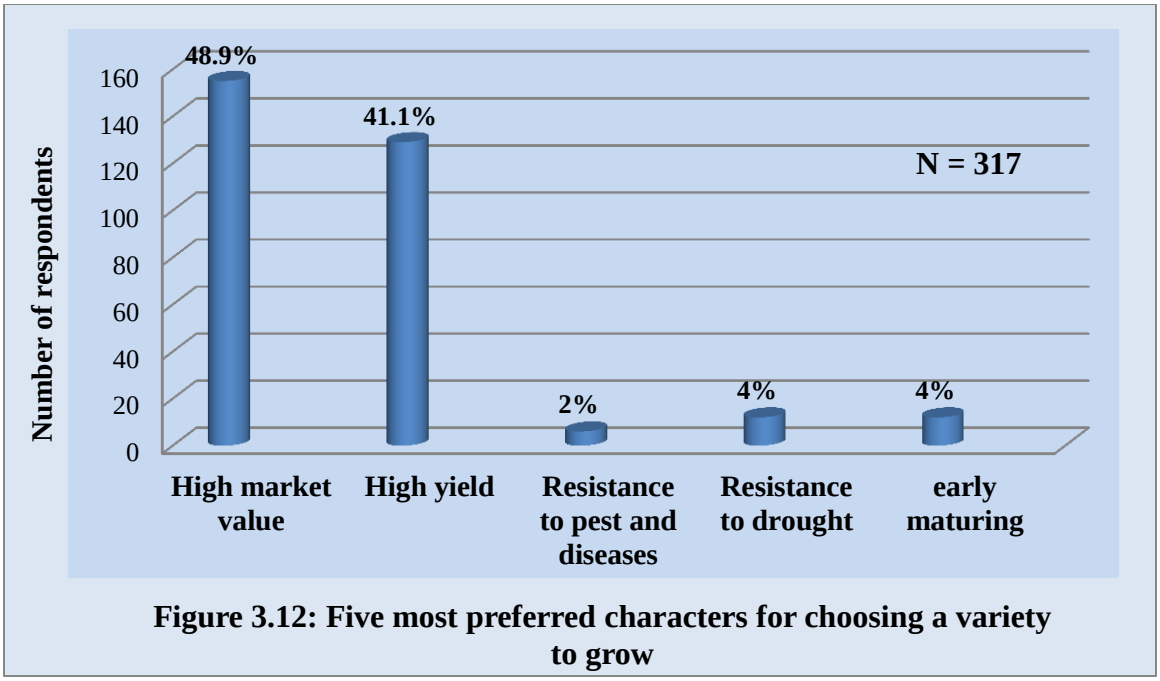


**Figure 3.12: Five most preferred characters for choosing a variety to grow**

**Figure 3.12: Five most preferred characters for choosing a variety to grow**

## 3.4 DISCUSSION

Client oriented research fosters farmers' ownership of a project and consequently facilitates the adoption of the developed technologies (Zeven, 2000; Odendo *et al.*, 2002; van de Fliert and Braun, 2002; Witcombe *et al.*, 2005; Gibson *et al.*, 2008). An attempt was made to obtain information from farmers through a PRA that was followed by a formal survey.

A large percentage of farmers (37 % uneducated, 44 % primary education, making a total of 81 % of farmers) had little or no education. Most of these farmers had no off-farm employment, and were therefore permanently employed in their farms. This coupled with their small acreages (averaging about 1.9 acres for all crops under cultivation), is a reflection of the subsistence livelihood of these farmers. Farming remains the major source of employment for many rural dwellers, whose often low educational status limits opportunities to obtain off-farm employment. Female farmers in this study were not only the least educated but were also the least engaged in

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off-farm employment. According to (Odendo *et al*., 2002), farmers' socio-economic status in addition to inappropriateness of the technologies and unavailability of required inputs, can constrain farmers' adoption of new technologies. The low educational status that characterized farmers in this study could therefore be a deterrent to technology adoption, which reinforces the need for client oriented research (van de Fliert and Braun, 2002; Witcombe *et al*., 2005), to ensure the adoption of new approaches by farmers. The involvement of farmers in this study therefore will enhance adoption of new approaches that may result from this study.

Even though farm lands were generally very small; averaging about two (2) acres, female farmers had even much smaller lands for cultivation as depicted by the sharp decrease in the number of female farmers as the number of hectares of farm size increased (Table 2 and 5). This could be attributed to the fact that apart from assisting husbands on their farms, women were also tasked with heavy household chores which makes it difficult to be heavily engaged in their own farming activities. They also did not own their farm lands but relied on their partners for land. These gender roles are socially defined, and so entrenched in rural communities that it is hard to advocate for change without appropriate education.

Land allotted to sweetpotato cultivation was also typically very limited and small. This was neither due to of farmers' inability to produce the crop, nor to low level of importance of sweetpotato, but rather to certain constraints which restricted expanded production. Among these constraints identified by the respondents were; unavailability of irrigation facility, lack of storage technology, high costs of labour, lack of financing, erratic payments for farm produce, low demand, unreliable markets, low prices and limited forms of utilization of sweetpotato.

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In all three regions surveyed, farmers relied heavily on rainfall for production. Cost of irrigation is so high that it is out of reach of subsistence farmers. Water is however, critical for storage root formation during the first few weeks after of sweetpotato growth and also for continues bulking. However current rainfall pattern is erratic and inadequate, and poses a serious threat to sweetpotato production. Drought therefore emerged as the most serious constraint to sweetpotato cultivation in two out of the three regions surveyed and emerged second in the third region.

Farmers indicated through informal discussions that harvest is good when climatic conditions, particularly rainfall were favorable. However, due to lack of storage facilities and technology, they are unable to store the crop from bumper harvests. To avoid spoilage, they are compelled to send all their produce to the market. This creates a glut at the market, with its attendant decline in prices, and erratic income generating potential of sweetpotato. Coupled with high costs of labour, inaccessible farm roads, and its attendant high costs of transportation, farmers' incomes dwindle, and the attraction to increase sweetpotato production is lost. To help improve on market prices and reduce marketing risks, there is the need for farmers' cooperatives that will serve as an advocacy and empowering tool for the negotiation of market prices, and for acquisition of policy support from government (Gabre-Madhin, 2004). Sweetpotato, especially OFSP varieties, could also be introduced into school feeding programs to boost demand. Research and education on utilization and nutritional benefits of sweetpotato should also be intensified so as to increase demand and hence production.

Regarding varieties grown by farmers, it was observed that most of the farmers grew both improved varieties and what the farmers referred to as their own 'local' varieties. Upon critical observation of the 'local' varieties however, it was realized that some of them bore close resemblance in morphology to released varieties and therefore could actually be released

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varieties that have been in farmers' fields for years. Some of these had been given names different from their original names. It was therefore difficult to confirm whether these were actually among the varieties released in 1998 by the CRI (Akoroda, 2009). The new names were based on some morphological or root trait that distinguished the variety. For example one variety that is highly preferred by farmers in the Central region, had purple young leaves and was referred to as Blue Blue'. This variety however had very close resemblance to a variety known as 'Jukwa Orange' or TIS 2 which was among varieties that were tried for release by CRI (Akoroda, 2009). 'Blue Blue' is currently the most popular variety in the Central region. It has yellow flesh colour and is moderately sweet.

The fact that majority of farmers selected market value as more important than yield when choosing a variety to grow (Table 11), emphasizes the importance that farmers accorded to sweetpotato for income over household food production. This is confirmed by farmers ranking of sweetpotato for income generation as highest among all crops under cultivation. Interestingly, the varieties they choose to grow, like "Blue Blue' in the Central Rregion, or 'Kadzie" in the Volta Region are all high in dry matter, firm and medium sweet. Farmers also mentioned that an orange fleshed variety that would appeal to their taste would be one that is higher in dry matter and with reduced sweetness. Many farmers had heard about the health benefits of these lines but disliked their high sugar levels and wateriness.

In contrast to its high rank for income generation, sweetpotato ranked very low as food. According to the farmers, they are not used to sweet staples, and that the high levels of sugar and low dry matter in sweetpotato, make it unsuitable for use in traditional cuisines. It has been suggested that sweetpotato often has distinct flavors (aroma and sweetness) that do not appeal to everyone, and that sweetness can be a deterrent to frequent consumption (Martin, 1988;

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McLaurin and Kays, 1992; Kays, 2006). According to these authors a sweet dish is unlikely to become a staple food. Contrary to this view however sweetpotato is a staple in countries like Papua New Guinea and Uganda (Ebregt, 2004; Gibson *et al*., 2008) where per capita consumption is high in spite of its high flavor impact. Varieties consumed in these regions may however, have lower flavor impact compared to the dessert types consumed in countries like the USA. Flavor preferences therefore vary from location to location and must be tailored to specific consumer preferences and product uses so as to increase the utilization of the crop (Kays *et al.*, 2005).

## 3.5 CONCLUSION

Constraints to sweetpotato production can essentially be put into two groups. 1. Constraints to cultivating the crop itself and 2. Factors affecting demand. With regards to constraints to cultivation, drought ranked highest. Factors affecting demand were linked to undesirable eating quality characteristics that resulted in low utilization of the crop in local cuisines. Farmers desired low sugar, high dry matter, and poundable sweetpotato. Seventy per cent of farmers disliked the high sugar levels of sweetpotato and were of the view that sweetpotato utilization in local dishes would increase with the availability of varieties that combine the desired attributes. Increased utilization along with its concurrent increases in production can therefore be achieved if the desires of farmers are factored into research goals that will eventually develop such varieties. Developing such varieties is achievable as a wide range of diversity in flavor types exists within the sweetpotato gene pool, that can be exploited to produce varieties with the required flavor levels (Kays and Wang, 2000).

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# CHAPTER FOUR

## 4.0 CHARACTERIZATION AND EVALUATION OF SWEETPOTATO GERMPLASM FOR SUGAR, DRY MATTER AND β-CAROTENE AND SELECTION OF PARENTAL GENOTYPES

### 4.1 INTRODUCTION

In most parts of sub-Saharan Africa preferred types of sweetpotato have higher dry matter (28-30%) and are low in sweetness, compared to varieties grown for example in the United States (Mwanga *et al.*, 2007a; Cervantes-Flores *et al.*, 2011). A sweet and low dry matter food has very low appeal as a staple for some consumers especially in sub-Saharan Africa (Kays, 1988; Mwanga *et al.*, 2007a). The market potential for low-sugar sweetpotato types for home consumption in Ghana is large (Adu-Kwarteng *et al.*, 2001; Adu-Kwarteng *et al.*, 2002; WAAPP, 2009). The availability of these types would increase home consumption and thereby boost production and farmers' incomes.

Sweetpotato germplasm worldwide is predominantly medium to high in sweetness but genotypes (Kays, 2005) are present within the gene pool, from which selection of new cultivars with distinctly higher or lower sweetness levels than current cultivars, can be made (Kays *et al.*, 2005). This diversity in flavor (sugar and aroma) types has also been observed by Mclaurin and Kays, 1992. The diversity however, remains to be systematically exploited in sweetpotato improvement.

The Crops Research Institute of Ghana has released 12 varieties of sweetpotato between 1998 (Akoroda, 2009) and 2013. According to farmers, current varieties do not adequately meet their varietal needs in terms of their eating quality. From the survey reported in Chapter 3, it appeared that these cultivars constitute most of the varieties currently cultivated by farmers, but it is

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possible that names of cultivars have been confused and farmers may still be growing local landraces. In various locations in regions where the PRA study was carried out, it appeared that farmers had given different names to the released varieties. There could therefore be duplications in the collection of farmers' material. It is therefore important to collect and characterize farmers' material so as to assess the variability that exists within farmers' collections and also evaluate them for their nutritional and eating qualities.

Vitamin A deficiency is a serious health concern in Ghana (Akoroda, 2009) and sweetpotato that is high in β-carotene has been proven as an effective means of combating vitamin A deficiency (Woolfe, 1992; Low *et al.*, 2007). The preferred low sugar and high dry matter types, however, have very low β- carotene content. As a result, it is necessary to introduce new high β-carotene lines, rich in vitamin A, as well as clones classified as high dry matter and non-sweet Kays *et al.*, 2001; Kays *et al.*, 2005) and evaluate them alongside collections within the country, so as to exploit the diversity within both local and exotic genotypes. From these evaluations parental genotypes with desired characteristics can be selected for further studies.

**The objectives of this study were to:**

1. assess diversity within farmers' varieties and exotic germplasm introduced from USDA germplasm repository.
2. evaluate accessions based on their sugar levels, dry matter and β-carotene content
3. identify suitable parents for hybridization

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## 4.2 MATERIALS AND METHODS

### 4.2.1 Local germplasm collection and introduction of exotic germplasm

A total of 43 farmers germplasm were collected from three regions of Ghana namely Central, Volta and the Upper East regions. These materials were collected from farms within the 28 farming communities where PRAs (Chapter 3) were conducted. Farmers were involved in the identification of their cultivars and their indigenous knowledge was also documented. Germplasm collection sites were geo-referenced with a global positioning system (GPS) and plotted on the map of Ghana (Figure 4.1). The GPS locations of these sites are presented in Appendix 4.1. Another set of 48 and 16 accessions were obtained from sweetpotato collections from the Crop Research Institute (CRI), Fumesua and Bunso germplasm repository respectively.

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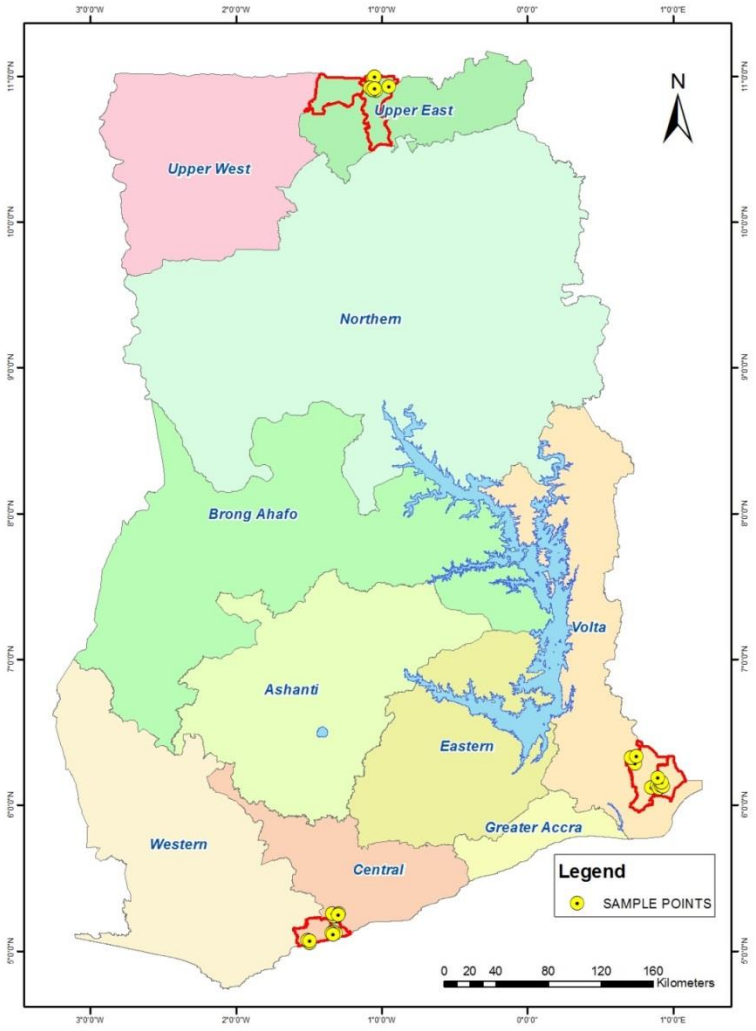


**Figure 4. 1: Map of Ghana showing germplasm collection sites in Central, Volta and Upper East Regions of Ghana. The sites are represented by yellow dots surrounded by red.**

Thirty-six exotic accessions of sweetpotato were introduced from the USDA sweetpotato germplasm repository. These materials had been characterized by previous workers (Kays *et al.*, 2001; Kays *et al.*, 2005b) as having diverse range of quality attributes including low sugar, high dry matter and high β-carotene. These were first multiplied *in-vitro* on hormone-free Murashige and Skoog (MS) medium and weaned on sand and vermiculite mixture in a screen house at the Biotechnology and Nuclear Agriculture Research Institute of the Ghana Atomic Energy

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Commission (BNARI – GAEC). All assembled germplasm were planted in pots in a multiplication nursery and maintained in a screen house at BNARI to generate enough vines for field evaluation.

### 4.2.2 Germplasm characterization

#### 4.2.2.1 Field experiment

A total of 143 clones were assembled. Of these only 128 and 2 checks namely Blue Blue and Apomuden were included in this study as the remaining thirteen showed signs of severe viral infection. The selected genotypes were planted in the research farm at BNARI during the rainy season in May 2011. The experimental design was a partially balanced 13x10 alpha lattice (Patterson and Williams, 1976), with three replications. Sweetpotato vines of about 25 cm long were planted to establish the experimental plots. The experimental plot consisted of single-rows of 7-plant with a spacing of 0.3 m between plants within a row and a spacing of 1 m between rows. The genotypes were randomized in each lattice. Weeding was carried out with hoes when required and 15:15:15 N:P:K fertilizer was applied at a rate of 170 kg/ha, 4 weeks after planting when the crop had established. No herbicides or pesticides were applied. At harvest, data was collected on the 5 central plants from a net plot area of 1.5 $m^2$.

#### 4.2.2.2 Morphological data collection

Above ground morphological data was collected at one hundred days after planting using prescribed sweetpotato descriptors (CIP-AVRDC-IBPGR, 1991). These were, plant type (PTP), vine internode length (VIL), vine internode diameter (VID), ground cover (GC), predominant color of vine (PVC), secondary color of vine (SVC), general leaf outline (GOL), type of leaf lobes (LLT), number of leaf lobes (LLN), shape of central leaf lobe (SCL), mature leaf size (MLS), abaxial leaf vein pigmentation (AVP), mature leaf color (MLC), immature leaf color

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(ILC), petiole length (PTL), petiole pigmentation (PPP), and flowering habit (FHT). These morphological traits were scored using a scale of 0-9 as prescribed (CIP-AVRDC-IBPGR, 1991) Roots were harvested with hand hoes at 5 months after planting. Data collected on root characters were; storage root shape (SRS), storage root defects (SRD), storage root size thickness (RS), predominant skin color (PSC), intensity of predominant skin color (IPC), secondary skin color (SSC), predominant root flesh color (PFC), secondary flesh color (SFC) and distribution of secondary flesh color (DSF). Flesh color was determined using a color chart developed by CIP.

#### 4.2.2.3 Yield data collection

Yield data collected were number of plants harvested, fresh root yield (t/ha), number of storage roots per plant, number and weight of marketable and unmarketable roots and vine weight, total biomass and harvest index. Harvest index (HI) was calculated as a ratio of fresh root yield to total biomass and expressed as a percentage.

#### 4.2.2.4 Dry matter determination

A random sample of four roots per genotype was selected and washed thoroughly. After air drying, the fresh roots were peeled, washed and cut longitudinally into four quarters. Two symmetrical pieces were then sliced into thin longitudinal slices of about 5 mm thick using a hand-held slicer. About 50 g of sliced fresh roots were weighed and freeze dried in a YK-118 vacuum freeze drier (TrueTen, Taiwan) for three days. After freeze drying, the weights of freeze dried samples were taken to obtain dry weights. The dry matter was then calculated as a ratio of dry weight to fresh weight expressed in percentage.

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#### 4.2.2.5 Sensory evaluation of cooked samples for sweetness

The remaining peeled fresh roots were steamed until well cooked and subjected to sensory evaluation by five trained panelist at CRI, Fumesua. Cooked samples were scored for sweetness, mouth feel, taste, fiber, color and aroma. Table 4.1 below shows the scores and their definitions.

**Table 4.1: Sensory scores and their definitions**

| | Description | |
|---|---|---|
| **Scores** | **Taste** | **sweetness** |
| **1** | Very good | Non-sweet |
| **2** | Good | Low-sweet |
| **3** | Average | Intermediate sweet |
| **4** | bad | Sweet |
| **5** | Very bad | Too sweet |

#### 4.2.2.6 Determination of sugars and β-carotene

Freeze dried raw and cooked samples were milled with a Willey mill into fine flour. Values for sugars, starch and β-carotene in raw roots were determined using a near infra-red spectrophotometer (NIRS) Foss XDS rapid content analyser (XM-1100), equipped with ISISCAN 2007 software at the sweetpotato lab at CSIR-CRI. The transmittance spectra of the flour samples were from 400 to 2500. After cooking, storage roots were also freeze dried, milled and subjected to NIRS for determination of cooked sugars and starch. Total sugars in raw and cooked roots were then computed. The relative sweetness of each accession expressed as sucrose equivalents (SE), was determined by the formula; SE = 1.73 fructose + 0.64 glucose + 1 sucrose + 0.33 maltose (Moskowitz, 1970) for both raw and cooked roots.

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### 4.2.3 Data standardization

The traits were not normally distributed so they were standardized (Milligan and Cooper, 1987) with the standardization equation below:

$$X' = \frac{S*(x_i - \overline{x})}{s_x} + M$$

Where;

x' = the new standardized value.

S = the value of standard deviation.

M = the value of mean

$x_i$= an observation's value.

$\overline{x}$= a variable's mean.

$s_x$= a variable's standard deviation.

Standardization allowed each variable to contribute to the overall variation such that a variable with a small variance could contribute as much as another variable with a larger variance (Sneath and Sokal, 1973).

### 4.2.4 Data analysis

#### 4.2.4.1 Morphological data analysis

Data for the morphological traits was analyzed with SAS version 9.3 (SAS Institute, Cary, NC, USA). A variable reduction technique was done using PROC VARCLUS procedure in SAS version 9.3, to select the most discriminating variables and eliminate redundant ones without losing information. The cluster structure was computed to display the correlations between the

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variables and their own clusters. Within each cluster the variable with the largest $R^2$ value was selected to represent that cluster. Further analysis was then performed using the selected variables.

Using PROC PRINCOMP of SAS 9.3, principal component analysis was performed on the selected variables to determine the structure of the correlations between variables and the percentage contribution of each trait to variation. Eigenvalues and eigenvectors of the correlation matrix were obtained. Using the eigenvalue, eigenvectors and the correlation matrix, variables were further reduced. The final set of 9 variables was used to determine the genetic relatedness of the genotypes in the study. Principal components were used as input variables for a cluster analysis. Agglomerative hierarchical cluster using the un-weighted pair-group method of averages (UPGMA) was performed to generate a dendrogram using the PROC CLUSTER procedure in SAS Version 9.3. DARwin 5.0.158 was used to estimate Rogers-Tanimoto pair-wise dissimilarity coefficient computed as a single and modality data.

#### 4.2.4.2 Root quality traits analysis

PROC GLM of SAS was performed to analyze differences among genotypes for the different quality traits under study. PROC UNIVARIATE of SAS 9.3 was also performed to obtain distribution curves and ranges for all variables. PROC STEPDISC was used to perform stepwise discriminant analysis to select the best discriminating root quality variables. The quality traits measured in uncooked roots were dry matter (DM), Starch (StarchR), fructose (fructoseR), glucose (glucoseR), sucrose (sucroseR), maltose (maltoseR), total sugars (TSraw), sucrose equivalents (SEraw) and β-carotene (BC). For cooked roots, variables comprised of Starch (StarchCk), fructose (fructoseCk), glucose (glucoseCk), sucrose (sucroseCk), maltose (maltoseCk), total sugars (TScooked), sucrose equivalents (SEcooked). Amount of β-carotene in

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cooked roots were not measured because NIRS had not been caliberated for measuring β-carotene in cooked roots. The variables contributing to the discriminating power of the model was measured using the Wilk's Lamda criterion (Costanza and Afifi, 1979). Variables were retained at a significance level of 0.15. Principal components analysis was subsequently conducted using PROC PRINCOMP to determine which traits contributed the most to the variation observed in the data and to examine the structure of correlations between variables. The eigenvalues and eigenvectors of the correlation matrix were derived and used to scale down the number of variables before cluster analysis. Agglomerative hierarchical cluster using the un-weighted pair-group method of averages (UPGMA) was performed to generate a dendrogram using the PROC CLUSTER procedure in SAS Version 9.3. Dissimilarity index was estimated using mean Euclidean distance computed as continuous data with DARwin 5.0.158.

## 4.3 RESULTS

### 4.3.1 Morphological characterization

#### 4.3.1.1 Discriminant analysis for morphological traits

The variable reduction technique (PROC VARCLUS) grouped the 26 variables into nine different clusters (Table 4.2). These nine cluster components accounted for 63% of the total variation in the data. Cluster one included the mature leaf traits GOL, LLT, LLN, and SCL while cluster two, a mixture of leaf, vine and root traits, VID, MLS, PTL, RS and VV. Clusters three and four, contained traits that were associated with plant pigmentation. These included PVC, SVC, AVP, PPP in cluster three and SFC and DSF in cluster four. Plant type (PTP)), VIL and principal skin color (PSC) were grouped into cluster five while PFC, storage root traits, PSC and SSC and FHT were in cluster six. Traits associated with leaf pigmentation (MLC and ILC) were in cluster seven. Clusters eight and nine were made up of only root traits. Storage root

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arrangement (SRA) and storage root shape (SRS) were in cluster 8 while storage root defect (SRD) was the only variable in cluster 9.

The correlation coefficients ($R^2$) for each variable are also presented in Table 4.2. Within each cluster, the variable with highest $R^2$ values was selected to represent that cluster. If there was a tie in $R^2$ values within a cluster as was the case with clusters four, seven and eight only one variable was selected. As such, a total of nine variables with discriminative power to differentiate among genotypes were selected from the 26 variables. These included shape of central leaf lobe (SCL) in cluster 1 with an $R^2$ of 0.84, vine vigor (GC) in cluster 2 with an $R^2$ of 0.68, petiole pigmentation (PPP) in cluster 3 with an $R^2$ of 0.76, distribution of secondary flesh color (DSF) in cluster 4 with an $R^2$ of 0.86, plant type (PTP) in cluster 5 with an $R^2$ of 0.81, flower habit (FHT) in cluster 6 with an $R^2$ of 0.59, immature leaf color (ILC) in cluster 7 with an $R^2$ of 0.67, storage root arrangement (SRA) in cluster 8 with an $R^2$ of 0.60 and storage root defects (SRD) in the ninth cluster with an $R^2$ of 1.0.

The variables that were not selected by the selection criteria included general leaf outline, leaf lobe number (LLN), leaf lobe type (LLT), vine internode diameter (VID), mature leaf size (MLS), petiole length (PTL), root shape (RS), principal vine color (PVC), secondary vine color (SVC), abaxial leaf vein pigmentation (AVP), secondary flesh color (SFC), vine internode length (VIL), principal skin color (PSC), principal flesh color (PFC), secondary skin color (SSC), mature leaf color (MLC) and storage root shape (SRS).

There was a wide variation in the distribution of morphological traits among the 130 clones evaluated. Within some descriptor types however not all categories specified in the prescribed descriptor (CIP-AVRDC-IBPGR, 1991) were observed. The distribution of the 9 variables that

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were selected as being discriminative among the 130 clones were as follows; For plant type (PTP) 15 % were erect (<75cm), 38% were semi erect (75-150cm), 29 % were spreading (151-250cm) while another 19 % were very spreading (>250m) . With respect to ground cover, 7 % of accessions had less than 50 %. Majority of the accessions (42 %) had medium coverage (50-74 % while 38 % and 12 % had high (75-90 %) and total (>90 %) ground cover respectively. The predominant shape of the central leaf lobe (SCL) was toothed (27 %), followed by triangular at 24 %, semi-elliptic at 22 %, lanceolate at 12 %, elliptic at 6 %. Five per cent of accessions had no central leaf lobe, while a very small number (0.8 %) had either linear broad or linear narrow central leaf lobe.

The immature leaf color was spread among seven of the nine different classes specified (CIP-AVRDC-IBPGR, 1991). Most of the accessions (43 %) had green immature leaves with purple edge and 20 % had green immature leaves. Slightly purple and mostly purple immature leaves were observed for 8 % and 3 % of the accessions, respectively while 12 % had immature leaves that were purple on both surfaces. No accession had green upper, purple lower or grayish-green immature leaves. Twenty five per cent and 9 % of the accessions had green and yellow-green immature leaves, respectively. For petiole pigmentation (PPP) most accessions (28 %) had green petioles with purple at both ends while 25 % and 24 % had green with purple near leaf and green with purple near stem petioles, respectively. While no accession had green with purple spots throughout petioles, 8 % had some petioles purple and others green. Ten percent of accessions had petioles that were totally or mostly purple.

The distribution of secondary flesh color varied as follows: no secondary flesh color (60 %), narrow ring in cortex (2 %), broad ring in cortex (2 %), scattered spots in flesh (13 %), narrow ring in flesh (4 %), broad ring in flesh (2 %), ring and other areas in flesh (5 %), longitudinal

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sections (0.3%) and covering most of the flesh (11%). With regards to storage root arrangement the predominant class was dispersed (45 %) followed by open cluster (27 %). Accessions with closed cluster and very dispersed roots were 12 % and 15 % respectively. Only about 1 % percent of the accessions had no storage root defects. Shallow longitudinal grooves on root surface, was the most frequent root defect (35%), followed by shallow horizontal constrictions (26 %). Other defects observed were deep longitudinal grooves (11 %), deep constrictions and deep grooves 11 %), alligator-like skin (1 %) and veins (1 %). During the period of evaluation most of the accessions (60 %) did not flower. Twelve per cent of accessions that flowered produced either sparse or profuse flowers, while 10% showed moderate flowering.

Although the selection criteria failed to select root flesh color and skin colors as discriminatory enough to differentiate between accessions, principal flesh color, secondary flesh color, principal skin color and secondary flesh colors were significantly different among accessions as shown in Table 4.3. The predominant skin color observed was cream (45 %), while other colors were white and yellow at 1 % each, orange (4 %), brownish orange (14 %), pink (15 %), purple red (17 %) and dark orange (5 %). No red root flesh color was observed.

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**Table 4. 2: Discriminant analysis of the 26 variables used to distinguish the 130 genotypes using PROC VARCLUS.**

| Cluster | Variable | $R^2$ with Own Cluster | $R^2$ with Next Closest | 1-R**2 Ratio |
|---|---|---|---|---|
| **Cluster 1** | **General outline of leaf (GOL)** | 0.7567 | 0.0593 | 0.2587 |
| | **Leaf lobe type (LLT)** | 0.8063 | 0.0140 | 0.1964 |
| | **Leaf lobe number (LLN)** | 0.6819 | 0.0115 | 0.3218 |
| | **Shape of central leaf lobe (SCL)** | 0.8351 | 0.0215 | 0.1685 |
| **Cluster 2** | **Vine internode diameter (VID)** | 0.4136 | 0.0577 | 0.6223 |
| | **Mature leaf size (MLS)** | 0.4457 | 0.0495 | 0.5832 |
| | **Petiole length (PTL)** | 0.5422 | 0.1061 | 0.5121 |
| | **Storage root size (RS)** | 0.2814 | 0.0455 | 0.7528 |
| | **Ground cover (GC)** | 0.6819 | 0.1261 | 0.3639 |
| **Cluster 3** | **Principal vine colour (PVC)** | 0.6842 | 0.1063 | 0.3534 |
| | **Secondary vine colour (SVC)** | 0.2281 | 0.0417 | 0.8055 |
| | **Abaxial vein pigmentation (AVP)** | 0.5767 | 0.0316 | 0.4371 |
| | **Petiole pigmentation (PPP)** | 0.7571 | 0.1130 | 0.2738 |
| **Cluster 4** | **Secondary flesh colour (SFC)** | 0.8594 | 0.0187 | 0.1433 |
| | **Distribution of secondary flesh colour (DSF)** | 0.8594 | 0.0079 | 0.1417 |
| **Cluster 5** | **Plant type (PTP)** | 0.8133 | 0.1474 | 0.2190 |
| | **Vine internode length (VIL)** | 0.7605 | 0.0632 | 0.2557 |
| | **Principal skin colour (PSC)** | 0.2707 | 0.0399 | 0.7596 |
| **Cluster 6** | **Principal flesh colour (PFC)** | 0.5510 | 0.0167 | 0.4566 |
| | **Secondary skin colour (SSC)** | 0.3946 | 0.0063 | 0.6092 |
| | **Flower habit (FHT)** | 0.5780 | 0.0617 | 0.4497 |
| **Cluster 7** | **Mature leaf colour (MLC)** | 0.6707 | 0.1386 | 0.3823 |
| | **Immature leaf colour (ILC)** | 0.6707 | 0.0180 | 0.3353 |
| **Cluster 8** | **Strorage root arrangement (SRA)** | 0.6016 | 0.0188 | 0.4061 |
| | **Storage root shape (SRS)** | 0.6016 | 0.0212 | 0.4071 |
| **Cluster 9** | **\|Storage root defects (SRD)** | 1.0000 | 0.0158 | 0.0000 |

**1 – R**2 = the maximum ratio of the value (1 – $R^2$) for a variable's own cluster to the value 1 – $R^2$ for its nearest cluster.**

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**Table 4. 3: Analysis of variance for root flesh and skin colour used to distinguish the 130 sweetpotato genotypes**

| Mean square for storage root flesh and skin colors | | | | | |
|---|---|---|---|---|---|
| **Sources** | **df** | **PFC** | **SFC** | **PSC** | **SSC** |
| **Genotype** | 129 | 13.48*** | 7.25*** | 17.00*** | 7.17*** |
| **Blk(rep)** | 38 | 0.16 | 0.19 | 0.19 | 0.75 |
| **Error** | 222 | 0.13 | 0.29 | 0.19 | 0.61 |

***** Significant at 0.1%. PFC=principal flesh color, SFC=secondary flesh color, PSC=principal skin color, and SSC=secondary skin color.**

### 4.3.1.2 Principal component analysis for phenotypic traits

Prior to cluster analysis, principal component analysis was done to determine the relative importance of the nine selected variables (Jackson, 1991). Table 4.4 shows the correlation matrix of these nine discriminative traits used for the analysis. The low correlations indicated effective removal of redundancy in the data before cluster analysis. Five principal components with eigenvalues greater than 1 accounted for 68.74 % of the variation (Table 4.5). The first principal component accounted for 17.75 % while the second, third, fourth and fifth explained 14.99 %, 12.95 %, 11.83 % and 11.22 % respectively. With reference to the high loadings in each PC (Table 4.6), the first PC was positively associated with traits related to the stem including ground cover (GC), plant type (PTP), and immature leaf color (ILC). The second PC was associated positively with shape of central leaf lobe (SCL) and storage root arrangement (SRA) but negatively with flower habit (FHT). The third PC had associations with the plant pigmentations including petiole pigmentation (PPP) and distribution of secondary flesh color (DSF). However it was negatively associated with PPP but positively with DSF. The fourth and fifth PCs associated positively with storage root traits; storage root arrangement (SRA) and storage root

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defects (SRD) respectively. The scree plot test (Figure 4.2) confirms the retention of these five principal components.

**Table 4. 4: Correlation matrix for 9 morphological descriptors that were used to distinguish the 130 sweetpotato accessions.**

| | SCL | GC | PTP | PPP | FHT | DSF | ILC | SRA |
|---|---|---|---|---|---|---|---|---|
| **Shape of central leaf lobe (SCL)** | | | | | | | | |
| **Ground cover (GC)** | 0.0482 | | | | | | | |
| **Plant type (PTP)** | -.0202 | 0.4032 | | | | | | |
| **Petiole pigmentation (PPP)** | 0.0545 | 0.0510 | 0.0718 | | | | | |
| **Flower habit (FHT)** | -.2180 | 0.1613 | 0.0577 | -.0378 | | | | |
| **Dis. of sec. flesh color (DSF)** | 0.1199 | 0.0609 | 0.0895 | -.0462 | 0.0154 | | | |
| **Immature leaf color (ILC)** | 0.0502 | 0.1771 | 0.1115 | 0.2331 | 0.0011 | -.0278 | | |
| **Storage root shape (SRA)** | -.0289 | 0.0193 | -.0221 | -.0182 | -.2203 | -.0130 | 0.0694 | |
| **Storage root defects (SRD)** | -.0228 | 0.0776 | 0.0295 | 0.0270 | -.0856 | 0.0738 | 0.0680 | -.0464 |

**Table 4. 5: Eigenvalue of the correlation matrix of the 9 morphological descriptors that were used to distinguish the 130 sweetpotato accessions.**

| Eigenvalues of the Correlation Matrix | | | | |
|---|---|---|---|---|
| | **Eigenvalue** | **Difference between successive eigen values** | **Proportion of total variation** | **Cumulative** |
| **1** | 1.59850101 | 0.24796697 | 0.1775 | 0.1775 |
| **2** | 1.34953403 | 0.18446288 | 0.1499 | 0.3274 |
| **3** | 1.16507116 | 0.10022710 | 0.1295 | 0.4569 |
| **4** | 1.06484405 | 0.05531092 | 0.1183 | 0.5752 |
| **5** | 1.00953313 | 0.14677066 | 0.1122 | 0.6874 |
| **6** | 0.86276247 | 0.07938910 | 0.0959 | 0.7832 |
| **7** | 0.78337338 | 0.12277442 | 0.0870 | 0.8703 |
| **8** | 0.66059896 | 0.15381715 | 0.0734 | 0.9437 |
| **9** | 0.50678181 | | 0.0563 | 1.0000 |

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**Table 4. 6: Eigenvectors from nine principal component axes used to classify 130 sweetpotato accessions.**

| | Prin1 | Prin2 | Prin3 | Prin4 | Prin5 | Prin6 | Prin7 | Prin8 | Prin9 |
|---|---|---|---|---|---|---|---|---|---|
| **Shape of central leaf lobe (SCL)** | 0.045 | **0.461** | 0.383 | 0.292 | -.460 | -.268 | 0.300 | 0.265 | 0.332 |
| **Ground cover (GC)** | **0.608** | -.085 | 0.105 | -.228 | -.058 | -.214 | 0.168 | 0.374 | **-.585** |
| **Plant type (PTP)** | **0.564** | -.085 | 0.135 | -.256 | -.073 | -.257 | -.397 | -.381 | **0.466** |
| **Petiole pigmentation (PPP)** | 0.265 | 0.289 | **-.429** | 0.421 | -.097 | 0.210 | **-.568** | 0.330 | -.028 |
| **Flower habit (FHT)** | 0.185 | **-.654** | -.114 | 0.130 | -.107 | 0.291 | 0.263 | 0.384 | **0.443** |
| **Dis. of sec. flesh color (DSF)** | 0.142 | 0.046 | **0.657** | 0.071 | -.004 | **0.702** | -.145 | -.100 | -.132 |
| **Immature leaf color (ILC)** | **0.399** | 0.288 | -.378 | 0.128 | 0.026 | 0.292 | 0.550 | **-.459** | 0.009 |
| **Storage root arrangement (SRA)** | -.0498 | 0.397 | -.137 | **-.723** | 0.078 | 0.295 | 0.038 | 0.360 | 0.274 |
| **Storage root surface defects (SRD)** | 0.157 | 0.139 | 0.186 | 0.243 | **0.867** | -.151 | 0.085 | 0.199 | 0.202 |
| **Eigenvalue** | **1.599** | **1.350** | **1.165** | **1.065** | **1.009** | **0.863** | **0.783** | **0.661** | **0.507** |
| **% variation** | **17.75** | **14.99** | **12.95** | **11.83** | **11.22** | **9.59** | **8.70** | **7.34** | **9.44** |
| **Cumulative %** | **17.75** | **32.74** | **45.69** | **57.52** | **68.74** | **78.32** | **87.03** | **94.37** | **100.0** |

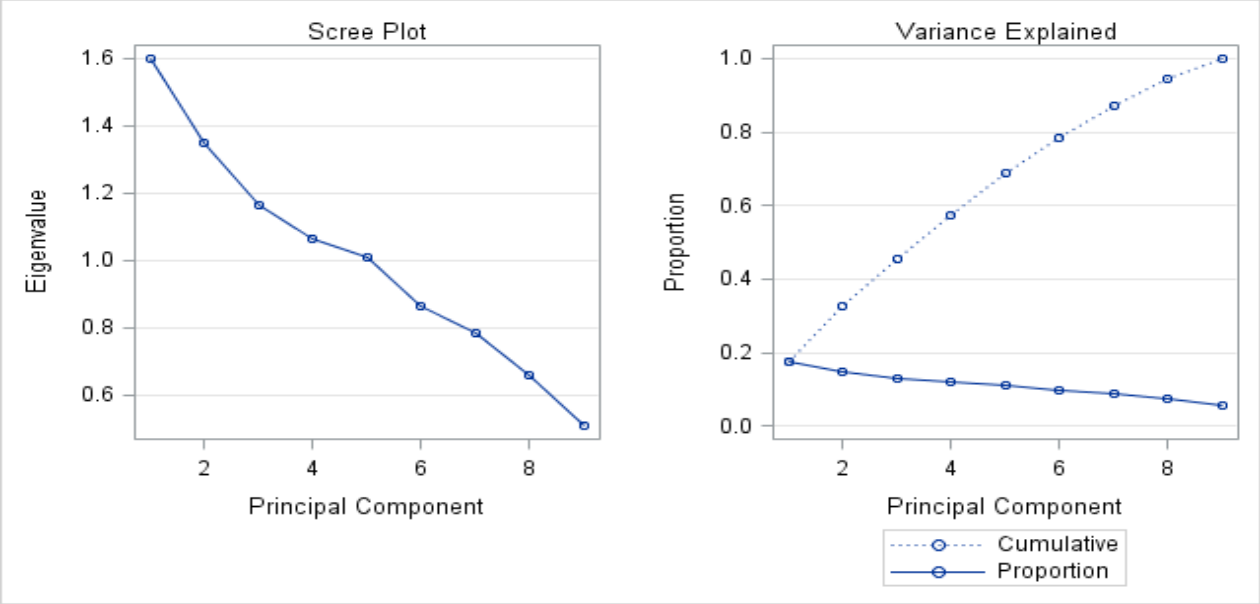


**Figure 4.2: Scree plot and total variance explained**

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#### 4.3.1.3 Cluster analysis based on nine morphological traits

Rogers-Tanimoto pairwise dissimilarity coefficient (Figure 4.3), revealed a dissimilarity index ranging from 0.42-1 with an average value of 0.85 implying high diversity in the 130 genotypes evaluated. The nine discriminative phenotypic variables grouped the accessions into 8 clusters based on their average linkage and Euclidean distance (Figure 4.4). Cluster VII was an outlier with only one member while cluster III contained two genotypes. Cluster V formed the largest cluster with 79 members, while clusters I and II had 6 accessions each. Clusters IV, VI, and VIII comprised of 4, 17 and 15 accessions respectively. A number of the clones from farmers' germplasm clustered with those released by the national program. Genotypes Blue Blue, TIS 2, TIS 2 (yellow local), and Jukwa Orange which appeared similar on farmers' fields, were all found in cluster V. Another set of germplasm (Fiaso local red, local1, local red, Santom Kokoo (local Faara), Santom Kokoo local, local 4 and local 3), with close resemblance to Faara, also clustered within cluster V, confirming their close relatedness. All clusters were divided into sub-clusters within which the relationship within sub-clusters was closer than the others within the larger cluster. In cluster I accessions were the spreading to very spreading plant types, most of which did not flower. Cluster II genotypes were characterized by dispersed storage root arrangement and strongly pigmented immature leaves with the exception of Trotroyeye whose immature leaves were not pigmented. Cluster III genotypes had many traits in common including very spreading plant type, profuse flowering, pigmented immature leaves and petioles, as well as storage roots that lacked secondary flesh color. All genotypes in cluster IV had low ground cover but Daak 08/001 and Shashango were semi-erect types, while local1 and Bot-03-028 were erect types. Genotypes at the top of cluster V shared more common traits than those at the bottom of the cluster. For example Nchidzitor and Nagodzie at the top of the cluster were characterized by semi erect, pigmented petioles, immature leaves and yellow flesh color, while AIS 0122-2,

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Naanunono and Keanja at the bottom of the cluster were non-flowering and very spreading genotypes. They also had high ground cover, toothed central leaf lobe and petioles that were predominantly green with purple at both ends. With the exception of Zapallo, genotypes in cluster VI were associated with the absence of secondary flesh color. Two genotypes W-183 and MD 844 formed a sub-cluster in cluster VI and were both orange fleshed and profuse flowering types. TIS 8504-op-1-53 and LA 54-89 also formed a sub-cluster that was characterized by very spreading plant type. Okumkom and 392 clustered together in cluster VI and were associated with green and purple petioles, absence of flowers, no secondary flesh color and green immature leaves with purple edges. Santom Fufuo local and Wagabolige, a sub-cluster in cluster VI associated with dispersed storage root arrangement, storage root defect, and no secondary flesh color. With the exception of Local orange flesh, W-209, J/7-13 and CN 1058-10, which are all orange-fleshed types, cluster VIII genotypes were characterized by yellow or white fleshed roots with secondary flesh colors covering most of the flesh. The white or cream fleshed genotypes were also high in dry matter.

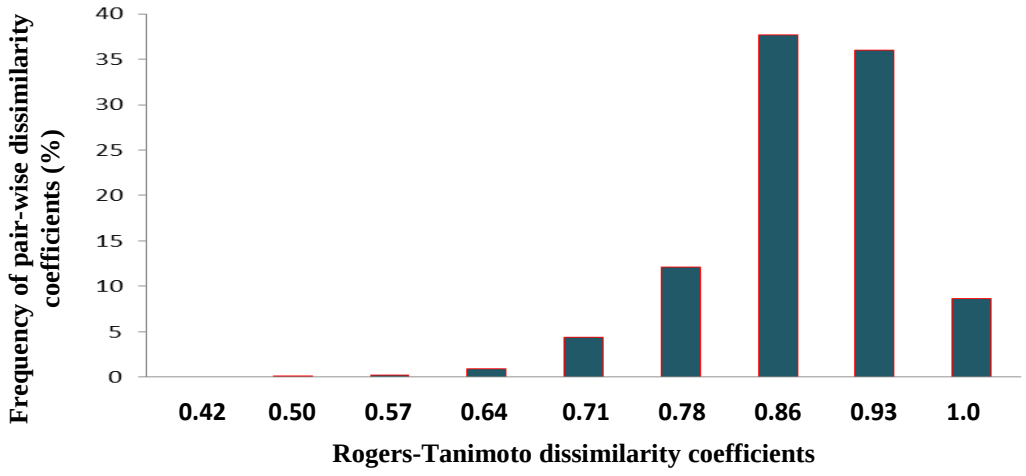


**Figure 4.3: Analysis of 130 sweetpotato genotypes based on Rogers-Tanimoto dissimilarity index using DARwin 5.0.158, mean = 0.85, min value = 0.42**

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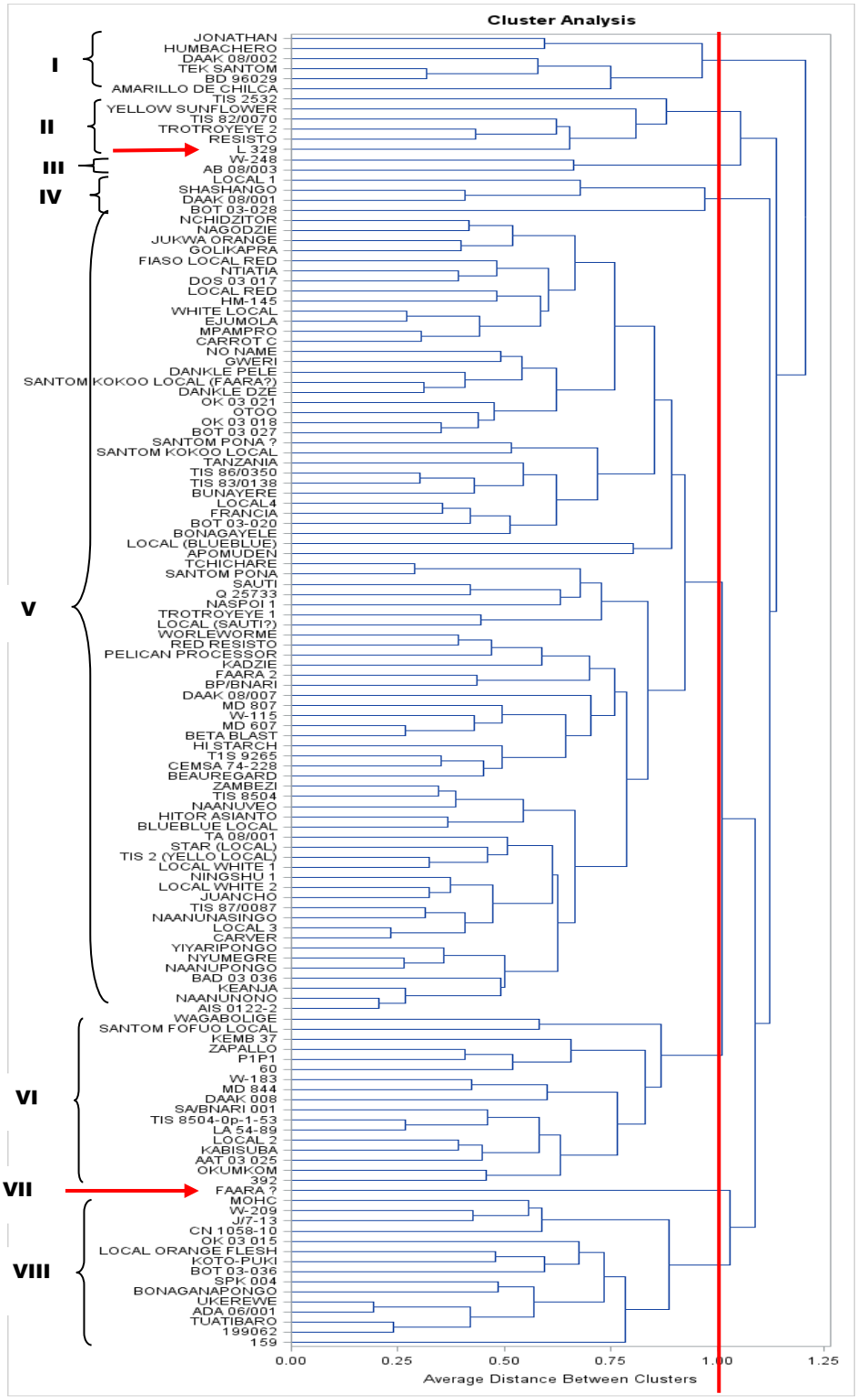


**Figure 4.4: Average linkage cluster analysis of 130 genotypes based on 9 discriminant phenotypic characters. Red arrows show outliers. Distance between clusters are expressed as average distances**

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### 4.3.2 Storage root quality traits analysis

#### 4.3.2.1 Means and distribution of sugars, sucrose equivalent, dry matter, starch and beta-carotene content in raw roots

Figure 4.5 shows the normal distribution curves for the uncooked storage root traits. Most traits except β-carotene were normally distributed, but total sugars (TSraw), starch (StarchR), sucrose equivalents (SEraw), and fructose (FructoseR) exhibited skewness. The principal sugars found in raw roots were fructose, glucose and sucrose with sucrose being predominant (Table 4.7). Maltose levels were very low as compared to the principal sugars. Total sugars ranged from 9.27- 45.94 % with a mean value of 19.05 %. Fructose, glucose and sucrose ranged from 0.30-8.36, 0.29-12.21 and 2.5-35.53% respectively. Mean values were 2.36% for fructose, 4.29% for glucose and 11.91% for sucrose. Sucrose equivalents ranged from 9.85-47.62% with an average of 19.33 %. Dry matter, starch and β-carotene ranged from 12.35-42.53 %, 38.01-75.04 % and 0.00-46.02 mg/100 g dry weight respectively. The large coefficient of variation for the sugar types could be due to the extent of variation that existed within the genotypes for the various sugars.

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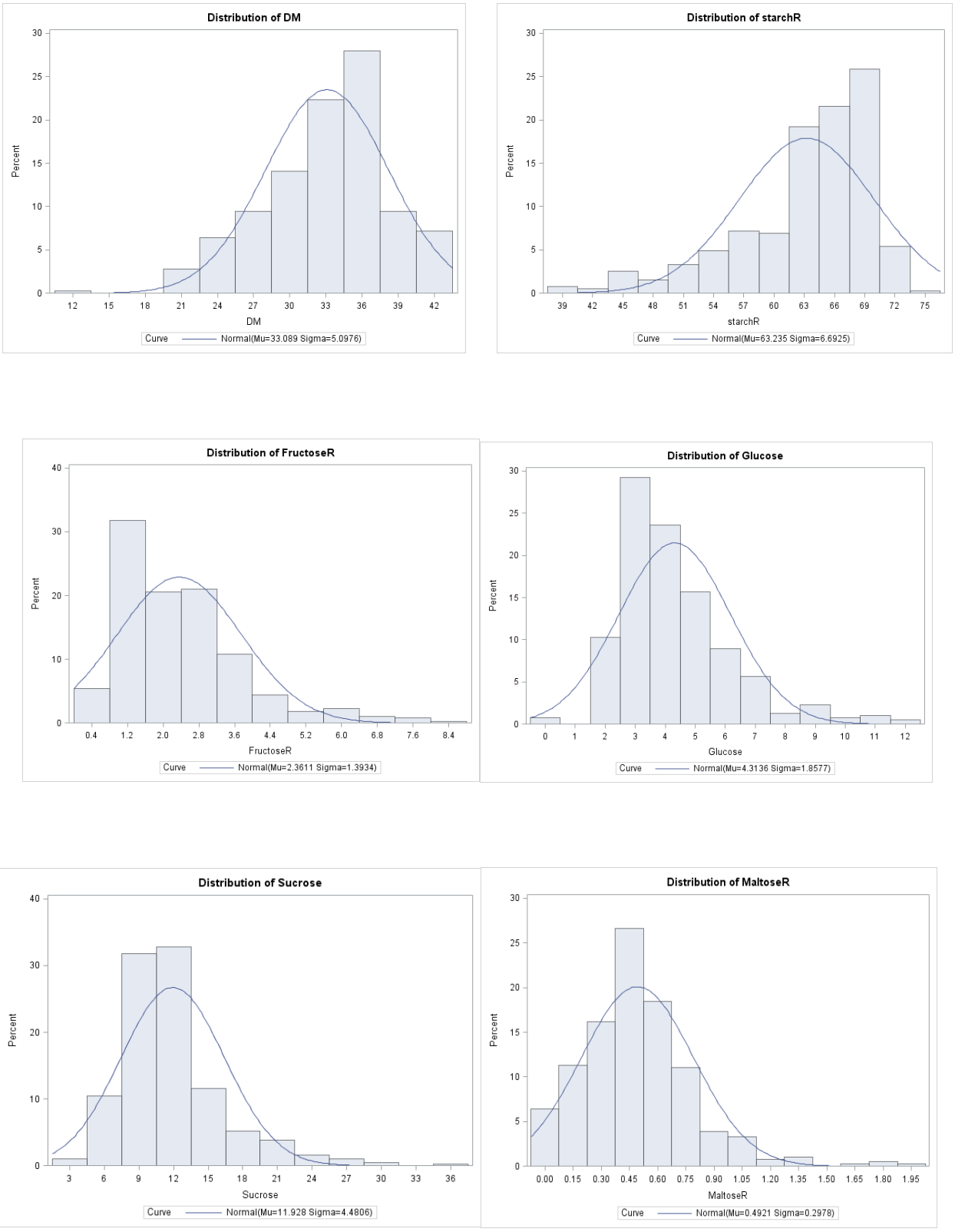


**Figure 4. 5: Distribution of dry matter, starch, sugars, β-carotene and sucrose equivalents in uncooked roots of 130 sweetpotato accessions**

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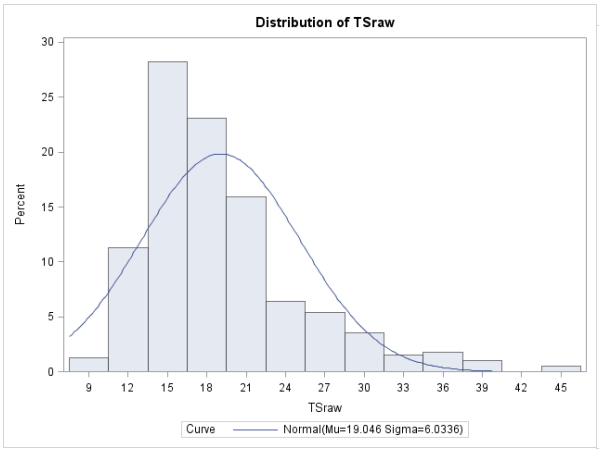


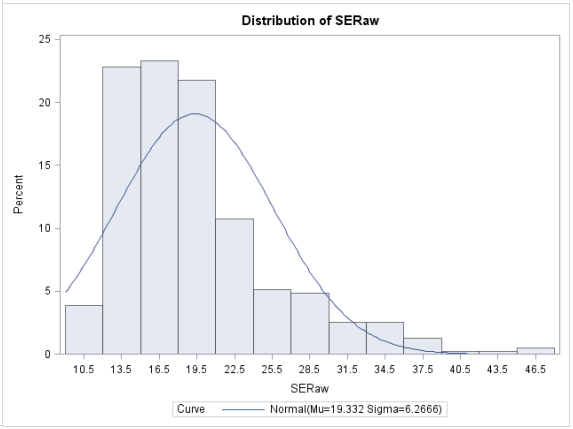


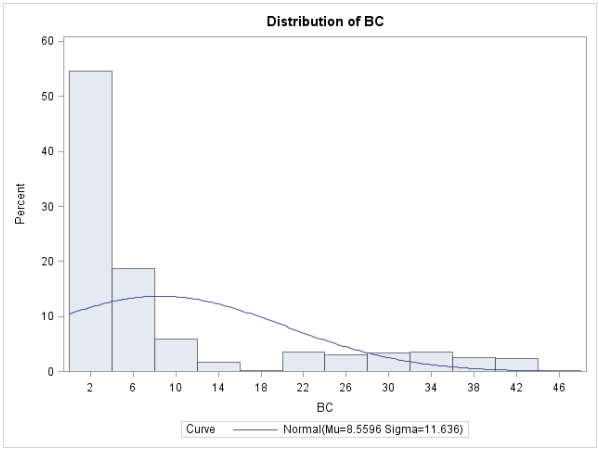


**Figure 4.5 (continued): Distribution of dry matter, starch, sugars, β-carotene and sucrose equivalents in uncooked roots of 130 sweetpotato accessions**

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**Table 4.7: Means, coefficient of variation (CV), standard error and range for sugars, sucrose equivalents, dry matter, starch and β-carotene in uncooked storage roots of the 130 genotypes**

| Traits | Mean | CV % | SED | Range |
|---|---|---|---|---|
| **Total sugars %** | 19.05 | 31.68 | 0.31 | 9.27- 45.94 |
| **Fructose %** | 2.36 | 59.01 | 0.07 | 0.30 - 8.36 |
| **Glucose %** | 4.29 | 42.46 | 0.09 | 0.29 - 12.21 |
| **Sucrose %** | 11.91 | 37.92 | 0.23 | 2.50 - 35.53 |
| **Maltose %** | 0.49 | 60.51 | 0.02 | 0.00 - 1.98 |
| **Sucrose equivalents (SE)** | 19.33 | 32.42 | 0.32 | 9.85 - 38.64 |
| **Dry matter %** | 33.26 | 15.41 | 0.29 | 12.35 – 42.53 |
| **Starch %** | 63.29 | 11.49 | 0.37 | 38.01 – 75.04 |
| **β-carotene mg/ 100g dry weight** | 8.56 | 25.26 | 0.59 | 0 – 46.02 |

### 4.3.2.2 Means and distribution of starch, sugars, sucrose, sucrose equivalent and sweetness in cooked roots

Distribution of sugars, SE, dry matter, and sweetness in cooked roots followed similar normal distribution. Starch, fructose, sucrose, and sucrose equivalents were however skewed (Figure 4.6). Mean values of these traits in cooked roots are presented in Table 4.8. Maltose was the most abundant sugar in cooked roots with a mean value of 14.89 % dry weight, representing about 2938 % increase over the value in raw roots. Similarly, total sugars, SE and sucrose levels in cooked roots increased by 74 %, 18 % and 22 % respectively. There was however a decrease in fructose, glucose and starch by 63 %, 41 % and 9.13 % respectively in cooked roots (Table 4.8).

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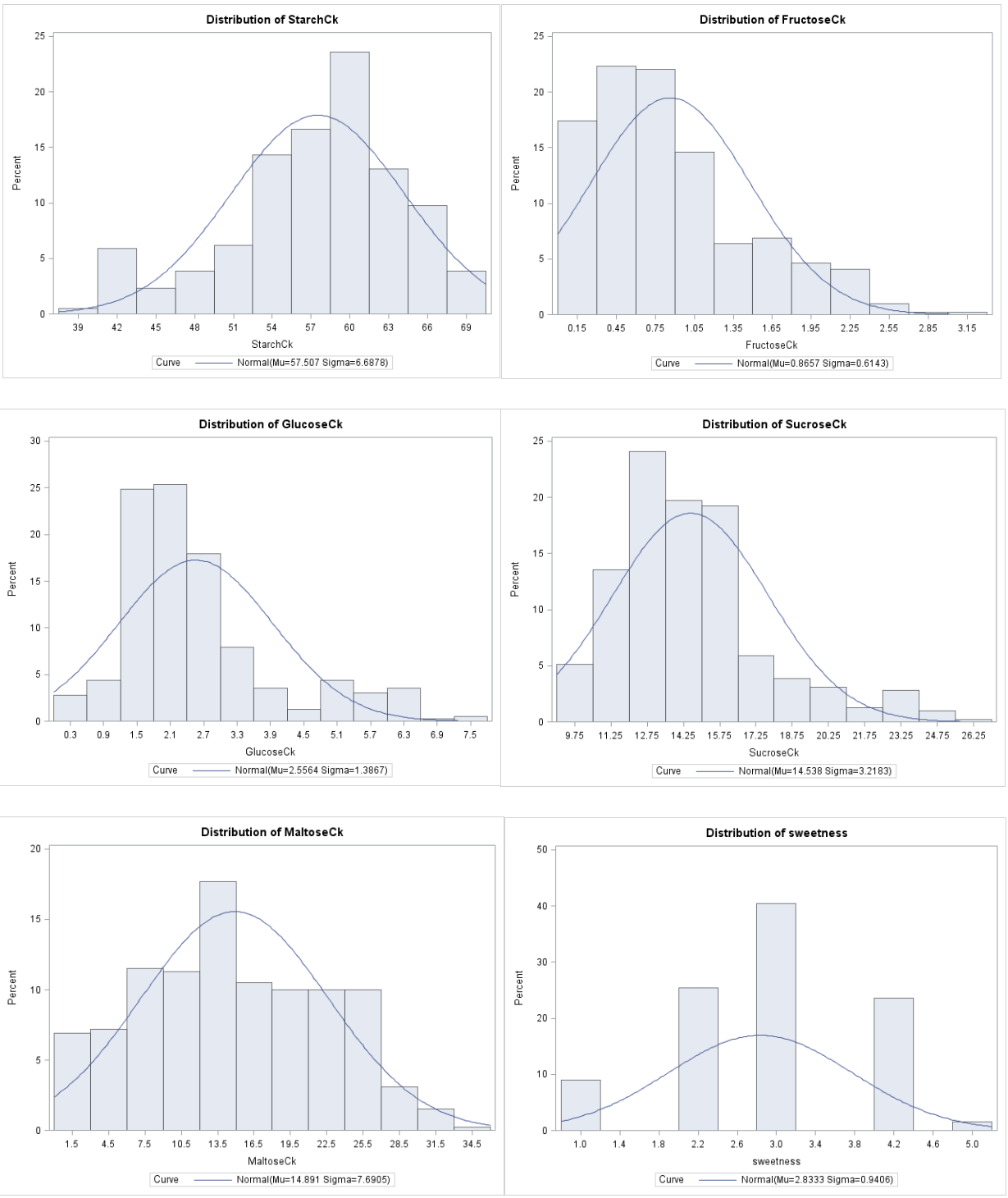


**Figure 4. 6: Distribution of starch, sucrose equivalents and sweetness in steamed roots of 130 sweetpotato accessions**

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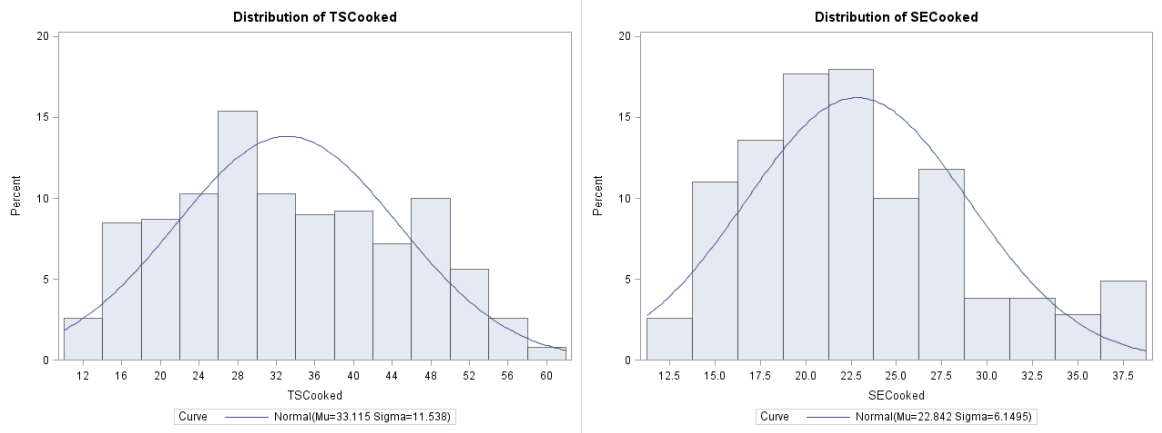


**Figure 4.6 (continued): Distribution of starch, sucrose equivalents and sweetness in cooked roots of 130 sweetpotato accessions**

**Table 4. 8: Means, coefficients of variation, standard error and ranges for sugars, sucrose equivalents, starch and sweetness in cooked storage roots and their percentage change over levels in raw roots of the 130 genotypes**

| Traits | Mean | CV % | SED | Range | % change in relation to values in raw roots |
|---|---|---|---|---|---|
| **Total sugars (%)** | 33.12 | 34.84 | 0.58 | 11.53 – 58.74 | **74 %** |
| **Fructose (%)** | 0.87 | 70.96 | 0.033 | 0.01 – 3.18 | -63 % |
| **Glucose (%)** | 2.56 | 54.24 | 0.07 | 0.1 – 7.73 | -41 % |
| **Sucrose (%)** | 14.54 | 22.13 | 0.16 | 9.52 – 26.33 | **22 %** |
| **Maltose (%)** | 14.89 | 51.65 | 0.39 | 0.05 – 34.87 | **2938.78 %** |
| **Sucrose equiv. (SE)** | 22.84 | 26.92 | 0.31 | 12.15 – 47.62 | **18 %** |
| **Starch (%)** | 57.51 | 11.63 | 0.34 | 39.47 – 69.65 | -9.13 % |
| **Sweetness** | 2.83 | 33.20 | 0.05 | 1 - 5 | |

**Note: β-carotene was determined in uncooked roots; SE = sucrose equivalents. Red fonts and green fonts represent percent increase and decrease in contents respectively**

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### 4.3.2.3 Analysis of variance

The analysis of variance (Table 4.9) indicated that the differences among genotypes in sugars, dry matter, starch and β-carotene levels were highly significant (P<0.0001). Differences between sucrose, total sugars and SE were however not significant in uncooked roots (Table 4.9). In cooked roots, significant differences (P<0.001) were recorded for all traits under study except for sweetness scores.

**Table 4.9: Analysis of variance for quality traits in storage roots of the 130 genotypes**

| | | Mean square for uncooked roots quality traits | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **sources** | **df** | **Dm** | **Starch** | **Fruc** | **Gluc** | **Sucr** | **Malt** | **TS** | **SE** | **BC** |
| **Genotype** | 129 | 68.20*** | 0.006*** | 0.08* | 0.04** | 17.5$^{NS}$ | 0.11** | 0.02$^{NS}$ | 0.02$^{NS}$ | 12.39*** |
| **Blk(rep)** | 38 | 19.94* | 0.001 | 0.06 | 0.03 | 22.5 | 0.09 | 0.02 | 0.02 | 4.59 |
| **Error** | 222 | 12.45 | 0.001 | 0.06 | 0.03 | 21.70 | 0.07 | 0.01 | 0.01 | 0.61 |

| | | Mean square for cooked roots quality traits | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| **Sources** | **df** | **Starch** | **Fruc** | **Gluc** | **Sucr** | **Malt** | **TS** | **SE** | **SW** |
| **Genotype** | 129 | 0.004*** | 0.22* | 2.63*** | 0.01** | 72.60** | 180.06*** | 0.018*** | 0.76$^{NS}$ |
| **Blk(rep)** | 38 | 0.002 | 0.09 | 1.18 | 0.007 | 45.22 | 89.89 | 0.009 | 0.84 |
| **error** | 222 | 0.002 | 0.18 | 1.59 | 0.006 | 47.82 | 102.30 | 0.01 | 0.96 |

***, **, *** Significance at 5%, 1% and 0.1% respectively. $^{NS}$ Not significant. Dm=dry matter, Fruc=fructose, Gluc=glucose, Sucr=sucrose, Malt=maltose, TS=total sugars in raw roots; SE=sucrose equivalents, BC=β carotene; SW = sweetness**

### 4.3.2.4 Discriminant analysis for quality traits in cooked and raw roots

Table 4.10 shows summary results of the stepwise discriminant analysis for root quality traits. Ten (10) root quality traits were identified as the most discriminative to differentiate the 130 genotypes based on their significant p values for Wilk's Lambda (P<0.0001) and p values for the average squared canonical correlations (P<0.0001). The discriminative variables were β-carotene, dry matter, starchR, starchCk, maltoseR, TScooked, maltoseCk, GlucoseCk and

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SECooked and SERaw . β-carotene R dry matter, starchR, and maltoseCk had the greatest discriminative power with F values of 34.63, 4.03, 3.30 and 1.98 respectively. The unselected traits were fructose, glucose, sucrose and total sugars in uncooked roots, and fructose sucrose and sweetness in cooked roots.

**Table 4.10: Stepwise discriminant analysis for root quality traits**

| Stepwise selection summary | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **Step** | **Entered** | **Partial R-Square** | **F Value** | **Pr > F** | **Wilks' Lambda** | **Pr < Lambda** | **Average Squared Canonical Correlation** | **Pr > ASCC** |
| **1** | **β-carotene R** | 0.945 | 34.63 | <.0001 | 0.0549952 | <.0001 | 0.00732562 | <.0001 |
| **2** | **Dry matter R** | 0.667 | 4.03 | <.0001 | 0.01829701 | <.0001 | 0.01244886 | <.0001 |
| **3** | **starchR** | 0.623 | 3.30 | <.0001 | 0.00690562 | <.0001 | 0.01690779 | <.0001 |
| **4** | **StarchCk** | 0.499 | 1.98 | <.0001 | 0.00346037 | <.0001 | 0.02066408 | <.0001 |
| **5** | **MaltoseR** | 0.487 | 1.89 | <.0001 | 0.00177446 | <.0001 | 0.02426374 | <.0001 |
| **6** | **TSCooked** | 0.486 | 1.87 | <.0001 | 0.00091301 | <.0001 | 0.02778356 | <.0001 |
| **7** | **MaltoseCk** | 0.512 | 2.06 | <.0001 | 0.00044589 | <.0001 | 0.03162702 | <.0001 |
| **8** | **GlucoseCk** | 0.463 | 1.69 | 0.0002 | 0.00023968 | <.0001 | 0.03505631 | <.0001 |
| **9** | **SECooked** | 0.432 | 1.49 | 0.0040 | 0.00013611 | <.0001 | 0.03836960 | <.0001 |
| **10** | **SERaw** | 0.388 | 1.23 | 0.0805 | 0.00008328 | <.0001 | 0.04122152 | <.0001 |

**Number of observetions = 130, variables in the analysis = 26, class level = 3, significant level to stay = 0.15; R = raw sample; ck = cooked samples; TS = total sugars**

### 4.3.2.5 Principal component (PC) analysis for root quality traits

Ten root quality traits namely, β-carotene (BC), dry matter (DM), starch in raw roots (starchR), starch in cooked roots (starchCk), maltose in raw roots (maltoseR), total sugars in cooked roots (TScooked), maltose in cooked roots (maltoseCk), glucose in cooked roots (GlucoseCk) and sucrose equivalents in cooked (SECooked) and raw (SERaw) roots were subjected to principal

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component (PC) analysis to ascertain the components that contributed most to the variation observed in the data.

The correlation between the ten traits (Table 4.11) and their eigen values formed the basis for identification of principal components. The eigen values together with the percentage of total variation accounted for by each component and the cummulative percentages are presented in Table 4.12. The relative discriminative power was high for principal axes 1 (5.01), 2 (1.68) and 3 (1.29). Only these three PCs had eigen values greater than 1. Principal components 1 (PC1) accounted for 50.13 % while PC2 and PC3 accounted for 16.81 % and 12.98 % respectively, to give a total of 79.92 % of the total variation in root quality traits. The principal component analysis also displayed a scree plot (Figure 4.7) which graphically shows the size of the eigen value associated with each component. The scree plot depicts a sharp bend at the second principal axes but the third axes was also retained because it had an eigen value greater than 1. The most relevant characters within these three principal axes were identified by examining their eigenvectors (Table 4.13). With respect to the high vector loadings, PC1 correlated with cooked root traits namely, cooked starch, total sugar in cooked roots and sucrose equivalence in cooked roots. PC2 correlated with raw root taits. It correlated negatively with BC but positively with DM and starch. The PC3 had positive associations with SE in raw roots as well as maltose in both cooked and raw roots.

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**Table 4. 11: Correlation matrix for 10 discriminative root quality traits used to distinguish the 130 genotypes**

| Correlation matrix | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | DM | starchR | MaltoseR | SERaw | BC | StarchCk | GlucoseCk | MaltoseCk | TSCooked |
| starchR | 0.5500 | | | | | | | | |
| MaltoseR | -.0254 | -.0713 | | | | | | | |
| SERaw | -.1444 | -.4025 | 0.5314 | | | | | | |
| BC | -.5385 | -.6811 | -.0059 | 0.1101 | | | | | |
| StarchCk | 0.2431 | 0.4191 | -.2408 | -.4818 | -.3200 | | | | |
| GlucoseCk | -.2248 | -.3987 | 0.2047 | 0.5143 | 0.2968 | -.8716 | | | |
| MaltoseCk | -.2077 | -.1900 | 0.1625 | 0.1147 | 0.2117 | -.6622 | 0.3853 | | |
| TSCooked | -.3175 | -.4073 | 0.2264 | 0.3302 | 0.3254 | -.8568 | 0.6671 | 0.8592 | |
| SECooked | -.2564 | -.4202 | 0.2943 | 0.4968 | 0.3225 | -.9514 | 0.8659 | 0.6981 | 0.8781 |

**Table 4. 12: Eigenvalues of the correlation matrix of the 10 discriminative root quality traits used to distinguish the 130 genotypes**

| Eigenvalues of the Correlation Matrix | | | | |
|---|---|---|---|---|
| | Eigenvalue | Difference | Proportion | Cumulative |
| 1 | 5.01267058 | 3.33122105 | 0.5013 | 0.5013 |
| 2 | 1.68144953 | 0.38377988 | 0.1681 | 0.6694 |
| 3 | 1.29766965 | 0.53377392 | 0.1298 | 0.7992 |
| 4 | 0.76389572 | 0.28910314 | 0.0764 | 0.8756 |
| 5 | 0.47479258 | 0.09462213 | 0.0475 | 0.9230 |
| 6 | 0.38017046 | 0.16485426 | 0.0380 | 0.9611 |
| 7 | 0.21531620 | 0.14865228 | 0.0215 | 0.9826 |
| 8 | 0.06666391 | 0.00163534 | 0.0067 | 0.9893 |
| 9 | 0.06502857 | 0.02268577 | 0.0065 | 0.9958 |
| 10 | 0.04234281 | | 0.0042 | 1.0000 |

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**Table 4. 13: Eigenvectors from ten principal component axes used to classify 130 sweetpotato accessions**

| | Eigenvectors | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | **Prin1** | **Prin2** | **Prin3** | **Prin4** | **Prin5** | **Prin6** | **Prin7** | **Prin8** | **Prin9** | **Prin10** |
| **DM** | -.199 | **0.516** | -.043 | -.314 | 0.751 | -.158 | -.047 | 0.033 | 0.047 | -.007 |
| **starchR** | -.273 | **0.470** | -.211 | 0.106 | -.230 | 0.470 | 0.596 | 0.135 | -.034 | 0.019 |
| **MaltoseR** | 0.150 | 0.290 | **0.556** | 0.589 | 0.176 | 0.357 | -.275 | -.020 | 0.004 | -.046 |
| **SERaw** | 0.253 | 0.150 | **0.605** | -.140 | -.127 | -.459 | 0.546 | 0.030 | 0.043 | -.020 |
| **BC** | 0.224 | **-.551** | 0.013 | 0.043 | 0.554 | 0.347 | 0.461 | 0.064 | 0.004 | -.001 |
| **StarchCk** | **-.416** | -.154 | 0.103 | 0.196 | 0.020 | -.108 | 0.040 | 0.056 | 0.732 | 0.450 |
| **GlucoseCk** | **0.373** | 0.120 | 0.044 | -.480 | -.136 | 0.402 | -.117 | -.148 | 0.585 | -.235 |
| **MaltoseCk** | 0.312 | 0.160 | **-.433** | 0.454 | 0.094 | -.293 | 0.187 | -.520 | 0.236 | -.165 |
| **TSCooked** | **0.401** | 0.110 | -.265 | 0.181 | 0.005 | -.162 | -.071 | 0.812 | 0.179 | -.034 |
| **SECooked** | **0.423** | 0.164 | -.088 | -.117 | -.011 | 0.103 | -.037 | -.143 | -.171 | 0.843 |
| **Eigenvalue** | **5.01** | **1.68** | **1.29** | **0.76** | **0.47** | **0.38** | **0.21** | **0.07** | **0.06** | **0.04** |
| **%variation** | **50.13** | **16.18** | **12.98** | **0.08** | **0.05** | **0.04** | **0.02** | **0.01** | **0.01** | **0.004** |
| **Cummulative %** | **50.13** | **66.94** | **79.92** | **87.56** | **92.30** | **96.11** | **98.26** | **98.93** | **99.58** | **100** |

**Bolded values indicate the most relevant characters (≥ 0.4) that contributed most to the variation in that axes: Ck, R, DM = cooked samples, raw samples and dry matter respectively**

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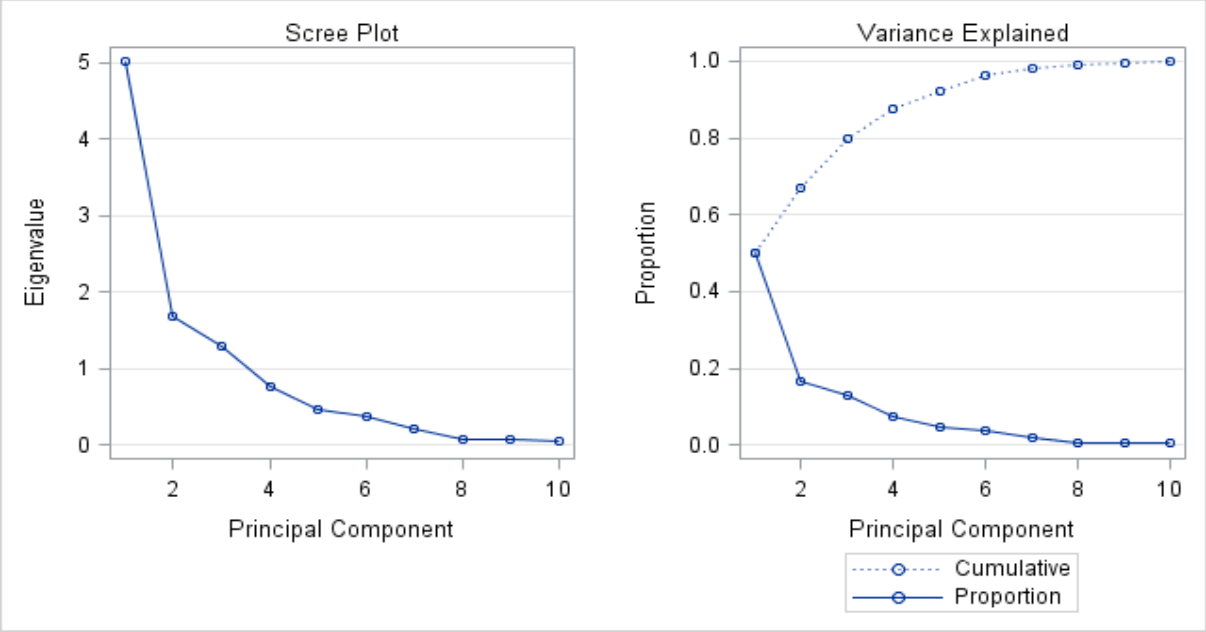


**Figure 4.7: Scree plot and total variance explained by the 10 discriminative root quality characters**

### 4.3.2.6 Cluster analysis based on eight root quality traits

Due to the high correlations among some variable (Table 4.11), total sugars and sucrose equivalents in cooked roots were not included in the traits used for cluster analysis. Mean Euclidean pair-wise dissimilarity coefficient computed as single and continuous data, revealed a dissimilarity index ranging from 0.82-19.66 with an average value of 7.41 (Figure 4.8) implying high diversity in quality traits among the 130 genotypes. The remaining 8 discriminative characters grouped the 130 genotypes into two major clusters and nine sub-clusters, five of which were outliers (Figure 4.9). Cluster A had two sub-clusters (I and IV) and two outliers while cluster B consisted of two sub-clusters (VIII and IX) and three outliers. Sub-cluster I to cluster VII consisted only of orange-fleshed genotypes but varied in the levels of β-carotene, from high levels in genotypes at the top of sub-cluster I to much lower levels in Zapallo of sub-cluster VIII.

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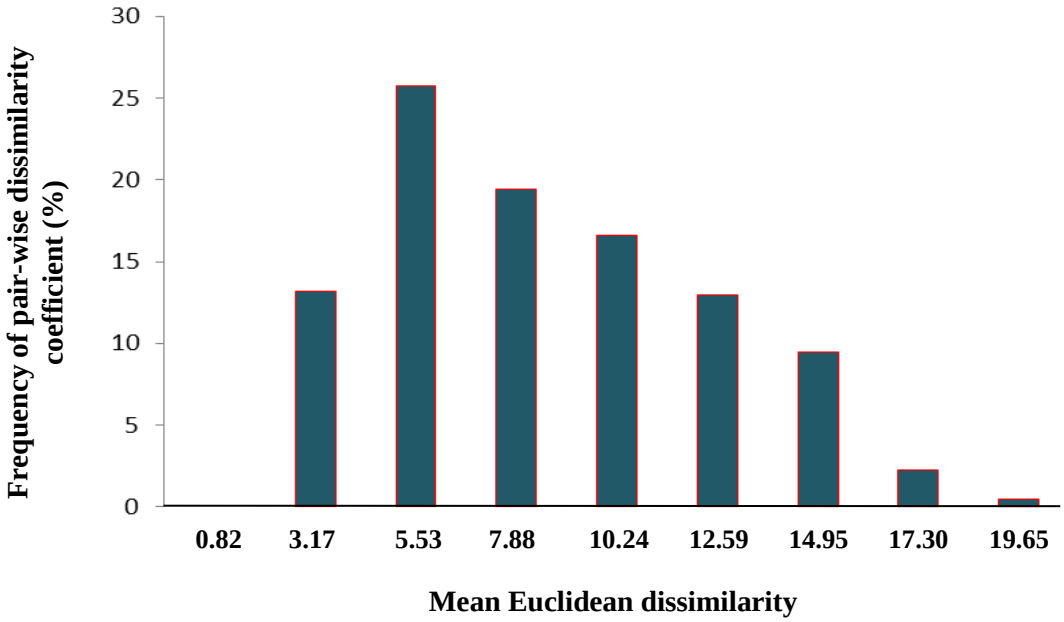


**Figure 4. 8: Mean Euclidean dissimilarity index of the 130 genotypes using DARwin 5.0.158, Mean = 7.41, Min value = 0.82**

The 14 genotypes in sub-cluster I were also characterized mostly by high levels of sugar and low dry matter and starch. They comprised mainly of very sweet accessions imported from the USDA germplasm repository. MD 844, W-248 and W 209 were however low in sweetness. Also among these 14 accessions were Ghanaian farmers' varieties, namely, Local orange flesh, Naanuveo and Tchichari. Naanunasingo, Dankledze and a released variety – Apomuden. All accessions in sub-cluster I had higher β-carotene levels than Apomuden, the check variety for high β-carotene. Within each sub-cluster were groups of genotypes forming smaller sub-clusters. The genotypes in a smaller sub-cluster were more closely related than the others in the same cluster. For example sub-cluster VIII comprised 65 genotypes related broadly by having low levels of β-carotene and high dry matter and intermediate sugar properties. The uppermost sub-cluster however, contained genotypes whose storage root flesh colors ranged from pale orange (e.g. Zpallo and Amarillo de Chilca) to yellow and were either sweet or intermediate sweet. High

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dry matter clones like Jonathan, Zambezi, Humbachero and Ejumula, from East Africa; Ghanaian clones like Santom Kokoo, Santom Fofuo local, Bonanyere and Naanunono; as well as USDA imports like Pelican Processor, Yellow Sunflower and Francia, were also found in sub-cluster VIII. In sub-cluster IX genotypes were very high in dry matter and starch but very low in β-carotene and low in both raw sugars and cooked sugars. In this sub-cluster genotypes had dry matter ranging from 33-42 % weight and had flesh colors ranging from yellow to white. Kadzie, a farmer variety and genotype 159 a USDA germplasm import were the least sweet cultivars in this sub-cluster having both low raw sugar and low maltose in cooked roots. These two and ten others that formed a sub-cluster at the bottom of the cluster IX were higher in dry matter than the local check, Blue Blue and were also the most bland.

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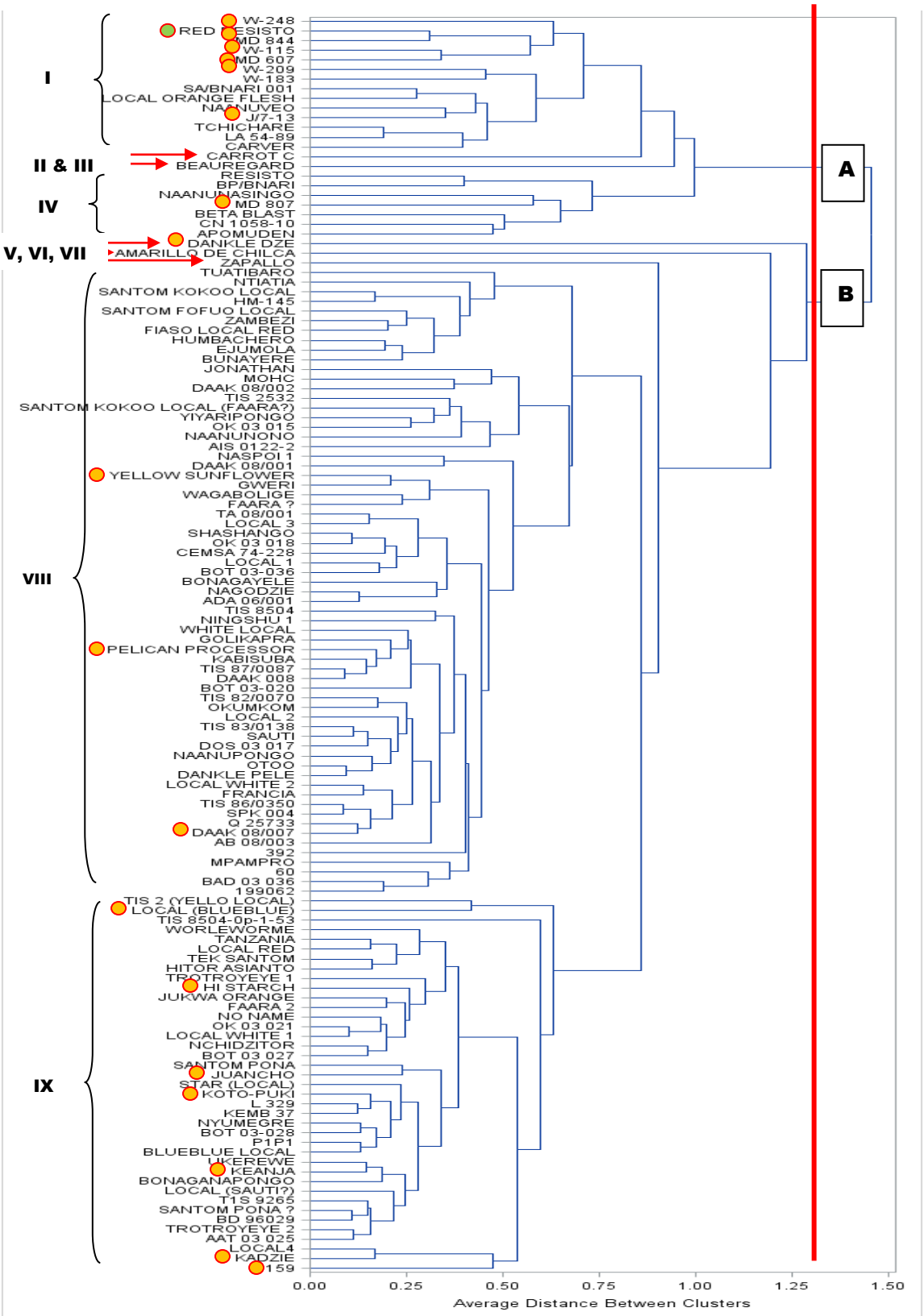


**Figure 4. 9: Dendrogram of the 130 accessions revealed by average linkage cluster analysis using the 8 discriminant quality traits. Yellow dots show the twenty selected parental genotypes.**

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#### 4.3.2.7 Correlations between morphological and root quality traits

As shown in Table 4.14 the only strong and significant correlations found between morphological and root quality traits were between flower habit and β-carotene. There was however weak but significant negative correlation ($p<0.0001$) between flower habit and dry matter and starch. This is because β-carotene clones in this study were mostly breeding lines that exhibit profuse flowering, as opposed to non-flowering to sparsely flowering types of high dry matter clones.

**Table 4. 14: Correlation between discriminative morphological and root quality traits used to classify the 130 genotypes**

| Pearson Correlation Coefficients, N = 390 | | | |
|---|---|---|---|
| | **Flower habit** | **Dry matter** | |
| **Dry matter** | -0.31438*** | | |
| **Raw root starch** | -0.28681*** | 0.39522*** | |
| **β-carotene** | **0.51370*** ** | -0.45745*** | -0.57209*** |

*** = significant at P < 0.0001 level

### 4.3.3 Comparison between morphological and root quality data.

Morphological data, grouped the 130 accessions into 8 clusters while root quality analysis grouped them into 2 major clusters. Each method generated sub-clusters within clusters, with closer relatedness among genotypes within a sub-cluster. No duplicates with 100% similarity were detected by either methods, but suspected duplicates were found in same clusters using both methods. While clusters generated by morphological data showed no distinct patterns with regard to origin of genotypes, some distinct patterns in relation to origin was observed in clusters generated by root quality data. Genotypes from Ghana, East Africa and USDA imports clustered

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together depending on their similarities with regard to levels of sugars dry matter and β-carotene. Apomuden, a released orange fleshed variety clustered with the orange-fleshed types while Okumkom, also a released variety fell within the cluster with intermediate sugar and dry matter properties. Morphological markers were unable to distinguish genotypes based on farmer preferred attributes, but quality markers separated genotypes based on farmer preferred traits.

### 4.3.4 Characteristics of selected parental genotype

Twenty genotypes with a range of quality attributes were selected as parents for hybridization. These were selected from the major clusters in Figure 4.9 and are shown as yellow dots. They ranged from high to low β-carotene content, very sweet to bland cultivars and low to high dry matter. Cluster analysis for these 20 genotypes is presented in Figure 4.10. Genotypes in cluster A, were orange-fleshed, low in dry matter and mostly sweet except W-209 and J/7-13 which were low sweet. In cluster B Dankledze was an outlier having intermediate root quality characteristics. The remaining clones were low-sweet to non-sweet, high in dry matter and yellow to white-fleshed. The varieties had different levels of sugars in uncooked roots, different levels of maltose formation in cooked roots and hence varying levels of sucrose equivalents (Table 4.15). Red Resisto for example had high SE in cooked roots due to the presence of high endogenous sugars and high maltose formation during cooking. Although MD 844 and W-115 had low sugars in raw roots, they both had higher SE due to higher amounts of maltose in cooked roots. Juancho on the other hand was relatively high in endogenous sugars but low in SE in cooked roots because of lower maltose in cooked roots. Accession 159 expressed low SE because of low endogenous sugars and low maltose in its cooked roots.

Yield and yield components for the selected genotypes are presented in Table 4.16. With the exception of W-248, Red Resisto, Daak 08/007, Juancho and Kadzie selected parents were

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higher in almost all yield and yield components than the check varieties Blue Blue and Apomuden. Most genotypes also performed better than the population means for all variables. Mean yield and yield components for selected genotypes were also higher than the overall population means.

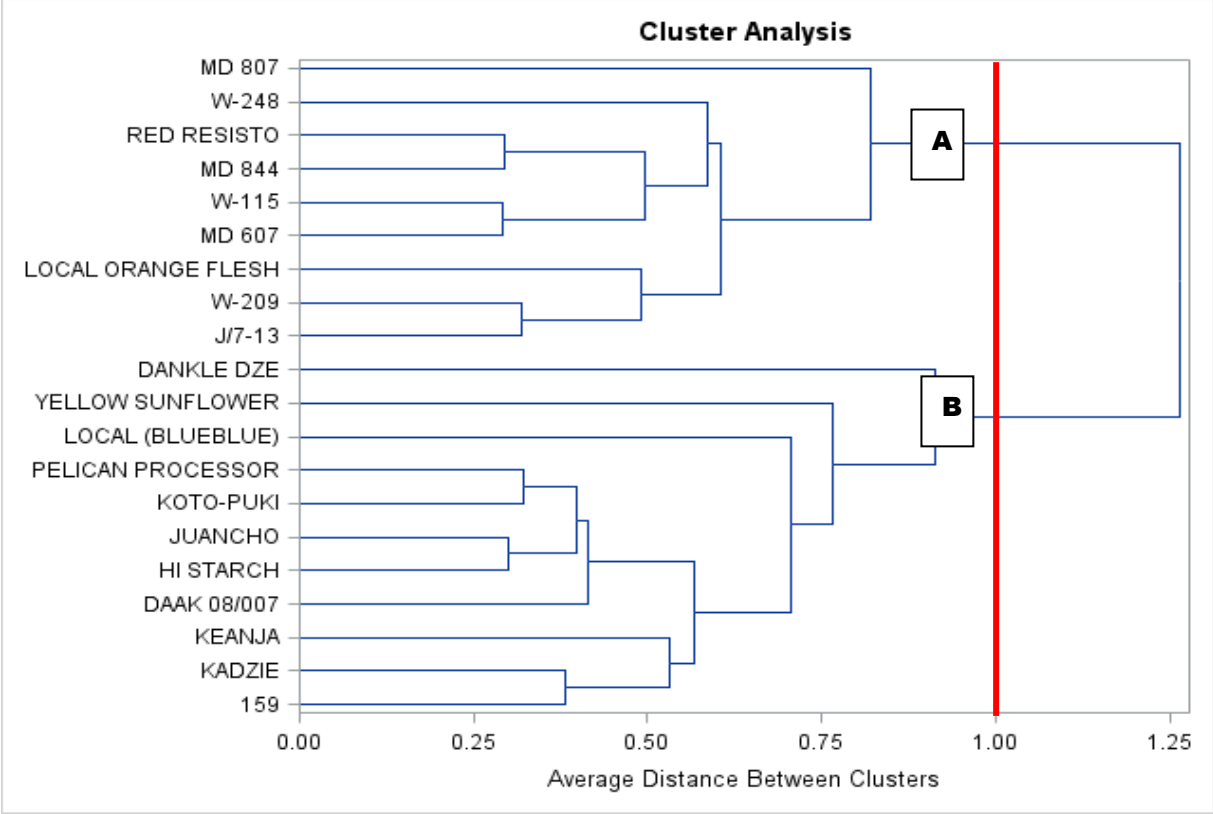


**Figure 4. 10: Dendrogram of the 20 selected parental accessions revealed by average linkage cluster analysis based on the 8 discriminant root quality traits**

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**Table 4.15: Means of root quality characteristics of the 20 selected parental genotypes and two checks**

| Genotype | DM (%) | StarchR (% DM) | StarchCk % | TSraw % | MTCk % | TSCooked % | SEraw | SEcooked | BC (mg/100g DM) |
|---|---|---|---|---|---|---|---|---|---|
| **MD 807** | 28.14 | 52.84 | 44.78 | 23.06 | 32.91 | 38.77 | 23.47 | 32.16 | 25.39 |
| **W-248** | 24.95 | 59.95 | 58.76 | 28.46 | 12.37 | 25.59 | 22.12 | 20.66 | 39.42 |
| **Red Resisto** | 24.88 | 53.69 | 59.97 | 12.28 | 42.83 | 33.53 | 12.26 | 20.43 | 37.89 |
| **MD-844** | 22.89 | 56.00 | 60.41 | 15.54 | 31.54 | 25.51 | 15.43 | 23.06 | 39.71 |
| **W-115** | 24.02 | 57.68 | 54.81 | 14.69 | 24.07 | 40.87 | 14.56 | 25.32 | 40.10 |
| **MD-607** | 21.31 | 54.04 | 57.56 | 19.10 | 27.85 | 36.91 | 19.41 | 23.65 | 40.70 |
| **Local OFSP** | 25.42 | 62.23 | 57.17 | 15.63 | 23.86 | 40.22 | 16.07 | 23.98 | 24.58 |
| **W-209** | 29.90 | 61.90 | 58.34 | 20.47 | 12.66 | 30.16 | 20.83 | 21.58 | 24.05 |
| **J/7-13** | 25.91 | 58.57 | 56.05 | 21.91 | 11.37 | 31.32 | 29.34 | 22.46 | 31.57 |
| **Dankle dze** | 33.07 | 53.05 | 65.01 | 19.90 | 1.17 | 19.38 | 19.99 | 16.65 | 23.14 |
| **Yellow sunflower** | 38.76 | 68.43 | 52.69 | 17.78 | 14.80 | 22.50 | 18.12 | 20.64 | 0.00 |
| **Blue Blue++** | 39.09 | 63.49 | 57.93 | 17.57 | 2.88 | 17.25 | 20.02 | 15.55 | 0.00 |
| **Pel. Processor** | 35.56 | 68.75 | 58.12 | 16.31 | 15.31 | 28.23 | 16.59 | 22.34 | 0.00 |
| **Koto-puki** | 34.63 | 68.14 | 62.50 | 16.54 | 11.19 | 19.66 | 16.49 | 16.92 | 0.00 |
| **Juancho** | 37.76 | 66.37 | 58.95 | 20.10 | 6.73 | 22.10 | 20.40 | 17.74 | 0.00 |
| **Hi Starch** | 33.13 | 68.18 | 60.89 | 21.72 | 9.70 | 25.86 | 22.43 | 19.01 | 0.00 |
| **Daak 08/007** | 35.15 | 63.93 | 59.10 | 19.60 | 14.17 | 24.80 | 19.93 | 19.68 | 0.00 |
| **Keanja** | 34.62 | 65.92 | 65.85 | 15.72 | 5.62 | 16.68 | 15.66 | 14.58 | 0.00 |
| **Kadzie** | 40.92 | 69.95 | 66.15 | 16.89 | 5.27 | 16.42 | 17.25 | 14.99 | 0.00 |
| **159** | 41.57 | 70.32 | 67.59 | 16.77 | 9.75 | 13.44 | 16.47 | 13.93 | 0.00 |
| **Apomuden** | 23.00 | 54.67 | 49.94 | 24.18 | 37.92 | 46.71 | 25.00 | 33.97 | 27.97 |
| **Mean of selected** | 31.18 | 61.81 | 58.69 | 19.05 | 16.86 | 27.42 | 19.13 | 20.72 | 16.88 |
| **Grand mean** | 33.26*** | 63.25*** | 57.51*** | 19.04*** | 14.87 | 33.11*** | 22.84*** | 2.88*** | 8.56*** |
| **SED** | 5.81 | 6.69 | 6.68 | 6.03 | 7.69 | 11.53 | 6.27 | 6.15 | 11.63 |
| **CV %** | 7.07 | 6.27 | 7.06 | 10.24 | 46.34 | 28.60 | 27.46 | 16.03 | 16.61 |
| **MD-807** | 28.14 | 52.84 | 44.78 | 23.06 | 32.91 | 38.77 | 23.47 | 32.16 | 25.39 |

*****Significant at 0.1%. DM = dry matter, starch = raw root starch,starchck = cooked root starch, TSraw = total sugars in raw roots, MTck = maltose in cooked roots, TScooked = total sugars in cooked roots,SEraw = sucrose equivalent in raw roots, SE cooked = sucrose equivalents in cooked roots and BC = β-carotene; ++ = Check varieties**

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**Table 4.16: Means of yield and yield components of 20 selected parental genotypes and two checks**

| Genotypes | HI | IRwt/kg | Comyld t/ha | Tyld t/ha | Nocr/plot |
|---|---|---|---|---|---|
| **MD 807** | 70.69 | 0.18 | 41.16 | 42.11 | 29.73 |
| **W-248** | 53.98 | 0.13 | 17.80 | 21.88 | 16.87 |
| **Red Resisto** | 46.02 | 0.19 | 12.30 | 14.45 | 7.62 |
| **MD 844** | 63.89 | 0.19 | 29.80 | 31.32 | 20.03 |
| **W-115** | 64.67 | 0.22 | 27.72 | 31.47 | 14.56 |
| **MD 607** | 64.94 | 0.27 | 32.73 | 33.26 | 14.74 |
| **Local ORF** | 59.95 | 0.18 | 23.33 | 25.34 | 14.24 |
| **W-209** | 67.21 | 0.27 | 34.12 | 34.88 | 16.87 |
| **J/7-13** | 53.24 | 0.12 | 20.16 | 21.86 | 15.60 |
| **Dankledze** | 59.16 | 0.29 | 23.62 | 25.25 | 10.11 |
| **Yellow Sunflower** | 58.72 | 0.26 | 24.26 | 25.57 | 10.49 |
| **++Blueblue** | 55.98 | 0.56 | 21.82 | 23.46 | 5.40 |
| **Pelican Processor** | 66.52 | 0.26 | 27.45 | 31.67 | 14.55 |
| **Kotopuki** | 61.84 | 0.27 | 25.82 | 29.65 | 11.82 |
| **Juancho** | 45.37 | 0.34 | 12.01 | 13.47 | 4.7 |
| **Histarch** | 60.05 | 0.35 | 24.34 | 24.71 | 7.8 |
| **Daak 08/007** | 48.95 | 0.34 | 11.22 | 16.15 | 3.5 |
| **Keanja** | 41.45 | 0.34 | 35.69 | 35.96 | 12.84 |
| **Kadzie** | 65.94 | 0.31 | 11.53 | 13.58 | 4.15 |
| **159** | 58.49 | 0.54 | 22.24 | 24.01 | 5.40 |
| **++Apomuden** | 6.28 | 0.04 | 2.26 | 3.62 | 1.2 |
| **Mean of selected** | **58.35** | **0.28** | **23.96** | **24.01** | **12.05** |
| **Grand mean** | **45.65*** ** | **0.26*** ** | **18.91*** ** | **20.82*** ** | **8.5*** ** |
| **CV%** | **17.51** | **58.16** | **38.15** | **38.27** | **35.04** |
| **SED** | **1.13** | **0.11** | **0.01** | **0.89** | **0.92** |

**++ = Check varieties; IRwt = individual root weight; Comyld = commercial yield; Nocr = number of commercial roots.**

## 4.4 DISCUSSION

Progress in plant breeding can be achieved through selection, if variability exists in the collection of germplasm. The presence of diverse range of genotypes increases the opportunity to select superior genotypes (Anshebo *et al*., 2004) for inclusion among breeding lines. There is therefore the need to assess the amount of variability in a germplasm for important economic characters as a first step at the inception of any breeding effort. One hundred and thirty genotypes were

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therefore assembled to provide an ample genetic base for the selection of parents for a low-sugar, high β-carotene and high dry matter breeding effort. The clones were characterized using morphological and root quality traits.

Nine discriminative morphological descriptors were identified, which revealed a high level of diversity among clones. They comprised plant type, ground cover, leaf characteristics (shape of central leaf lobe, immature leaf color and petiole pigmentation), root characters (storage root arrangement, storage root surface defects, distribution of secondary flesh color) and flower habit. Storage root surface defects, distribution of secondary flesh color, shape of central leaf lobe and petiole pigmentation had the highest $R^2$ values and were the most discriminative. None of the skin color descriptors were useful in differentiating genotypes in this study, but Yada *et al*. (2010) found principal skin color as discriminatory for Ugandan germplasm. Plant type and ground cover were found discriminatory by Gichuru *et al*. (2006), shape of central leaf lobe and immature leaf color by Yada *et al*. (2010) and storage root surface defects by Some (2013). In Uganda twenty discriminatory morphological traits were identified among forty (Yada *et al.*, 2010a), as opposed to the nine identified in this study. However, only two descriptors general leaf outline and the shape of central leaf lobe were identified to differentiate between accessions in Kenya (Karuri *et al*., 2010). The same authors found flower habit as not discriminative but flower habit was discriminative in the current study. The high diversity index in sweetpotato populations reported by Karuri *et al*. (2010) is in agreement with this study.

The cluster analysis did not reveal any geographically distinguishable relationship among the various groups of accessions. This supports reported study in Uganda to assess diversity among East African land races using morphological and SSR markers (Gichuru *et al*., 2006).

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Only three PCs were necessary to explain the variation (78.9 %) in root traits while five PCs (68%) were needed for morphological traits. This could be explained by the fact that there is high level in variability associated with morphological traits than there is with root quality traits. Hence when analyzing morphological traits a larger number of PCs are necessary to account for total variance in the germplasm. Seven PCs accounting for 89.2% of total variance in a morphological data were also identified by earlier authors (Yada *et al.*, 2010a). There have been no documented reports on the use of storage root quality traits to identify discriminative variables or for cluster analysis in sweetpotato. This study identified ten storage root quality traits as discriminative, but to prevent redundancy due to high correlation between some variables, only 8 were used in the cluster analysis. The most discriminative among these were β-carotene, dry matter, starch and maltose. Taste (sweetness) did not enter into the discriminatory factors for quality classification probably because taste is subjective and the large number of samples involved may have made it difficult to discern significant differences between samples. A number of farmers' varieties clustered with those released by national programs. It is possible that some of these 'farmer varieties' are actually released varieties that have been adopted by farmers. Some key morphological descriptors like skin colour, flesh colour, and mature leaf colour were excluded from the analysis, and may have reduced the efficiency of morphological markers in clarifying the likelihood of similarity between the accessions.

Even though the phenotypic and quality data employed in this study were useful for utilitarian purposes, they would have been even more helpful if complemented by assessment of genetic diversity via molecular data (Yada *et al.*, 2010b). This would have provided a more in-depth analysis of the germplasm and helped to guide breeding decisions more effectively. However, published reports on breeding methods that incorporate molecular marker approaches for

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organoleptic traits are uncommon and genome maps in sweetpotato are sparsely saturated. To circumvent these bottlenecks, selection methods that do not require a priori genetic maps and are capable of analyzing multiple traits simultaneously as described by (Mcharo, 2005) would be useful. Mcharo (2005) used discriminant analysis to select a total of 8 markers for total sugars in raw roots but each of the markers accounted for just a small percentage of the variation for total sugar content as would be expected of a quantitative trait like sugars (Mcharo, 2005). The selection of these markers was based on raw root sugars. However, since maltose accumulates only when sweetpotato is cooked, molecular marker studies involving maltose as a classification variable would be more informative to breeders. A more recent study has also identified a number of QTLs associated with total sugar, dry matter and starch in Beauregard and Tanzania, a US and East African variety respectively (Todd, 2013). Cervantes-Flores *et al*. (2006) reported the significant effect of 8 QTLs on variation in β-carotene in sweetpotato. These findings provide a stepping stone for further molecular work that would extend the knowledge base on the genetics of sweetpotato sugars, β-carotene and other quality characteristics.

The Crops Research Institute of Ghana has carried out a number of sensory evaluations to determine varieties with desired quality characteristics that suit consumers and farmers (Adu-Kwarteng *et al.*, 2001; Adu-Kwarteng *et al.*, 2002; Sam and Dapaah, 2009; WAAPP, 2009). Traits mostly considered in these studies have been dry matter content and sweetness levels and their effects on cultivars suitability for local cuisines. Measurements for dry matter have been easy to undertake, but until now, actual quantification of different sugars and their effect on sweetness has not been done. This is because chemical analysis costs are so high that unless a simple screening tool is available it is difficult to include these chemical traits in routine screening. Progress in breeding however, requires not only genetic variation for the traits being

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selected but also reliable and simple screening procedures for identifying desired genotypes (Lebot *et al.,* 2009). In the past as was the case in many breeding programs around the world, early generation lines of sweetpotatoes are tested for many years and are retained because they possess good agronomic characteristics. These are later rejected by farmers or discarded by breeders if analysis shows a deficiency in quality attributes like starch, dry matter, or sugar concentration (Katayama *et al*., 1996). Traditional assay methods, particularly for starch and sugars, are too laborious to efficiently screen many progeny produced in a breeding program (Katayama *et al*., 1996). With the advent of NIRS proximate analysis for quality attributes is no longer a constraint since many compounds can now be readily quantified (Lebot *et al.,* 2009). NIRS was used to quantify sugars and starch in uncooked as well as in cooked roots, and β-carotene in the uncooked roots of 130 genotypes evaluated in this study.

Sucrose was the most abundant sugar in raw roots as also reported by others (Palmer, 1982; Walter, 1992; Wang and Kays, 2003). Compared to the sucrose, glucose, and fructose, maltose levels were very low in raw roots. Glucose content was a little higher than that of fructose. This finding is in agreement with that reported by Lewthwaite *et al*. (1997) and Wang and Kays (2003). Total sugars in raw roots ranged from 9.27-45.94 % dry weight, while in cooked roots, they ranged from 11.53-58.74 % dry weight, representing a 74 % increase in sugars after cooking (Table 4.8). This increase was primarily due to the accumulation of maltose during cooking. The accumulation of maltose in cooked sweetpotato has been widely documented (Kumagai *et al.*, 1990; Koehler and Kays, 1991; Lewthwaite *et al.*, 1997; Kays *et al.*, 1999; La Bonte and Picha, 2000; Kays *et al.*, 2005a; Kays, 2006) and occurs as a result of hydrolysis of starch to sugars during cooking by the activity of β-amylases (McLaurin and Kays, 1992; Morrison *et al*., 1993). In this study starch content reduced by 9.13 % in cooked roots. The hydrolysis of starch into

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maltose by this enzyme may have been responsible for the decline. While maltose increased during cooking, fructose and glucose concentration on the other hand decreased. Decreases in fructose and glucose contents during cooking have been reported from studies using methods such as HPLC to quantify sugars (Truong *et al.*, 1986; Lewthwaite *et al.*, 1997). Increased concentrations of fructose, glucose and sucrose after cooking have also been reported (Picha, 1987; Takahata *et al.*, 1992)

According to La Bonte and Picha (2000), the selection of sweetpotato based on sweetness levels is complicated by a number of factors. First, sugars are not equal in their contribution to sweetness thus necessitating comparison at similar levels of sweetness by determining their sucrose equivalents (SE). A second factor according to the authors is that, even though higher sugar content in raw sweetpotato implies a sweeter baked product, high sugar content in a raw sweetpotato does not necessarily result in higher sugar content in a cooked sweetpotato. This is evidenced in the study by Picha (1987) and La Bonte and Picha (2000) in which a particular variety (Travis) had higher levels of total sugars before cooking, than afterwards. This was because Travis had low Alcohol Insoluble Solids or crude starch, making less starch available for conversion to maltose by β-amylase. These phenomena were also observed in this study where varieties like MD 844 and W-115, had low total sugars when raw but higher cooked sugars occasioned by higher maltose in cooked roots. In addition, varieties like Juancho which had higher sugar content before cooking, but lower maltose in cooked roots confirms the existence of cultivars with high endogenous sugars and low starch hydrolysis (McLaurin and Kays, 1992). Cultivars 159 and Kadzie were low in both total sugars and starch conversion to maltose and were thus high in starch and dry matter. They were also the blandest of all cultivars in this study and may have some potential for Ghana. Other factors that can significantly alter the storage root

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sugar content before cooking and thereby complicate sugar selection, include postharvest curing treatments (Picha, 1987; Lewthwaite *et al.*, 1997), physiological changes during storage (La Bonte and Picha, 2000) and methods of sample preparation and cooking (Lewthwaite *et al.*, 1997).

In this study sucrose equivalents in raw and cooked roots of the 130 genotypes were determined and a range of 9.85 - 38.64 and 12.15 – 47.62 was obtained for raw and cooked roots respectively, representing an 18 % increase in cooked roots. Kays *et al*. (2005) classified sweetpotato into five categories based on their SE, as follows; [very high (≥ 38 SE), high (29-37 SE), moderate (21-28 SE), low (13-20 SE), non-sweet (≤ 12 SE)]. Based on this classification five accessions from the 130 clones namely; 159, Kadzie, Keanja, high starch, kotopuki and Dankledzi can be classified as low SE accessions while MD 807, Red Resisto and W-115 are high SE accessions. The means for dry matter (DM), starch and β-carotene were 33.26 % dry weight, 63.25 % dry weight and 17.77 mg/100g dry weight. There were however, clones with higher values than the means. Selected parents were also high in dry matter and starch. Values, as high as 46 % dry matter and 75.04 % starch were observed. The large variation in these traits implies that genotypes can be selected for subsequent breeding to increase the population means. With the high heritability for dry matter (Zhang and Li, 2004), starch and β-carotene (Hernandez *et al.*, 1967; Jones *et al.*, 1986b; Tsegaye *et al.*, 2007) rapid genetic gain can be realized.

## 4.5 CONCLUSION

Large variation was observed for both morphological and root quality traits in the 130 genotypes analyzed. Nine discriminant morphological and 8 quality traits were identified which generated different clusters of genetic relatedness. Regarding farmer preferred traits, the use of root quality traits in characterizing genotypes was most useful. Sugar, dry matter and β-carotene varied

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widely offering an opportunity for selection and genetic improvement. The sucrose equivalent, a measure of sweetness, was calculated for each genotype and clones that were low or high in sucrose equivalents were identified. Twenty of these clones namely; W-248, Red Resisto, MD 844, W-115, MD 607, Local ORF, W-209, J/7-13, Dankledze, Yellow Sunflower, Blueblue, Pelican Processor, Kotopuki, Juancho, Histarch, Daak 08/007, Keanja, Kadzie, Apomuden and 159 (Table 4.14) with varying range of quality and yield characteristics have been selected for genetic improvement through hybridization.

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# CHAPTER FIVE

## EVALUATING GENOTYPE X ENVIRONMENT INTERACTION OF SWEETPOTATO FOR YIELD, DRY MATTER, SUGARS AND BETA-CAROTENE

### 5.1 INTRODUCTION

The phenotype of an individual is not only determined by its genetic make-up but also by non-genetic factors referred to as the environment (Kempthorne, 1957; Carpena *et al.*, 1982). Genotypes x environment interaction (GEI) therefore involve the differences in performance of genotypes in different locations, years and seasons within a year (Wrickle and Weber, 1986; Dixon and Nukenine, 2000). According to Grüneberg *et al*. (2005) GEI can be explained as subsets of genotypes and environments.

Knowledge of the magnitude of GEI on phenotypes improves the accuracy in characterizing genotypes and improves gain in selection by enabling the identification of locations and input systems to use (Grüneberg *et al.*, 2005). In plant breeding multi-environment trials are carried out primarily to identify superior cultivars by comparing the mean performance of genotypes across test environments (Yan and Hunt, 2002) so as to select genotypes for specific or wide adaptation. A variety is said to have specific adaptation if it ranks among the highest yielders at some locations, but not at others as a result of differences in biotic and abiotic factors *(Abidin et al.*, 2002). A widely adapted variety has high mean yields across environments (Abidin *et al.*, 2005). Such an ideal cultivar is referred to as a stable variety in that its yields vary relatively little around the average yield for that variety, after correction for the average differences that will always exist between environments (Shukla, 1972).

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In many breeding programs wide and specific adaptations are assessed and allow the breeder to make informed decisions as to which genotypes to select. In sweetpotato breeding, G x E assessment should also play a central role (Abidin *et al.*, 2005). There have been many reports on sweetpotato, showing high G x E interaction in sweetpotato for various traits (Abidin *et al.*, 2002; Manrique and Hermann, 2002; Abidin *et al.*, 2005; Grüneberg *et al.*, 2005; Lin *et al.*, 2007; Lebot, 2008). Multi- environment testing is therefore essential if selection gain is to be made (Grüneberg *et al.*, 2009b; Grüneberg *et al.*, 2010).

In recent years, particularly in Sub Saharan Africa, there has been a growing interest to combine yield increases and micronutrient improvements in sweetpotato breeding (Manrique and Hermann, 2002; Kapinga *et al.*, 2003; Grüneberg *et al.*, 2005; Andrade *et al.*, 2009; Chiona, 2009 ; Cervantes-Flores *et al.*, 2011). Yield is the most important trait and its maintenance or improvement must always compliment high micronutrient breeding to ensure widespread farmer acceptance. As with yields, studies related to sweetpotato nutritional traits indicate substantial variation for food quality in different genotypes (Collins and Walter, 1985; Woolfe, 1992; Mwanga *et al.*, 2003; Mcharo and La Bonte, 2007). There is however a paucity of information on the extent to which this variation is associated with GEI effects (Grüneberg *et al*., 2005).

Chiona (2009) conducted a study to evaluate G x E effects on yield, dry matter and carotene in five environments in Zambia and found the magnitude of G x E for carotene and dry matter to be small. In another study conducted in Burkina Faso, genotype by location effect was not significant for β-carotene but significant for dry matter (Some, 2013). In Peru, Manrique and Hermann (2001) reported that none of the nine cultivars tested showed yield stability across environments but beta-carotene levels were higher in higher altitudes for all genotypes tested.

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With respect to dry matter content, Grüneberg *et al*. (2005) reported significant G x E interaction in a study in Peru. In Burkina Faso, West Africa, Some, (2013) obtained similar results of G x E interactions for dry matter. Significant G x E effect on dry matter were also reported when orange-fleshed sweetpotato varieties were evaluated in Uganda, with higher values for dry matter being recorded when the varieties were grown at higher altitudes (Tumwegamire, 2011). These results contrast those of Chiona, (2009), who obtained stable dry matter content across all environments under study. With respect to the relative magnitudes of variance components, the proportion of G x E variance for yield is usually higher than for quality attributes including dry matter and carotenoid content (Grüneberg *et al.*, 2005)

The importance of sugars in determining consumer acceptability of sweetpotato has been reported by many investigators (Koehler and Kays, 1991; Lewthwaite *et al.*, 1997; Grüneberg *et al.*, 2005; Kays *et al.*, 2005a). Considerable variation exists in sweetness due to sugars in raw roots and maltose in cooked roots. This variation can be exploited in breeding to increase or decrease sugar content (Wang and Kays, 2000). Nothing however, has been reported on the extent to which this variation is associated with G x E effects.

In chapter four of this study, a range of genotypes with good yields and varying levels of farmer preferred quality attributes, specifically dry matter, sugars and β-carotene were identified. Due to their high yields, and good agronomic characteristics, they merit further evaluation in multi environments to ascertain their potential as new cultivars in Ghana, while using them to develop new populations.

**The objectives of this study were therefore to:**

1. determine the magnitude of G x E variation in these range of genotypes for yield, β-carotene, dry matter and sugars

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2. determine accessions with stable and superior performance in yield, DM, low sugar and β-carotene.
3. determine the phenotypic correlations among these traits over multiple environments
4. determine broad sense heritability of the traits under study

## 5.2 MATERIALS AND METHODS

### 5.2.1 Description of environments

The experiment was conducted in four environments consisting of locations, years and seasons. In the first environment genotypes were planted on the research field of Biotechnology and Nuclear Agriculture Research Institute (BNARI) during the major rainy season in May, 2011. The trial was repeated under irrigation in 2012, in three locations, during the minor season. The three locations for the 2012 planting were; BNARI research field in Accra, a Coastal Savanna zone; Council for Scientific and Industrial Research – Crops Research Institute (CSIR-CRI) station, Kumasi, a Semi-deciduous forest zone, and on a farmer's field in Kitase, a highland and a Moist deciduous Forest zone. Annual rainfall and temperatures for these three agroecologies are presented in Appendix 5.1. Soil texture and nutrient analysis for the four sites as well as rainfall and temperature regimes for the four months growth period are also presented in Appendix 5.2.

### 5.2.2 Plant material and Field experiment

Eleven (11) genotypes comprising seven introduced varieties, one released variety and three farmer varieties were used in this study. Within these clones were high dry matter clones, high and low-sugar types, and β-carotene lines (Table 5.1) One local and one elite clone were used as check varieties. All trials were set up in randomized complete block designs with three

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replications. Each experimental plot comprised three 2 m long ridges, spaced 1m apart. Seven vines were planted on each ridge at 30cm apart to give a total of 21 hills per genotype per plot. Five plants within the middle ridge were used for data collection and the rest served as border plants. In all locations and seasons, the trials were harvested four months after planting.

**Table 5. 1: Characteristics and origin of 11 genotypes involved in the GxE analysis**

| Clone | origin | characteristics | Clone | origin | characteristics |
|---|---|---|---|---|---|
| **1 Daak/08/007** | Local variety | IS, HDM, YF | **7 J/7-13** | USDA | LS, LDM, ORF |
| **2 kadzie** | Local variety | LS, HDM, YF | **8 MD 807** | USDA | S, LDM, ORF |
| **3 Hi-starch** | Released | LS, HDM, CF | **9 MD-607**** | USDA | S, LDM, ORF |
| **4 Yellow sunflower** | USDA | IS, HDM, YF | **10 W-248** | USDA | LS, LDM, ORF |
| **5 Pelican processor** | USDA | LS, HDM, YF | **11 MD-844** | USDA | S, LDM, ORF |
| **6 Blue Blue ++** | Local variety | LS, HDM, YF | | | |

**S = High sugar; IS = intermediate sugar: LS = low-sugar; LDM = low dry matter; HDM = high dry matter; Cf = cream fleshed; YF = yellow-fleshed; ORF = orange-fleshed; ++, ** = Local and elite check varieties.**

### 5.2.3 Data collection

At harvest, four months after planting, data were recorded on number of plants harvested, number of plants with roots, number of commercial roots, number of non-commercial roots, commercial and non-commercial root weight, vine weight and weevil damage scored on a scale of 1-5 (CIP-AVRDC-IBPGR, 1991). Dry matter data for raw and cooked roots, sweetness scores and weevil damage scores are as described in chapter 4. NIRS data for starch, endogenous sugars in raw and cooked roots, maltose in cooked roots and β-carotene in raw and cooked roots are also described in Chapter four. Sucrose equivalents (SE) were also computed as described in Chapter 4.

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### 5.2.4 Data analysis

Data was analyzed with CloneSelector edition 3.1, an Excel-based data management tool associated with the statistical software R (R, core team 2013). Multi-environment trial (MET) analysis was generated in CloneSelector to estimate the means by genotypes, environment and genotype by environment GE) interaction means and interaction effects. Analysis of variance (ANOVA) was conducted using genotypes as fixed and environment and block as random. Coefficient of variation (CV%) and variance components of each trait were also computed. The assumption made in the linear model used was that variances for genotypes across all environments were the same and that the data was normally distributed. Barlett test for homogeneity of variances and the Shapiro-Wilk normality test were therefore computed. Stability analysis was based on regression and Additive Main effects and Multiplicative Interaction (AMMI). Regression slopes, principal components (PC) and standard errors for the regression slopes, mean square errors, mean square interactions and variances of genotypes across environments were computed. Additive Main effects and Multiplicative Interaction (AMMI) was analyzed using fixed effect model and biplots for the individual traits were generated to visualize GxE interaction effects graphically. The ANOVA was computed for the experiment over the environments according to the model:

$$\mathbf{Y = \mu + G + E + (G \times E) + e}$$

Where Y is the value for the observed trait, μ is the overall mean of the response for all genotypes in all environments, G is the effect due to genotype, E the environment effect, G x E is the genotype by environment effect and e is component of unexplained response or experimental error. The linear mathematical model for an RCBD is

$$\mathbf{y_{ijk} = \mu + \alpha_i + \beta_j + e_{ijk}}$$

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Where $y_{ijk}$ denotes the value of the observed trait for $i_{th}$ treatment received in the $k_{th}$ block within $j_{th}$ replicate; μ is the overall mean, $\boldsymbol{\alpha_i}$ is the fixed effect of the $i_{th}$ treatment; $\boldsymbol{\beta_j}$ is the effect of the $j_{th}$ replicate; eijk is the experimental error associated with the observation of the $i_{th}$ treatment in the $j_{th}$ replicate and $k_{th}$ block.

## 5.3 RESULTS

### 5.3.1 Mean performance of genotypes and environments for agronomic traits

The analysis of variance for fixed effects for genotypes, random environment and random blocks showed significant differences among genotypes, environments and their interaction effects for most agronomic traits (Table 5.2). Genotype main effect was however not significant for total root yield, commercial yield, weevil damage and biomass yield. Environmental effect was also not significant for harvest index.

**Table 5.2:Analysis of variance for selected agronomic traits of 11 genotypes evaluated in four environments in Ghana in 2011 and 2012**

| | | Mean square for agronomic components | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **sources** | **df** | **Tyld** | **Comyld** | **Mktrt** | **WED** | **Biomyld** | **HI** | **Irwt** |
| **G** | 10 | 137.05 | 93.14 | 1042.2** | 0.68 | 517.3 | 0.22*** | 0.024* |
| **E** | 3 | 2127.4*** | 1729.62*** | 8370.2*** | 57.63*** | 8920.6*** | 0.06 | 0.129*** |
| **R:E** | 8 | 44.5 | 22.4* | 372.7* | 0.78 | 372.2458** | 0.03* | 0.002 |
| **GxE** | 30 | 100.9*** | 119.88*** | 738.0** | 0.94* | 515.4*** | 0.05*** | 0.011*** |
| **Residual** | 74 | 28.4803 | 17.29 | 2.2.3 | 0.61 | 97.89783 | 0.01162 | 0.003583 |

*** if P ≤ 0.05, ** if P ≤ 0.01, *** if P ≤ 0.001; Tyld = total yield; Comyld = commercial yield in t/ha; Mktrt = number of marketable roots per plot; WED = weevil damage; Biomyld = biomass yield in t/ha; HI = harvest index; Irtwt = individual root weight in kg; R:E = R:E = replications nested into the environments**

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**Table 5.3: Magnitude of variance components and their importance on agronomic traits measured on 11 genotypes evaluated in four environments in Ghana in 2011 and 2012**

| | $\sigma^2_G$ | $\sigma^2_E$ | $\sigma^2_{R:E}$ | $\sigma^2_{GXE}$ | $\sigma^2_E$ |
|---|---|---|---|---|---|
| | **Magnitude of variance for agronomic traits** | | | | |
| **Tyld** | 3.12 | 60.71 | 1.12 | 24.00 | 28.41 |
| **Comyld** | 1.0E-8 | 48.81 | 0.46 | 32.03 | 17.26 |
| **Mktrt** | 24.37 | 226.98 | 11.88 | 172.91 | 14.71 |
| **WED** | 0 | 1.77 | 0.02 | 0.09 | 0.61 |
| **Biomyld** | 0.20 | 246.38 | 23.09 | 139.90 | 97.62 |
| **HI** | 0.01 | 0 | 0.001 | 0.01 | 0.01 |
| **Irwt** | 0.001 | 0.004 | 1.03E-16 | 0.003 | 0.003 |

**Tyld = total yield; Comyld = commercial yield in t/ha; Mktrt = number of marketable roots per plot; Ncyld = non-commercial yield in t/ha; WED = weevil damage; Biomyld = biomass yield in t/ha; HI = harvest index; Irtwt = individual root weight in kg.**

Considering the mean square values and the magnitude of variance components for each agronomic trait (Table 5.3), environment effect contributed more to the total variation in all traits than genotype and GEI effects except for harvest index. GEI effect were also important for all agronomic traits but to a lesser magnitude. G effects were, however, important for only marketable roots per plot, harvest index and individual root weight.

The mean performance of the four environments across the 11 genotypes showed that, BNARI 2012 trial recorded higher values for all agronomic traits than the other three environments (Table 5.4). Total storage root yield ranged from 21.06 t/ha for the 2011 trial in BNARI to 8.31, 6.86 and 2.32 for the 2012 trial at Kumasi, BNARI and Kitase respectively. Commercial root yield and number of marketable roots also followed a similar trend. Kitase 2012 was a low performance environment in that, mean values for all agronomic traits were consistently lower than the other environments. Harvest index was, however, higher in 2012 for kitase than for

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Kumasi and BNARI. Weevil damage was highest for Kitase 2012 trial. In 2011, the trial at BNARI was set up in the main season while all 2012 trials were carried out in the minor season under irrigation. Higher and consistent rainfall in 2011 may have contributed to the better performance with regard to agronomic traits for 2011 BNARI trial. The coefficient of variation (CV %) for agronomic traits ranged from 21.79 % to 55.37 % with total root yield, commercial yield and biomass yield exhibiting highest values of 55.37 % and 50.69 % and 48.2 % respectively.

The highest storage root yields of 35.56 t/ha, 29.56 t/ha, 28.89 t/ha and 20.71 t/ha were obtained by MD-807, MD-607, Blue Blue and Hi Starch respectively (Table 5.5). These high yields were obtained from the 2011 trial in BNARI with the exception of the 28.89 t/ha obtained by Blue Blue in Kumasi 2012. Five accessions performed better in yield than the mean of 9.91 for all genotypes across all environments. However, mean values across all accessions were lower than the mean for the check variety – Blue Blue. Kadzie had the lowest yield across all environments. Kadzie is a late maturing farmer variety and may not have fully bulked at four months after planting.

**Table 5.4: Environment mean performance and coefficient of variation of agronomic traits across 11 genotypes evaluated in four environments in Ghana in 2011 and 2012**

| TRAITS | BNARI 2011 | BNARI 2012 | KITASE 2012 | KUMASI 2012 | CV% |
|---|---|---|---|---|---|
| | | | Mean performance for agronomic traits | | |
| **Tyld (t/ha)** | 21.06 | 6.86 | 2.32 | 8.31 | 55.37 |
| **ComYld (t/ha)** | 18.52 | 5.00 | 1.90 | 7.40 | 50.69 |
| **MktRt/plot** | 69.72 | 31.43 | 25.65 | 48.43 | 28.40 |
| **WED** | 2.70 | 1.60 | 4.00 | 1.00 | 33.34 |
| **Biomyld (t/ha)** | 43.21 | 14.19 | 4.70 | 19.51 | 48.42 |
| **HI** | 0.57 | 0.48 | 0.52 | 0.44 | 21.79 |
| **Irwt (kg)** | 0.25 | 0.11 | 0.12 | 0.15 | 37.23 |

**NOTE: Sugar values were from cooked roots**

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**Table 5.5: Comparison of storage root yield of the 11 genotypes evaluated in four environments in Ghana in 2011 and 2012**

| GENOTYPE | BNARI 2011 | BNARI 2012 | KITASI 2012 | KUMASI 2012 | MEAN |
|---|---|---|---|---|---|
| **Blue Blue++** | 20.47 | 5.78 | **4.69** | **28.89** | 14.96 |
| **Daak 08/007** | 14.67 | 3.56 | 1.20 | 7.16 | 6.65 |
| **Hi Starch** | 20.71 | 12.22 | 2.53 | 2.93 | 9.60 |
| **J/7-13** | 14.67 | 5.22 | 2.38 | 6.66 | 7.22 |
| **Kadzie** | 8.91 | 1.31 | 1.38 | 1.91 | 3.38 |
| **MD-607** | 27.11 | 2.00 | 1.22 | 2.64 | 8.24 |
| **MD-807** | **35.56** | 5.64 | 1.18 | 2.16 | 11.13 |
| **MD-844** | 29.56 | **13.78** | 3.38 | 6.22 | 13.23 |
| **Pelican Processor** | 24.00 | 6.18 | 2.84 | 18.22 | 12.81 |
| **W-248** | 15.33 | 9.00 | 3.18 | 4.00 | 7.88 |
| **Yellow Sunflower** | 20.67 | 10.77 | 1.59 | 10.67 | 10.93 |
| **MEAN** | 21.06 | 6.86 | 2.32 | 8.31 | 9.91 |
| **SED** | 4.23 | 2.25 | 0.63 | 4.59 | 0.93 |
| **CV %** | 34.79 | 56.90 | 46.82 | 45.60 | 32.51 |

**++ = Check variety. Bold fonts indicates highest mean per environment.**

### 5.3.2 Mean performance of genotypes and environments for quality traits

Dry matter and β-carotene analysis were based on raw root data. Analysis of sugars were however based on cooked roots due to the profound changes that occur in sugar content after cooking in addition to the fact that the final end-users utilize cooked sweetpotato. β-carotene values were also based on raw roots because NIRs was not calibrated for cooked β-carotene.

Genotype, environment and their interaction main effects were significant for all quality traits under consideration (Table 5.6), except for SE where environment effect was not significant. With respect to the magnitude of variance components however, genotypic effects contributed more to the total variance except for fructose and total sugars, where G x E and environment effects respectively, were more important (Table 5.7). For all other quality traits, GEI and genotypic effects were also important but contributed to a lesser extent to the observed variance.

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**Table 5.6: Analysis of variance for selected root quality traits of 11 genotypes evaluated in four environments and three replications in Ghana in 2011 and 2012**

| | | Mean square for quality attributes | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Sources of variance | df | DM | Starch | Fructose | glucose | Sucrose | Maltose | Total sugars | Sucrose equivalents (SE) | β-carotene |
| G | 10 | 420.4*** | 424.9*** | 2.2*** | 22.5*** | 93.3*** | 296.7** | 685.4*** | 241.18*** | 2685.4*** |
| E | 3 | 98.8** | 117.6** | 3.2*** | 18.8*** | 22.2*** | 189.7*** | 798.1*** | 122.74 | 82.3** |
| R:E | 8 | 5.1 | 14.2 | 0.04 | 1.2 | 5.2 | 5.0 | 39.0 | 11.95 | 4.3 |
| GxE | 30 | 17.6*** | 72.2*** | 0.35*** | 2.9*** | 16.7*** | 86.3*** | 145.6*** | 41.73*** | 25.25*** |
| Residual | 79 | 3.9 | 20.3 | 0.09 | 0.82 | 5.4 | 16.7 | 32.8 | 11.70 | 2.8 |

*if $P \leq 0.05$, ** if $P \leq 0.01$, *** if $P \leq 0.001$. Analysis of sugars and starch was based on cooked roots. R:E = replications nested into the environments

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**Table 5.7: Magnitude of variance components and their importance on quality traits measured on 11 genotypes over four environments in Ghana in 2011 and 2012**

| | $\sigma^2_G$ | $\sigma^2_E$ | $\sigma^2_{R:E}$ | $\sigma^2_{GXE}$ | $\sigma^2_e$ |
|---|---|---|---|---|---|
| **Dry matter** | 33.56 | 2.42 | 0.11 | 4.56 | 3.93 |
| **Starch** | 29.39 | 1.38 | 2.3E-10 | 17.49 | 19.70 |
| **Fructose** | 0.16 | 0.07 | 0 | 0.09 | 0.09 |
| **Glucose** | 1.63 | 0.47 | 0.03 | 0.71 | 0.82 |
| **Sucrose** | 6.38 | 0.17 | 6.17E-15 | 3.80 | 5.34 |
| **Maltose** | 17.53 | 3.13 | 0 | 23.51 | 15.79 |
| **Total sugars** | 44.98 | 19.58 | 0.57 | 37.61 | 32.77 |
| **Sucrose equivalents** | 16.62 | 2.45 | 0.02 | 10.01 | 11.70 |
| **β –carotene** | 221.69 | 1.68 | 0.14 | 7.49 | 2.80 |

Comparing the four environments for their mean performance for quality traits across genotypes (Table 5.8), higher values were observed for 2011 BNARI trial, with the exception of dry matter, starch and total sugars in cooked roots. Dry matter was higher for Kitase 2012 and ranged from 34.75 % dry weight to 30.52 % for BNARI 2011. Total sugars varied from 33.90 % dry weight for Kumasi 2012 to 33.35, 26.52 and 24.07 % for BNARI 2011, Kitase 2012 and BNARI 2012 respectively. Cooked roots from Kumasi 2012 trial produced the highest values for maltose and total sugars. The values for fructose, glucose and sucrose were higher in cooked roots of BNARI 2011. Sucrose equivalents (SE) were higher for BNARI 2011 followed by Kumasi 2012. β-carotene ranged from 16.97 mg/100g dry weight for BNARI 2012 to the lowest of 13.35 mg/100 g dry weight for Kitase 2012. Dry matter, starch and β-carotene exhibited the lowest CV % of 6.10 %, 7.82 % and 11.34 % respectively among the quality traits. Except for dry matter and starch, genotypes generally performed better in BNARI 2012 for the studied traits, followed by Kumasi 2012, BNARI 2012 and Kitase 2012.

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**Table 5. 8: Environment mean performance and coefficient of variation of quality traits across 11 genotypes evaluated in four environments in Ghana in 2011 and 2012**

| TRAITS | BNA 2011 | BNARI 2012 | KITASE 2012 | KUMASI 2012 | CV% | SED |
|---|---|---|---|---|---|---|
| | | | Mean performance for root quality traits | | | |
| **Dry matter (%)** | 30.52 | 32.53 | **34.75** | 32.55 | 6.10 | 0.75 |
| **Starch (%)** | 54.77 | **59.09** | 58.23 | 57.93 | 7.82 | 0.82 |
| **Fructose (%)** | **1.24** | 0.48 | 0.82 | 0.83 | 35.19 | 0.13 |
| **Glucose (%)** | **3.37** | 1.55 | 2.17 | 2.37 | 38.24 | 0.33 |
| **Sucrose (%)** | **15.59** | 13.81 | 13.90 | 14.43 | 16.03 | 0.35 |
| **Maltose (%)** | 13.61 | 13.57 | 13.92 | **18.48** | 27.57 | 1.04 |
| **Total sugars (%)** | 33.35 | 24.07 | 26.52 | **33.90** | 19.43 | 2.13 |
| **Sucrose equivalents** | **25.09** | 21.21 | 22.27 | 24.89 | 14.64 | 0.83 |
| **β-carotene mg/100g dry weight** | 16.15 | 13.89 | 12.01 | 13.72 | 11.38 | 0.74 |

**NOTE: Sugar values were from cooked roots. Bold fonts indicate highest value per variable across environments**

### 5.3.2.1 Comparison of genotypes for individual sugars and total sugars in cooked roots

Tables 5.9, 5.10 and 5.11 show amount of fructose, glucose and sucrose produced in cooked roots of the 11 genotypes over the four environments. The highest amount of fructose, 2.4 % dry weight, was produced by MD-607 in BNARI 2011. MD 807 and MD 607 produced the highest amount of glucose with 6.4 and 5.7 % dry weight respectively. In general, fructose was present in the lowest concentrations in all genotypes across all environments with an overall mean of 0.84 % dry weight (Table 5.9) followed by glucose with a mean of 2.37 % dry weight (Table 5.10). MD-607, MD-807 and MD-844 had the highest amounts for glucose across genotypes and environments while MD-607 attained the highest amount of fructose across environments (Table 5.9). Sucrose, with a general mean of 14.43 % dry weight (Table 5.11) was the second highest

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sugar in cooked roots and MD-844 gave the highest amount with a mean of 19.52 % dry weight across the four environments. Maltose, the most abundant sugar in cooked roots had a mean of 14.9 % dry weight (Table 5.12) across all environments. Daak 08/007 was the highest in maltose with a mean of 23.07 % dry weight followed by MD-607 and Yellow Sunflower with a mean of 18.24 and 18.04 % dry weight respectively.

The highest ranking genotypes for total sugar in cooked roots were MD-607, MD-844, Daak 08/007 and MD-807 with 40.12, 39.14, 37.25 and 35.54 % dry weight respectively (Table 5.13). In decreasing order, Hi Starch, Kadzie, Blue Blue, W-248 and J/7-13, were among the lowest ranking genotypes for total sugars in cooked roots producing 23.79, 21.48, 21.25 and 20.42 % dry weight respectively. MD-607 was the highest ranking genotype for sucrose equivalent (SE) (Table 5.14) and BNAR 2011 trial was the highest ranking environment for SE

Table 5.15 shows mean values for individual sugars in raw and cooked roots across genotypes and environments and their percentage change in cooked roots. The most abundant sugar in raw roots was sucrose, with a mean of 14.13 % dry weight. Apart from fructose which decreased by 50 % in cooked roots all other sugars increased in quantity. Maltose gave the biggest increase of 3448 %. The increase in total sugars and sucrose equivalent by 59 % and 30 % respectively, was mostly due to the accumulation of maltose in cooked roots. Generally high coefficients of variation were obtained for almost all variables measured in Kitase 2012, the environment with the least performance.

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**Table 5.9: Comparison of fructose content in cooked roots of 11 sweetpotato genotypes evaluated in four environments in Ghana in 2011 and 2012.**

| Genotypes | BN2011 | BN2012 | KIT2012 | KUM2012 | MEAN |
|---|---|---|---|---|---|
| **Blue Blue++** | 0.72 | 0.54 | 0.26 | 0.86 | 0.59 |
| **Daak 08/007** | 0.78 | 0.15 | 0.15 | 0.27 | 0.34 |
| **Hi Starch** | 0.65 | 0.14 | 0.20 | 0.69 | 0.42 |
| **J/13-7** | 1.74 | 0.58 | 1.22 | 1.02 | 1.14 |
| **Kadzie** | 0.41 | 0.61 | 0.16 | 0.21 | 0.35 |
| **MD-607** | **2.40** | **0.88** | **1.98** | **1.52** | **1.70** |
| **MD-807** | 1.52 | 0.39 | 1.21 | 1.33 | 1.11 |
| **MD-844** | 1.55 | 0.24 | 1.51 | 1.13 | 1.11 |
| **Pelican Processor** | 1.03 | 0.67 | 0.52 | 0.41 | 0.66 |
| **W-248** | 1.98 | 0.45 | 1.47 | 0.67 | 1.14 |
| **Yellow Sunflower** | 0.83 | 0.59 | 0.40 | 1.06 | 0.72 |
| **Mean** | 1.24 | 0.48 | 0.82 | 0.83 | 0.84 |
| **SED** | 0.35 | 0.13 | 0.37 | 0.24 | 0.12 |
| **CV %** | 2.88 | 3.20 | 27.28 | 4.90 | 4.13 |

**++ = Check variety; Bold fonts indicates the highest values for each environment and genotype**

**Table 5.10: Comparison of glucose content in 11 sweetpotato genotypes evaluated in four environments in Ghana in 2011 and 2012.**

| Genotype | BN2011 | BN2012 | KIT2012 | KUM2012 | MEAN |
|---|---|---|---|---|---|
| **Blue Blue++** | 1.28 | 2.28 | 0.47 | 1.18 | 1.30 |
| **Daak 08/007** | 2.63 | 0.33 | 1.05 | 1.61 | 1.40 |
| **Hi Starch** | 1.58 | 0.32 | 0.82 | 1.31 | 1.01 |
| **J/13-7** | 3.96 | 1.19 | 2.25 | 1.17 | 2.14 |
| **Kadzie** | 1.31 | 1.45 | 0.28 | 0.21 | 0.81 |
| **MD-607** | 5.72 | **2.65** | **4.63** | 4.05 | **4.26** |
| **MD-807** | **6.40** | 1.38 | 3.82 | 4.75 | **4.09** |
| **MD-844** | 5.22 | 1.42 | 5.12 | **5.39** | **4.29** |
| **Pelican Processor** | 2.51 | 2.22 | 0.70 | 0.99 | 1.61 |
| **W-248** | 4.29 | 1.81 | 3.97 | 3.62 | 3.42 |
| **Yellow Sunflower** | 2.21 | 2.04 | 0.78 | 1.81 | 1.71 |
| **Mean** | 3.37 | 1.55 | 2.17 | 2.37 | 2.37 |
| **SED** | 1.01 | 0.42 | 1.02 | 0.96 | 0.38 |
| **CV %** | 8.32 | 10.48 | 76.16 | 20.06 | 13.17 |

**++ = Check variety. Bold fonts indicates the highest values for each environment and genotype**

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**Table 5.11: Comparison of sucrose content in 11 sweetpotato genotypes evaluated in four environments in Ghana in 2011 and 2012.**

| Genotype | BN2011 | BN2012 | KIT2012 | KUM2012 | Mean |
|---|---|---|---|---|---|
| **Blue Blue++** | 10.77 | 14.96 | 10.07 | 11.74 | 11.89 |
| **Daak 08/007** | 14.91 | 11.57 | 15.64 | 14.38 | 14.13 |
| **Hi Starch** | 10.64 | 10.84 | 12.47 | 12.48 | 11.61 |
| **J/13-7** | 14.89 | 14.15 | 10.09 | 10.56 | 12.42 |
| **Kadzie** | 13.94 | 12.55 | 13.22 | 12.14 | 12.96 |
| **MD-607** | 22.37 | 15.79 | 17.88 | 17.87 | 18.48 |
| **MD-807** | 19.00 | 13.59 | 14.77 | 16.19 | 15.89 |
| **MD-844** | **23.64** | 13.22 | **19.94** | **21.31** | 19.53 |
| **Pelican Processor** | 12.01 | **16.23** | 11.48 | 12.23 | 12.99 |
| **W-248** | 18.31 | 13.58 | 17.06 | 17.98 | 16.73 |
| **Yellow Sunflower** | 11.04 | 15.42 | 10.28 | 11.89 | 12.16 |
| **Mean** | 15.59 | 13.81 | 13.90 | 14.43 | 14.43 |
| **SED** | 2.55 | 0.95 | 1.88 | 1.89 | 0.77 |
| **CV %** | 28.33 | 11.89 | 23.44 | 22.64 | 18.43 |

**GENERAL MEAN = 14.43; LSD = 3.41; CV% = 16.03; ++ = Check variety; Bold fonts indicates the highest values for each environment and genotype**

**Table 5.12: Comparison of maltose content in cooked roots of 11 sweetpotato genotypes evaluated in four environments in Ghana in 2011 and 2012.**

| | BN2011 | BN2012 | KIT2012 | KUM2012 | MEAN |
|---|---|---|---|---|---|
| **Blue Blue++** | 3.39 | 13.27 | 7.11 | 19.31 | 10.77 |
| **Daak 08/007** | **25.03** | 16.46 | **23.45** | **27.35** | **23.07** |
| **Hi Starch** | 4.77 | 16.61 | 17.86 | 19.35 | 14.65 |
| **J/13-7** | 2.55 | 14.89 | 5.77 | 17.65 | 10.22 |
| **Kadzie** | 13.89 | 16.64 | 15.41 | 12.70 | 14.66 |
| **MD-607** | 16.84 | 9.33 | 21.38 | 25.41 | 18.24 |
| **MD-807** | 19.19 | 13.64 | 12.00 | 20.17 | 16.25 |
| **MD-844** | 16.14 | **16.81** | 12.09 | 18.38 | 15.85 |
| **Pelican Processor** | 22.61 | 7.86 | 18.44 | 21.91 | 17.71 |
| **W-248** | 2.11 | 13.13 | 1.97 | 0.50 | 4.43 |
| **Yellow Sunflower** | 23.19 | 10.74 | 17.63 | 20.64 | 18.05 |
| **Mean** | 13.61 | 13.57 | 13.92 | 18.48 | 14.90 |
| **SED** | 4.89 | 1.72 | 3.74 | 3.91 | 1.37 |
| **CV %** | 28.03 | 22.01 | 29.51 | 22.66 | 31.81 |

**++ = Check variety; Bold fonts indicates the highest values for each environment and genotype**

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**Table 5.13: Comparison of total sugars in cooked roots of 11 sweetpotato genotypes evaluated in four environments in Ghana in 2011 and 2012.**

| | BN2011 | BN2012 | KIT2012 | KUM2012 | MEAN |
|---|---|---|---|---|---|
| **Blue Blue++** | 15.42 | 25.62 | 14.13 | 30.74 | 21.48 |
| **Daak 08/007** | 44.83 | 22.78 | 37.92 | 43.49 | 37.25 |
| **Hi Starch** | 17.24 | 22.42 | 29.42 | 32.60 | 25.42 |
| **J/7-13** | 18.12 | 24.76 | 10.58 | 28.24 | 20.42 |
| **Kadzie** | 27.24 | 24.93 | 23.42 | 19.60 | 23.80 |
| **MD-607** | **50.13** | 23.13 | **41.66** | 45.58 | **40.13** |
| **MD-807** | 47.68 | 24.66 | 27.81 | 42.05 | 35.55 |
| **MD-844** | 47.94 | **26.60** | 37.07 | **45.79** | 39.35 |
| **Pelican Processor** | 37.71 | 20.43 | 26.02 | 32.40 | 29.14 |
| **W-248** | 23.83 | 24.40 | 19.16 | 17.65 | 21.26 |
| **Yellow Sunflower** | 36.77 | 25.08 | 24.56 | 34.78 | 30.30 |
| **Mean** | 33.35 | 24.07 | 26.52 | 33.90 | 29.48 |
| **SED** | 7.39 | 0.95 | 5.38 | 5.37 | 2.08 |
| **CV %** | 38.39 | 6.86 | 35.15 | 27.43 | 24.44 |

**++ = Check variety; Bold fonts indicates the highest values for each environment and genotype**

**Table 5.14: Comparison of sucrose equivalents in cooked roots of 11 sweetpotato genotypes evaluated in four environments in Ghana in 2011 and 2012**

| Genotype | BN2011 | BN2012 | KIT2012 | KUM2012 | Mean |
|---|---|---|---|---|---|
| **Blue Blue++** | 13.92 | **22.77** | 13.74 | 21.83 | 18.07 |
| **Daak 08/007** | 28.29 | 19.04 | 26.57 | 27.49 | 25.35 |
| **Hi Starch** | 14.47 | 18.36 | 20.90 | 22.46 | 19.05 |
| **J/13-7** | 20.61 | 22.01 | 15.47 | 20.12 | 19.55 |
| **Kadzie** | 21.24 | 21.36 | 20.21 | 17.98 | 20.20 |
| **MD-607** | **36.15** | 22.55 | **32.41** | 33.21 | **31.08** |
| **MD-807** | 33.17 | 20.82 | 23.82 | 29.50 | 26.83 |
| **MD-844** | 35.78 | 21.64 | 30.23 | **34.01** | 30.42 |
| **Pel Proc** | 24.58 | 21.82 | 20.49 | 22.78 | 22.42 |
| **W-248** | 24.33 | 20.93 | 22.21 | 21.31 | 22.19 |
| **Yellow Sunflower** | 23.42 | 22.05 | 18.85 | 23.20 | 21.88 |
| **Mean** | 25.09 | 21.21 | 22.27 | 24.90 | 23.37 |
| **SED** | 4.22 | 0.76 | 3.15 | 2.95 | 1.23 |
| **CV %** | 24.15 | 6.23 | 29.48 | 20.49 | 18.29 |

**++ = Check variety; Bold fonts indicates the highest means per genotype across environment**

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**Table 5.15: Comparison of starch and sugars in raw and cooked storage roots across genotypes and environments**

| TRAIT | RAW ROOTS | COOKED ROOTS | % CHANGE |
|---|---|---|---|
| **Starch** | 59.59 | 57.51 | **-3.5** |
| **Fructose** | 1.68 | 0.84 | **-50** |
| **Glucose** | 2.36 | 2.37 | 0.4 |
| **Sucrose** | 14.13 | 14.43 | 2.1 |
| **Maltose** | 0.42 | 14.90 | 3448 |
| **Total sugars** | 18.60 | 29.48 | 59 |
| **Sucrose equivalent** | 18.23 | 23.65 | 30 |

**Note: Red font indicates % increase and green indicates % reduction in cooked roots**

### 5.3.2.2 Comparison of genotypes across environments for dry matter, starch and β-carotene

Dry matter ranged from a lowest of 21.31 % fresh weight by MD-607 in BNARI 2011 to a highest of 44 % fresh weight by Kadzie in Kitase 2012 (Table 5.16). The general mean for all genotypes across environments was 32.59 % with the highest mean of 40.82 % fresh weight attained by Kadzie. MD-607 had the lowest mean of 24.82 % .fresh weight. Kadzie, Pelican Processor, Blue Blue and Yellow Sunflower were among the highest in dry matter across all environments. Hi Starch, Blue Blue, Kadzie and Yellow Sunflower and J/7-13 (Table 5.17). were among the genotypes with the highest starch yields across the four environments. MD-607 had the lowest starch yield. Mean starch across genotypes and environments was 57.51 % dry weight. The highest mean for dry matter was attained in roots of Kitase 2012 trial.

Among the orange-fleshed genotypes, W-248 produced the highest β-carotene across all environments with a mean of 35.13 mg/100 g dry weight followed by MD-607 and MD-844 with

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32.93 and 32.45 mg/dry weight respectively (Table 5.18). Mean β-carotene across genotypes and environment was 13.72/100 g dry weight with a CV of 11.38 %. The highest environment mean across all genotypes was attained in BNARI 2011 trial while the lowest was from Kitase 2012 trial.

**Table 5.16: Comparison of dry matter content of cooked storage roots of 11 sweetpotato genotypes evaluated in four environments in Ghana in 2011 and 2012.**

| Genotype | BNARI 2011 | BNARI 2012 | KITASE 2012 | KUMASI 2012 | MEAN |
|---|---|---|---|---|---|
| **Blue Blue++** | 37.02 | 40.54 | 40.93 | 35.65 | 38.53 |
| **Daak 08/007** | 28.95 | 32.45 | 29.75 | 30.13 | 30.32 |
| **Hi Starch** | 32.61 | 32.36 | 34.09 | 32.47 | 32.88 |
| **J/13-7** | 25.91 | 34.32 | 33.15 | 37.47 | 32.71 |
| **Kadzie** | **41.73** | 39.15 | **44.11** | 38.32 | **40.83** |
| **MD-607** | 21.31 | 23.56 | 29.48 | 24.93 | 24.82 |
| **MD-807** | 28.14 | 28.86 | 30.52 | 28.11 | 28.91 |
| **MD-844** | 22.89 | 24.13 | 29.29 | 24.93 | 25.31 |
| **Pel Proc** | 33.50 | **40.89** | 39.85 | **43.17** | 39.35 |
| **W-248** | 24.95 | 24.03 | 29.60 | 27.55 | 26.53 |
| **Yellow Sunflower** | 38.76 | 37.52 | 41.60 | 35.34 | 38.30 |
| **MEAN** | **30.52** | **32.53** | **34.75** | **32.55** | **32.59** |
| **SED** | 3.70 | 3.66 | 3.16 | 3.28 | 1.63 |
| **CV %** | 21.01 | 19.50 | 15.73 | 17.44 | 17.32 |

**++ = Check variety; Bold fonts indicates highest mean per genotype across environment**

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**Table 5.17: Comparison of starch content in cooked roots of 11 sweetpotato genotypes evaluated in four environments in Ghana in 2011 and 2012.**

| Genotypes | BN2011 | BN2012 | KIT2012 | KUM2012 | MEAN |
|---|---|---|---|---|---|
| **Blue Blue++** | 66.03 | 52.88 | **69.78** | 64.28 | 63.24 |
| **Daak 08/007** | 53.38 | **64.08** | 55.92 | 57.53 | 57.73 |
| **Hi Starch** | **66.75** | 65.12 | 61.75 | 62.61 | **64.06** |
| **J/13-7** | 57.53 | 58.97 | 64.16 | **65.59** | 61.56 |
| **Kadzie** | 61.84 | 61.01 | 63.13 | 65.19 | 62.79 |
| **MD-607** | 42.87 | 56.15 | 44.34 | 45.68 | 47.26 |
| **MD-807** | 45.31 | 60.82 | 53.36 | 50.23 | 52.43 |
| **MD-844** | 42.43 | 60.29 | 47.08 | 45.69 | 48.87 |
| **Pelican Processor** | 56.39 | 55.74 | 62.29 | 60.61 | 58.76 |
| **W-248** | 50.42 | 58.43 | 52.63 | 55.76 | 54.31 |
| **Yellow Sunflower** | 59.58 | 56.53 | 66.20 | 64.07 | 61.60 |
| **MEAN** | **54.775** | **59.092** | **58.239** | **57.931** | **57.51** |
| **SED** | 4.79 | 2.02 | 4.48 | 4.20 | 1.64 |
| **CV %** | 15.16 | 5.92 | 13.32 | 12.56 | 9.86 |

**++ = Check variety; Bold fonts indicates highest mean per genotype across environment**

**Table 5.18: Comparison of beta-carotene content in raw storage roots of 11 sweetpotato genotypes evaluated in four environments in Ghana in 2011 and 2012.**

| Genotypes | BN2011 | BN2012 | KIT2012 | KUM2012 | MEAN |
|---|---|---|---|---|---|
| **++Blue Blue** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| **Daak 08/007** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| **Hi Starch** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| **J/13-7** | 31.57 | 26.35 | 22.14 | 22.77 | 25.71 |
| **Kadzie** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| **MD-607** | **40.70** | 34.99 | 25.41 | 30.66 | 32.94 |
| **MD-807** | 25.39 | 22.12 | 22.56 | 24.30 | 23.59 |
| **MD-844** | 39.71 | 33.41 | 28.29 | 28.41 | 32.46 |
| **Pelican Processor** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| **W-248** | 39.42 | **35.22** | **32.40** | **33.50** | **35.14** |
| **Yellow Sunflower** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| **MEAN** | 16.15 | 13.89 | 12.01 | 13.72 | 13.72 |
| **SED** | 10.43 | 8.98 | 7.67 | 8.18 | 4.40 |

**MEAN =++ = Check variety; Bold fonts indicates highest mean per genotype across environments**

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### 5.3.3 Stability analysis and its interpretation using regression and AMMI 1 biplot

The AMMI biplots presented in (Figure 5.1 – 5.9) have ordinates that represent the mean performance for all genotypes across environments and separates high performance genotypes and environments from those with low performance. Genotypes and environments to the left of the ordinate have mean performance lower than the overall mean performance across genotypes and environments for the parameter being considered. Genotypes and environments on the right of the ordinate have higher means than the overall mean. The perpendicular line (abscissa) that passes through the center of the biplot separates the most responsive genotypes and environment from those with higher stability. Genotypes and environments located further away from the abscissa in either direction have higher interaction effect and thus are less stable. Genotypes and environments with large PC1 scores irrespective of the direction have high interaction and are less stable, while those with PC1 Scores closer to zero, are the most stable. Another measure of stability provided by AMMI is the slopes derived from linear regression (Table 5.19, 5.20a and 5.20b). A regression coefficient ($\beta_i$) approximating unity indicates average responsiveness (Finlay and Wilkinson, 1963). When this is associated with high mean performance the variety has general adaptability; when associated with low mean performance the variety has poor adaptability. Slopes greater than 1 imply below average stability or very sensitive to changes in the environments. According to Eberhart and Russel (1966) a stable variety has a mean higher than the mean of a group, unity regression coefficient and deviation from regression that is as small as possible ($S^2d_i = 0$).

#### 5.3.3.1 Stability analysis for yield

Figure 5.1 shows the AMMI biplot for yield with the PC1 accounting for 65.7 % of the total yield variation due to GEI. Together, PC1 and PC2 accounted for 94.62 % of the variation in

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yield (Table 5.19). Based on the linear regression slopes (Finlay and Wilkinson, 1963) in Table 5.19 and the suggestion on identification of stable genotypes (Eberhart and Russell, 1966), BNARI 2011 and Kumasi 2012 with high mean yield, larger than unity regression slope and larger than zero deviation from regression, are the least stable environments for storage root yield and contributed more to the G x E interaction. BNARI 2011 was the only environment that appeared to have average stability for yield. By extension, MD-844, Pelican Processor and Yellow Sunflower with yields higher than the mean, unity slope and almost zero deviation from slope were the most stable genotypes. The yields of W-248, J/7-13, Daak 08/007 and Kadzie were lower than the average yield and the lowest yield was obtained from Kadzie.

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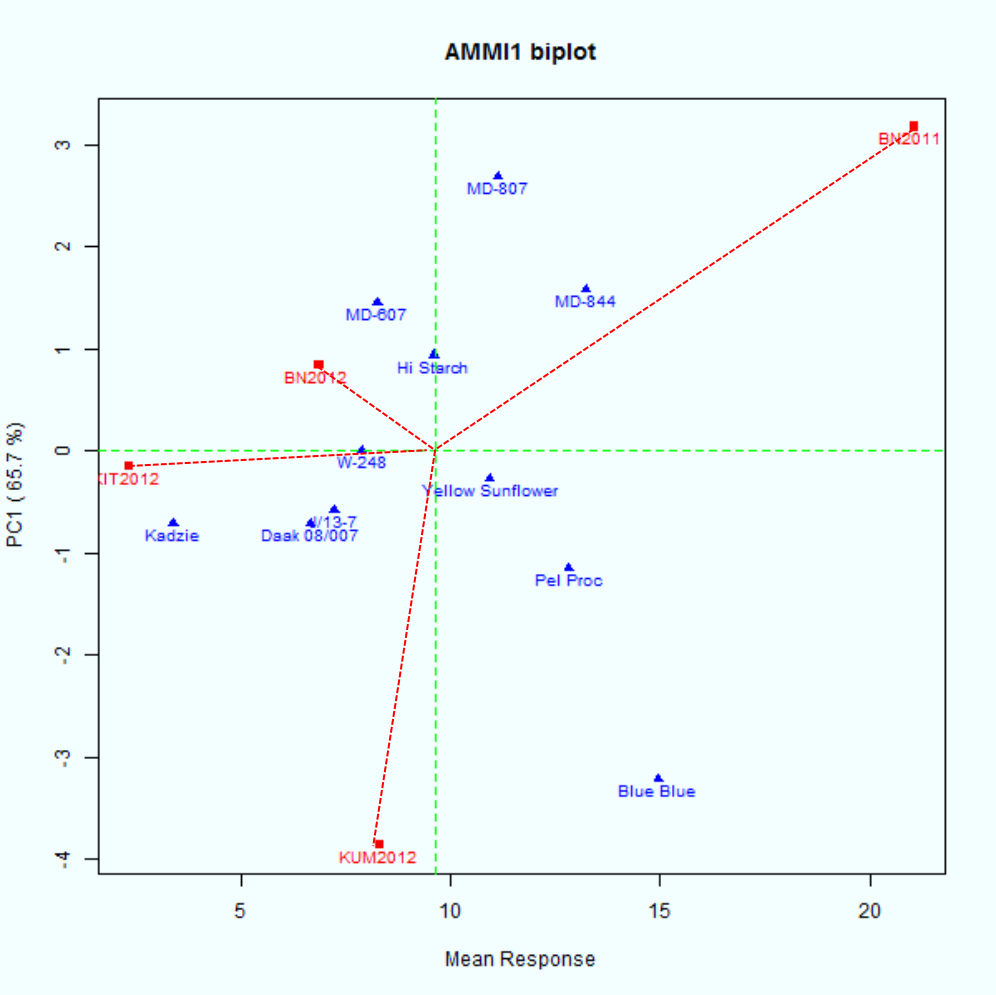


**Figure 5.1: AMMI biplot of the interactions of genotypes and environments for storage root yield of the 11 genotypes evaluated in four environments in Ghana in 2011 and 2012. The four environments are shown in red font and the genotypes are in blue font. BN, Kum and Kit are BNARI, Kumasi and Kitase sites respectively**

### 5.3.3.2 Stability analysis for individual sugar types and total sugars

Considering the AMMI biplot for individual sugars, the PC1 for fructose (Figure 5.2), glucose (Figure 5.3), sucrose (Figure 5.4) and maltose (Figure 5.5) explained 75.7 %, 81 %, 81.4 % and 63.3 % of variation due to GxE interaction respectively. PC1 and PC2 values for the sugars as well as regression slopes are presented in Tables 5.19, 5.20a and 5.20b. Judging by the means, regression slopes and their deviations, BNARI 2011 was the most stable for fructose and glucose while Kumasi was the most stable for sucrose and maltose. The AMMI plots (Figure 5.2 – 5.5

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also depict the same trend. BNARI 2012 was the most unstable environment for all sugar types The biplots (Figures 5.2 – 5.4) revealed that the lowest means for fructose, glucose and sucrose over all environments were mostly obtained from the cream and yellow-fleshed varieties; Kadzie, Blue Blue and Yellow Sunflower. J/7-13, an orange-fleshed clone was also among the clones with the lowest means for glucose and sucrose (Figures 5.3 and 5.4). The highest means for fructose, glucose and sucrose over all environments were obtained from MD-607, MD-844 and MD-844 respectively. The biplot for maltose (Figure 5.5) revealed that Daak 08/007 had the highest maltose yield while W-248 had the lowest.

The genotypes exhibited variation in stability for the individual sugars. Accession J/7-13 was the most stable for fructose (Figure 5.2) while accession W-248 and MD-607 were most stable for glucose (Table 5.3). No genotype showed clear stability for sucrose and maltose. Regression slopes and values for the deviation from regression (Tables 5.19, 5.20a and 5.20b) confirm this trend. MD-807 and MD-844 appeared to be the most stable for maltose but the deviation of their regression slopes were significantly different from zero.

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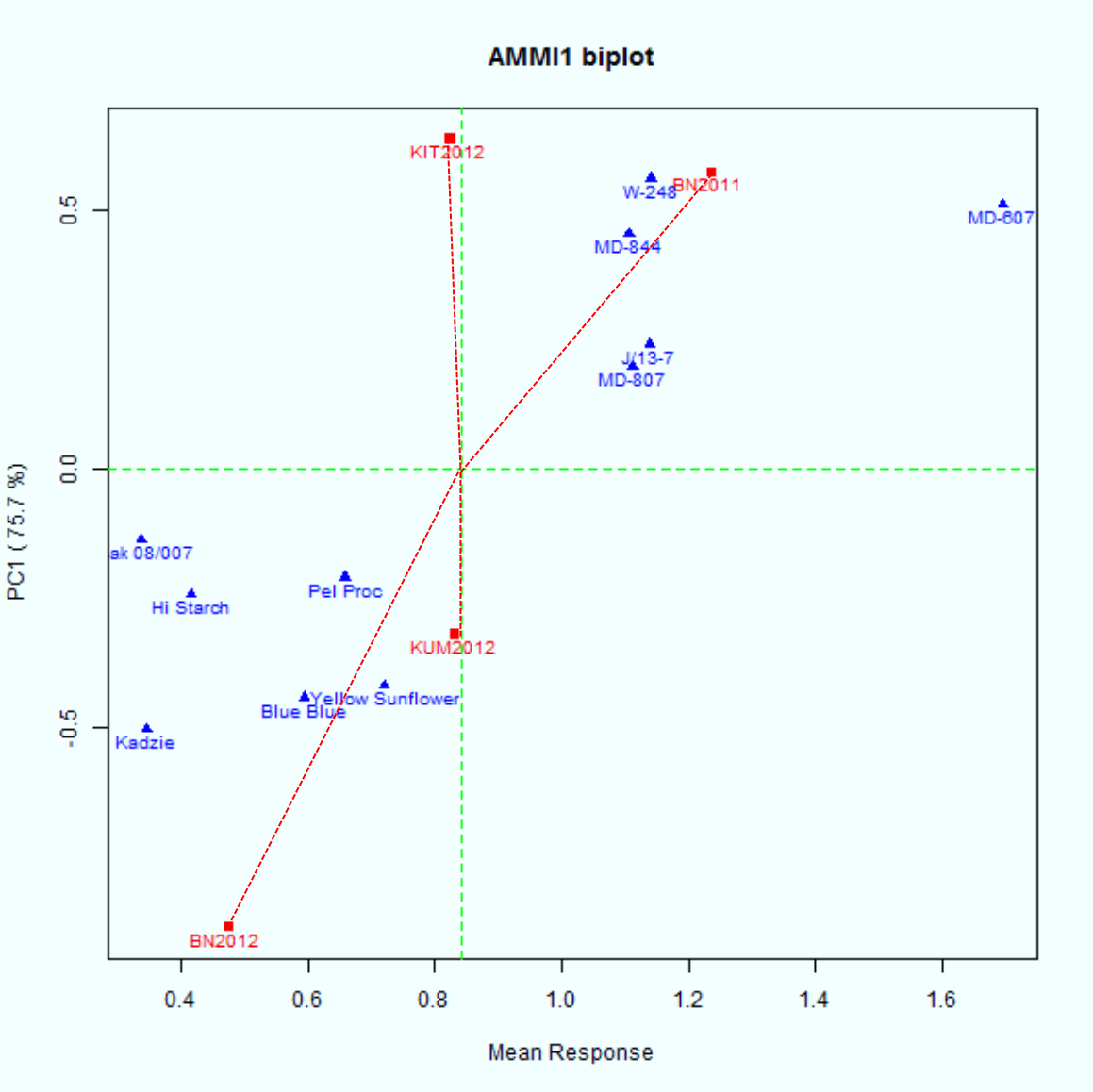


**Figure 5.2: AMMI biplot of the interactions of genotypes and environments for fructose in cooked storage roots of the 11 genotypes evaluated in four environments in Ghana in 2011 and 2012. The four environments are shown in red font and the genotypes are in blue font. BN, Kum and Kit are BNARI, Kumasi and Kitase sites respectively**

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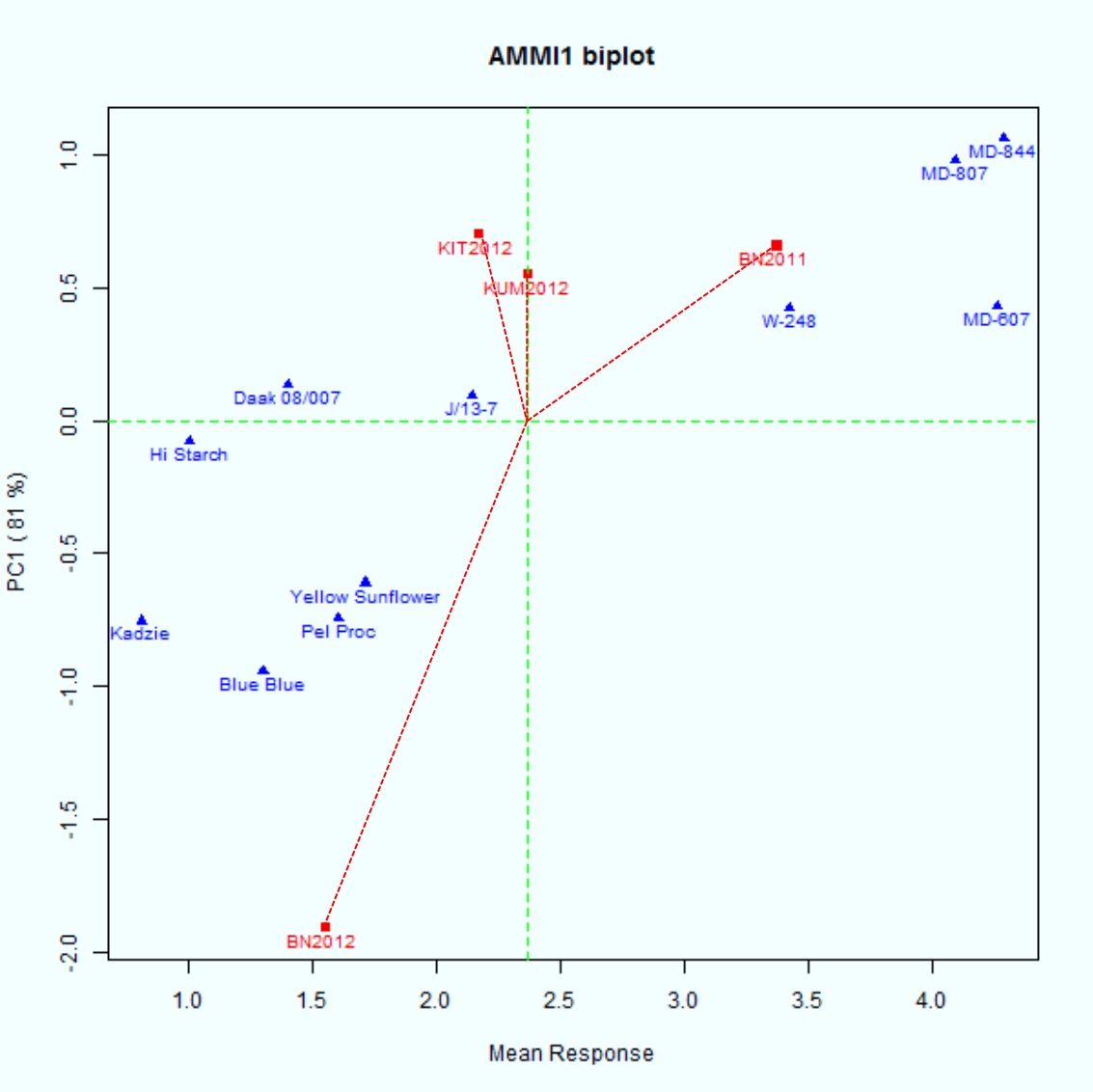


**Figure 5.3: AMMI biplot of the interactions of genotypes and environments for glucose in cooked storage roots of the 11 genotypes evaluated in four environments in Ghana in 2011 and 2012. The four environments are shown in red font and the genotypes are in blue font. BN, Kum and Kit are BNARI, Kumasi and Kitase sites respectively**

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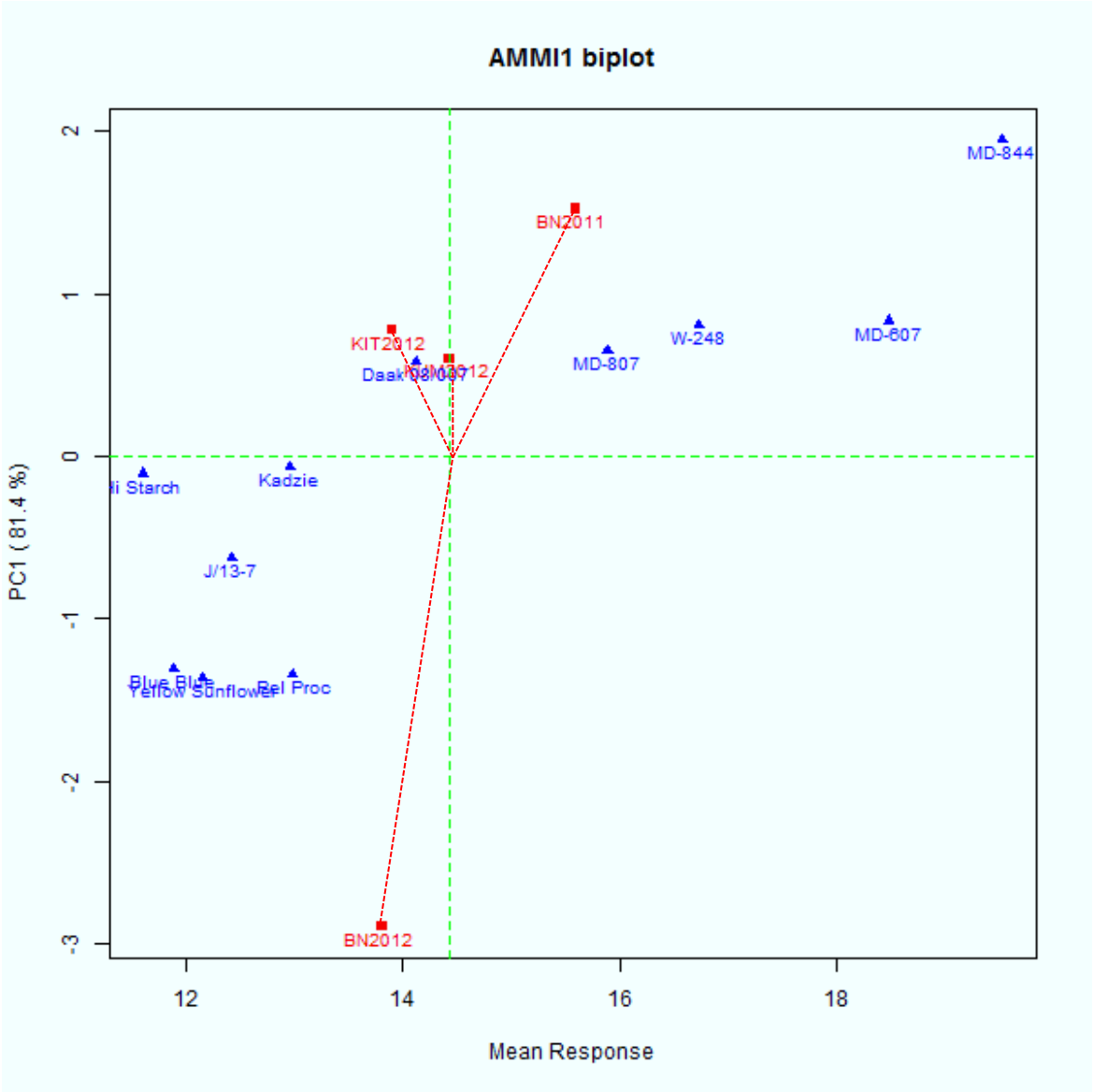


**Figure 5.4: AMMI biplot of the interactions of genotypes and environments for sucrose in cooked storage roots of the 11 genotypes evaluated in four environments in Ghana in 2011 and 2012. The four environments are shown in red font and the genotypes are in blue font. BN, Kum and Kit are BNARI, Kumasi and Kitase sites respectively**

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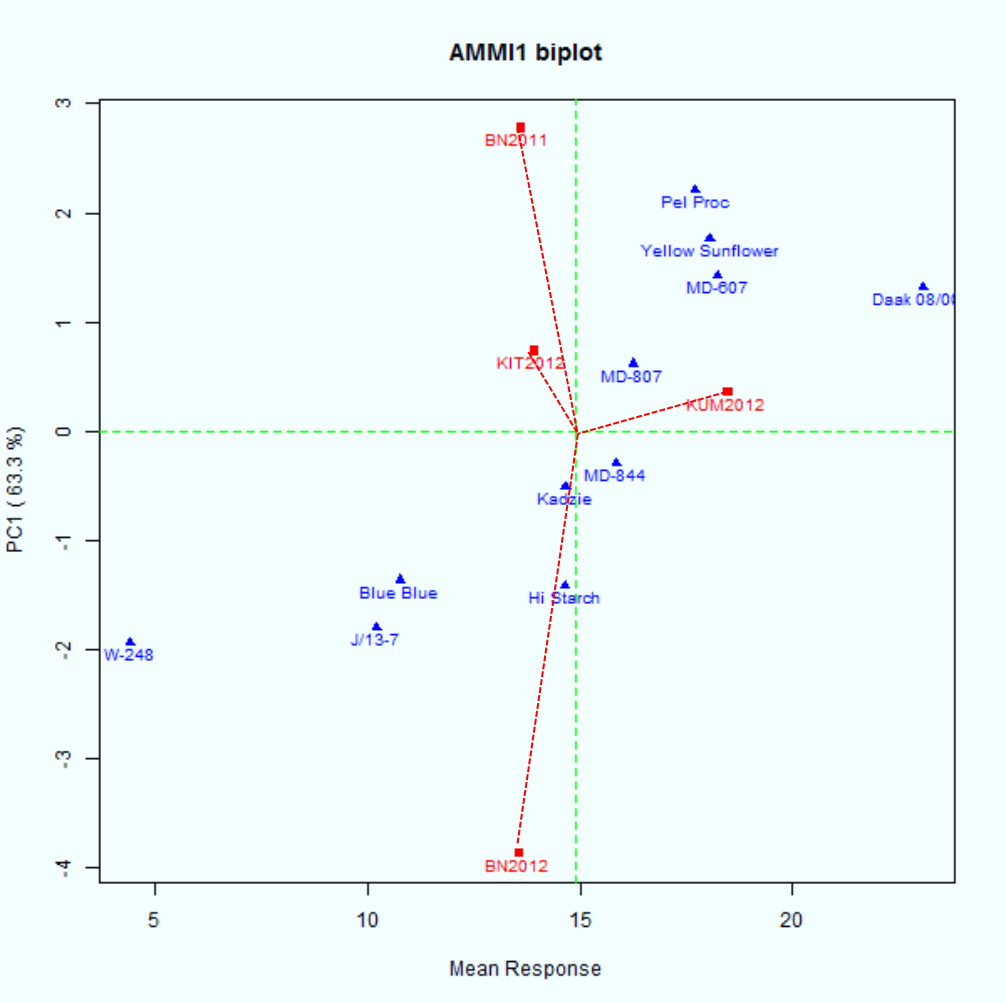


**Figure 5.5: AMMI biplot of the interactions of genotypes and environments for maltose in cooked storage roots of the 11 genotypes evaluated in four environments in Ghana in 2011 and 2012. The four environments are shown in red font and the genotypes are in blue font. BN, Kum and Kit are BNARI, Kumasi and Kitase sites respectively**

With respect to the AMMI biplot for total sugars (Figure 5.6), PC1 captured 65.7 % of the variation due to GxE, while PC1 and PC2 together accounted for 84.01 % (Table 5.20b). Kumasi 2012 was the most stable environment with respect to total sugar as depicted by its biplot (Figure 5.6) and its regression slope (Table 5.20b). BNARI 2011 and 2012 were the most responsive environments and contributed more to the GxE effect. The genotypes that contributed most to the GxE effect were MD-607 and Blue Blue. Yellow Sunflower was the most stable genotype but

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Pelican processor, W-248, Hi Starch and Kadzie with close to average stability and lower total sugars may be the most suitable as stable and low-sugar breeding lines.

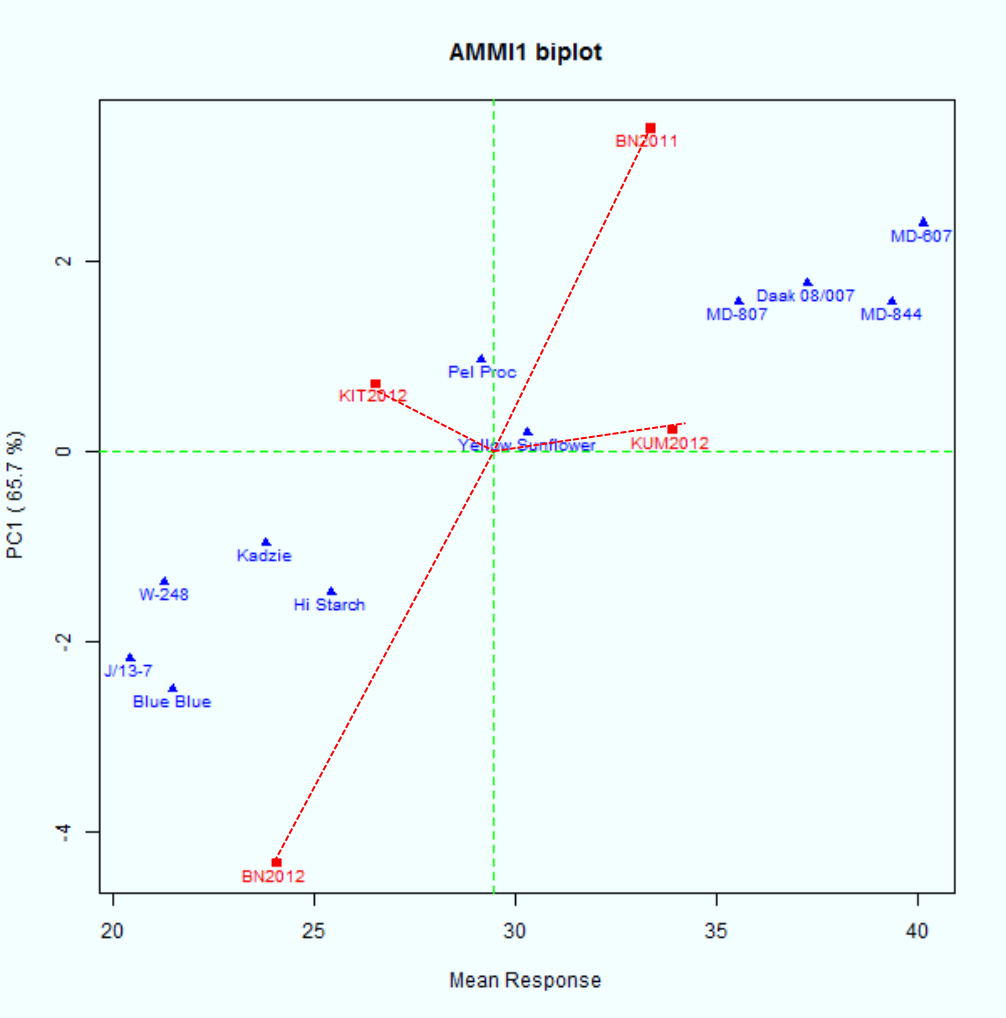


**Figure 5.6: AMMI biplot of the interactions of genotypes and environments for total sugars in storage roots of the 11 genotypes evaluated in four environments in Ghana in 2011 and 2012. The four environments are shown in red font and the genotypes are in blue font. BN, Kum and Kit are BNARI, Kumasi and Kitase sites respectively**

### 5.3.3.3 Stability analysis for sucrose equivalents

Principal component 1 of the biplot for sucrose equivalents captures 73.2 % of the variation due to β-carotene (Figure 5.7). Together, PC1 and PC2 explained 89.71 % of the total variation (Table 5.20b). Judged by both AMMI plot and regression, BNARI 2011was the most responsive

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environment while Kumasi 2012 and Kitase 20 12 were the most stable environments. The most responsive genotypes were MD-607, MD-807 and MD-844 while Pelican Processor, W-248, Yellow Sunflower, Kadzie were the most stable and low SE genotypes.

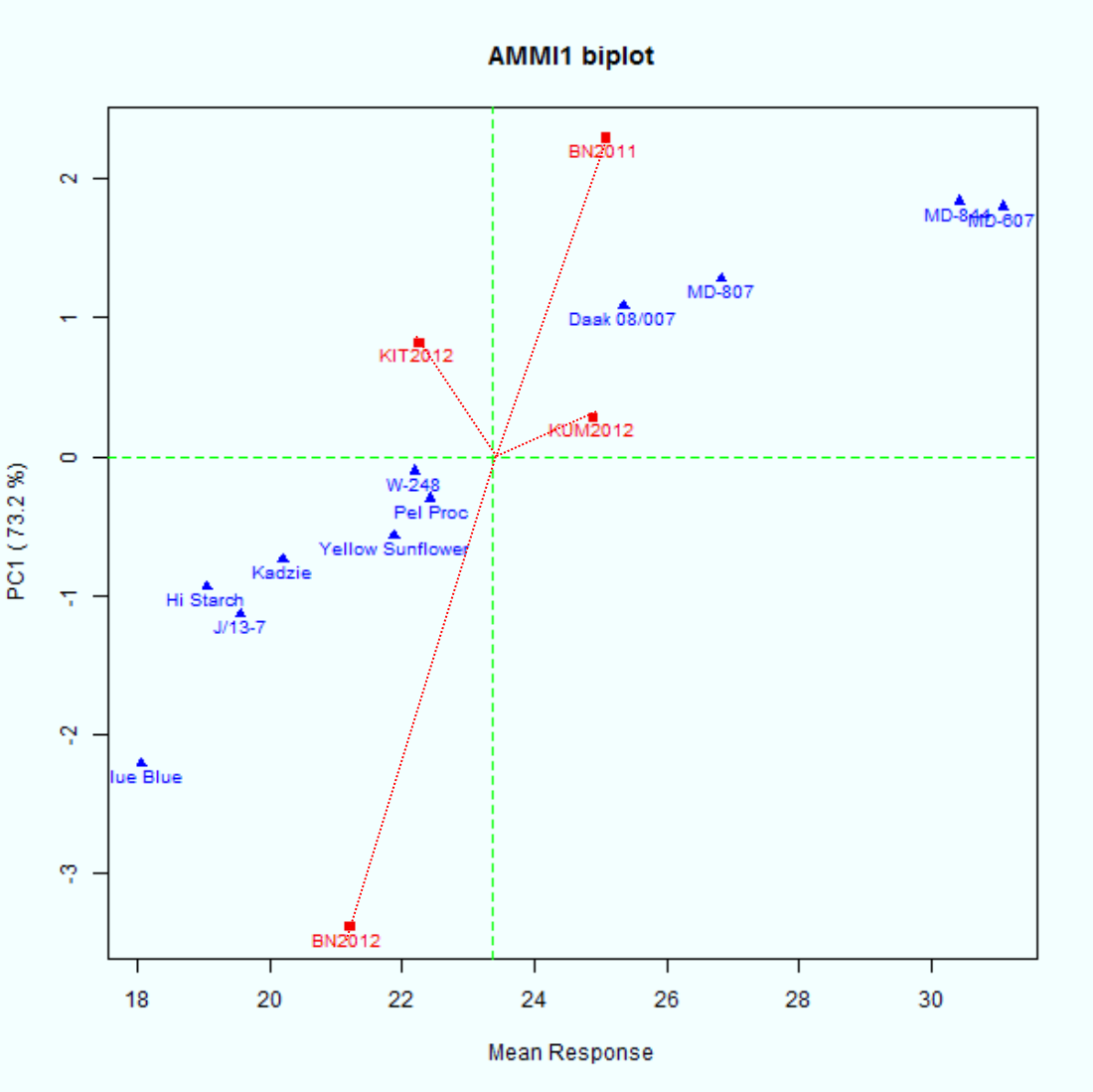


**Figure 5.7: AMMI biplot of the interactions of genotypes and environments for sucrose equivalents of storage roots of the 11 genotypes evaluated in four environments in Ghana in 2011 and 2012. The four environments are shown in red font and the genotypes are in blue font. BN, Kum and Kit are BNARI, Kumasi and Kitase sites respectively**

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#### 5.3.3.4 Stability analysis for dry matter and β-carotene

Figure 5.8 is the biplot for dry matter which captures 72.6 % of the dry matter variation due to GxE. The most unstable environments were Kumasi 2012 and BNARI 2011. BNARI 2012 and Kumasi 2012 obtained average yields similar to the mean across genotypes and environments. The highest DM content was obtained in Kitase 2012 trial and the least was in BNARI 2011. Kitase 2012 was also the most stable with unity repression slope (Table 5.19). The most unstable genotypes for dry matter were J/7-13 and Pelican Processor. Hi Starch was the most stable for dry matter but Yellow Sunflower with better storage root yields, unity slope and close to average stability (Table 5.12) for dry matter could be the most ideal as breeding line or for intended release after further evaluation.

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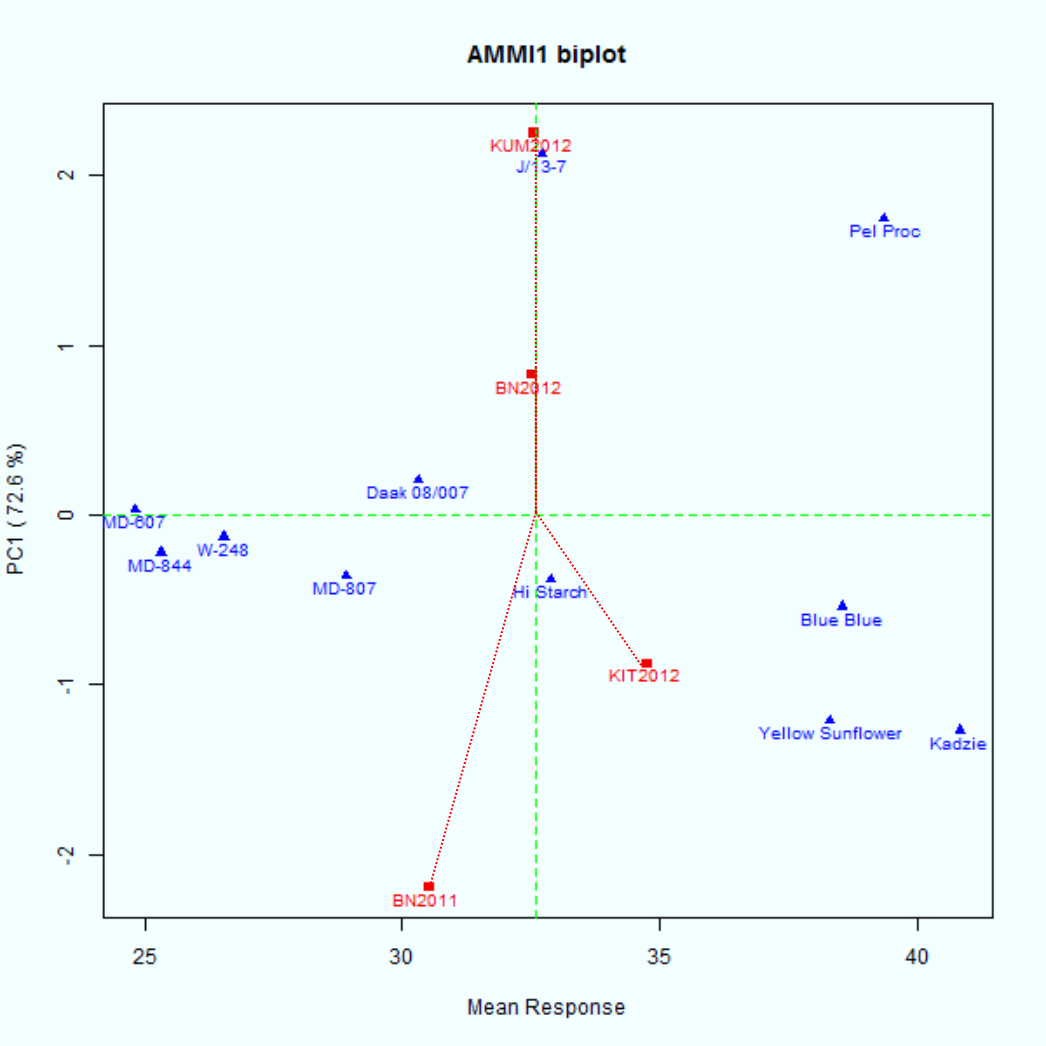


**Figure 5.8: AMMI biplot of the interactions of genotypes and environments for storage root dry matter of the 11 genotypes evaluated in four environments in Ghana in 2011 and 2012. The four environments are shown in red font and the genotypes are in blue font. BN, Kum and Kit are BNARI, Kumasi and Kitase sites respectively**

The AMMI biplot for β-carotene explained 91.3 % of the β-carotene variation due to GXE interaction (Figure 5.9). As expected the genotypes that produced the lowest β-carotene in all environments were the cream to yellow-fleshed clones; namely Hi starch, Daak 08/007, Pelican Processor, Yellow Sunflower, Blue Blue and Kadzie. These clustered together because they had similar β-carotene contents across all environments. Mean β-carotene content was higher for

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BNARI 2011 trial while the least was obtained from the 2012 trial in Kitase. BNARI 2012 was the most stable environment for β-carotene while MD-807 was the most stable clone.

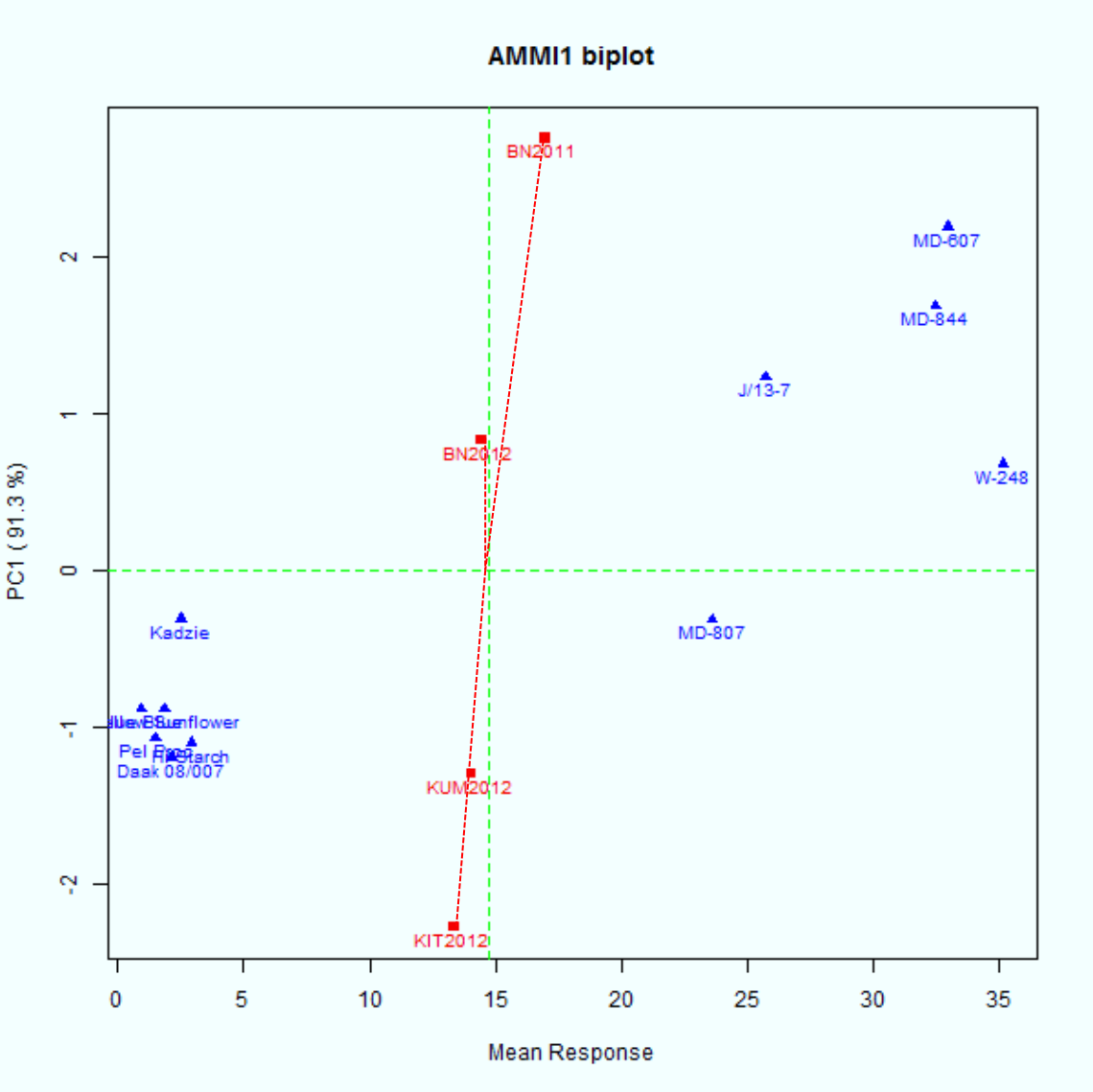


**Figure 5.9: AMMI biplot of the interactions of genotypes and environments for β-carotene in raw roots of the 11 genotypes evaluated in four environments in Ghana in 2011 and 2012. The four environments are shown in red font and the genotypes are in blue font. BN, Kum and Kit are BNARI, Kumasi and Kitase sites respectively**

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**Table 5.19: Means, regression slopes, deviation from regression, heritability estimates, principal components and Barlett's test of homogeneity for the traits under study in the 11 genotypes evaluated in 2011 and 2012**

| | Yield | | | Dry matter | | | Starch | | | β-carotene | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Genotype** | ***Xi*** [a] | $\beta_i$ [b] | $S^2d_i$ [c] | ***Xi*** [a] | $\beta_i$ [b] | $S^2d_i$ [c] | ***Xi*** [a] | $\beta_i$ [b] | $S^2d_i$ [c] | ***Xi*** [a] | $\beta_i$ [b] | $S^2d_i$ [c] |
| **++Blue Blue** | **14.96** | **0.75** | 0.89* | **38.53** | **0.93** | 0.84* | **63.24** | -1.76* | 2.42* | 0.96 | -0.35* | **0.05** |
| **Daak 08/007** | 6.65 | **0.72** | **0.09** | **30.31** | 0.16* | 0.60* | **57.73** | 1.92* | 1.04* | 2.14 | **-0.64** | **0.34** |
| **Hi Starch** | 9.60 | **0.93** | **0.38** | **32.88** | 0.36* | **0.21** | **64.06** | **-0.75** | 0.68* | 2.93 | -0.31* | 0.77 |
| **J/7-13** | 7.22 | **0.66** | **0.02** | **32.71** | 1.64* | 1.63* | **61.56** | **0.98** | 1.29* | **25.71** | 2.66* | **0.46** |
| **Kadzie** | 3.38 | 0.44 | **0.09** | **40.82** | **0.61** | 0.98* | **62.79** | 0.10* | 0.68* | 2.52 | **0.56** | **0.07** |
| **ººMD-607** | 8.24 | **1.51*** | **0.30** | 24.82 | 1.94* | **0.31** | 47.26 | 2.18* | 1.65* | **32.94** | 3.85* | 1.02 |
| **MD-807** | **11.13** | 1.96* | **0.41** | 28.90 | **0.57** | **0.22** | 52.43 | 3.04* | 1.14* | **23.59** | **0.72** | **0.46** |
| **MD-844** | **13.23** | **1.38** | **0.35** | 25.31 | 1.53* | **0.36** | 48.87 | 3.09* | 1.97* | 32.46 | 3.28* | 0.67 |
| **Pelican Processor** | **12.81** | **1.10** | **0.41** | **39.35** | **1.44** | 1.35* | **58.76** | **0.47** | 1.15* | 1.50 | **-0.53** | **0.42** |
| **W-248** | 7.88 | **0.63** | **0.21** | 26.53 | **1.12** | 0.67* | 54.31 | 1.55* | 0.73* | **35.14** | 1.94* | **0.18** |
| **Yellow Sunflower** | **10.93** | **0.93** | **0.19** | **38.30** | **0.71** | 0.94* | **61.60** | 0.18* | 1.63* | 1.87 | -0.17* | 0.68 |
| **BN2011** | **21.06** | **1.49** | 0.57* | 30.52 | **1.06** | **0.14** | 54.78 | **1.42** | **0.11** | **16.97** | **1.208** | **0.03** |
| **BN2012** | 6.86 | **0.63** | **0.35** | 32.53 | **1.09** | **0.09** | **59.09** | 0.04* | **0.21** | 14.45* | **1.050** | **0.02** |
| **KIT2012** | 2.32 | 0.21* | **0.09** | **34.76** | **0.93** | **0.09** | **58.24** | **1.29** | **0.15** | 13.35 | **0.836** | **0.03** |
| **KUM2012** | 8.31 | 1.67* | 0.61 | 32.55 | **0.92** | **0.14** | **57.93** | **1.25** | **0.10** | 14.04 | **0.906** | **0.02** |
| **Overall mean** | **9.91** | | | **32.59** | | | **57.51** | | | **14.79** | | |
| **Heritability** | **27.18** | | | **95.80** | | | **83.01** | | | **99.00** | | |
| **PC1** [d] | **65.66*****| | | **72.60***** | | | **86.20***** | | | **91.30***** | | |
| **PC2** [d] | **28.96***** | | | **20.10***** | | | **9.78** | | | **6.48** | | |
| **B-test** | ∞∞ | | | ∞∞ | | | ∞∞ | | | ∞∞ | | |

**[a] values in bold are higher than the overall mean; [b] values in bold are not significantly different from unity at P < 0.05 while those with *, are either smaller than or more than unity at P < 0.05; [c] values in bold are not significantly different from zero at P < 0.05; while those with *, are significantly different from zero at P < 0.005; [d] **, *** = Significant at 0.1% and 0.01% respectively; B-test = Barlett's test of homogeneity of variances; ∞∞ = P < 0.0001; *Xi* = means for genotypes; $\beta_i$ = Regression slope; $S^2d_i$ = deviation from regression slope; ++ = local check; ºº = elite check clone**

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**Table 5.20a: Means for sugars, regression slopes, deviation from regression, heritability estimates, principal components and Barlett's tests for the traits under study in the 11 genotypes evaluated in 2011 and 2012**

| | Fructose | | | Glucose | | | sucrose | | |
|---|---|---|---|---|---|---|---|---|---|
| **Genotype** | ***Xi*** [a] | $\beta_i$ [b] | $S^2d_i$ [c] | ***Xi*** [a] | $\beta_i$ [b] | $S^2d_i$ [c] | ***Xi*** [a] | $\beta_i$ [b] | $S^2d_i$ [c] |
| **++Blue Blue** | 0.59 | **0.25*** | 0.56* | 1.30 | -0.38* | 0.64* | 11.89 | **-1.11** | 1.69* |
| **Daak 08/007** | 0.34 | **0.85** | **0.33** | 1.40 | **1.27** | **0.13** | 14.12 | **0.84** | 1.42* |
| **Hi Starch** | 0.42 | **0.67** | 0.46* | 1.01 | **0.68** | **0.19** | 11.61 | **-0.55** | 0.77* |
| **J/7-13** | **1.14** | **1.53** | **0.19** | 2.14 | **1.50** | 0.61* | 12.42 | **1.50** | 1.83* |
| **Kadzie** | 0.35 | **-0.23*** | **0.44** | 0.81 | 0.05* | 0.62* | 12.96 | **0.62** | 0.52* |
| **ººMD-607** | **1.70** | 1.98* | 0.49* | **4.26** | **1.58** | **0.43** | **18.48** | 3.22* | 0.72* |
| **MD-807** | **1.11** | **1.45** | 0.47* | **4.09** | 2.68* | 0.52* | **15.89** | 2.79* | **0.37** |
| **MD-844** | **1.11** | 1.68* | 0.72* | **4.29** | 1.81* | 1.25* | **19.53** | 4.20* | 2.46* |
| **Pelican Processor** | 0.66 | **0.52** | 0.50* | 1.61 | 0.34* | 0.80* | 12.99 | **-1.16** | 1.69* |
| **W-248** | **1.14** | 2.00* | 0.77* | **3.42** | **1.21** | 0.58* | **16.73** | 1.79* | 1.37* |
| **Yellow Sunflower** | 0.72 | **0.31*** | 0.61* | 1.71 | 0.24* | 0.58* | 12.16 | **-1.15** | 1.78* |
| **BNARI 2011** | **1.24** | **1.43** | **0.13** | **3.37** | **1.28** | **0.13** | 15.59 | 1.61* | **0.13** |
| **BNARI 2012** | 0.48 | 0.25* | **0.16** | 1.55 | 0.18* | **0.17** | 13.81 | 0.06* | **0.20** |
| **KITASE 2012** | 0.82 | **1.50** | **0.12** | 2.17 | **1.32** | **0.10** | 13.90 | **1.15** | **0.15** |
| **KUMASI 2012** | 0.83 | **0.82** | **0.19** | **2.37** | **1.22** | **0.13** | **14.43** | **1.19** | **0.11** |
| **Overall mean** | **0.84** | | | **2.37** | | | **14.43** | | |
| **Heritability** | **84.34** | | | **86.92** | | | **82.06** | | |
| **PC1** | **75.76*** ** | | | **80.99*** ** | | | **81.36*** ** | | |
| **PC2** | **21.21**** | | | **12.82** | | | **15.73** | | |
| **B-test** | **** ** | | | **** ** | | | **** ** | | |

**[a] values in bold are higher than the overall mean; [b] values in bold are not significantly different from unity at P < 0.05 while those in red front are either smaller than or more than unity at P < 0.05; [c] values in bold are not significantly different from zero at P < 0.05; ; while those with *, are significantly different from zero at P < 0.005; [d]**, *** = Significant at 0.1% and 0.01% respectively; B-test = Barlett's test of homogeneity of variances; *Xi*= means for genotypes; $\beta_i$ = Regression slope; $S^2d_i$ = deviation from regression slope; ++ = Local check; ºº = elite check clone; Tsugars = Total sugars.**

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**Table 5.20b: continued: Means for sugars, regression slopes, deviation from regression, heritability estimates, principal components and Barlett's tests for the traits under study in the 11 genotypes evaluated in 2011 and 2012**

| | Maltose | | | Total sugars | | | Sucrose equivalent | | |
|---|---|---|---|---|---|---|---|---|---|
| **Genotype** | ***Xi*** [a] | $\beta_i$ [b] | $S^2d_i$ [c] | ***Xi*** [a] | $\beta_i$ [b] | $S^2d_i$ [c] | ***Xi*** [a] | $\beta_i$ [b] | $S^2d_i$ [c] |
| **++Blue Blue** | 10.77 | 2.35 | 1.23* | 21.48 | 0.23* | 1.14* | 18.07 | **-0.61** | 1.75* |
| **Daak 08/007** | **23.07** | **1.23** | 1.08* | 37.25 | 1.84* | 0.65* | 25.35 | 1.84* | 0.86* |
| **Hi Starch** | 14.65 | **1.38** | 1.71* | 25.42 | 0.06* | 0.99* | 19.05 | -0.29* | 1.26* |
| **J/7-13** | 10.22 | 2.02* | 1.58* | 20.42 | 0.43* | 1.08* | 19.55 | 0.17* | 1.03* |
| **Kadzie** | 14.66 | -0.54* | **0.33** | 23.80 | **-0.14*** | 0.45* | 20.20 | -0.37* | **0.51** |
| **ººMD-607** | **18.24** | 2.10* | 1.39* | **40.13** | 2.07* | 0.87* | **31.08** | 2.59* | 1.16* |
| **MD-807** | **16.25** | 1.04* | 0.94* | **35.55** | 2.17* | **0.42** | **26.83** | 2.80* | **0.47** |
| **MD-844** | **15.85** | **0.65** | 0.65* | **39.35** | 1.89* | **0.40** | **30.42** | 3.03* | 0.85* |
| **Pelican Processor** | **17.71** | **1.22** | 1.82* | 29.14 | **1.43** | **0.38** | 22.42 | **0.69** | **0.40** |
| **W-248** | 4.43 | -1.17* | 1.51* | 21.26 | -0.23* | **0.46** | 22.19 | 0.45* | **0.46** |
| **Yellow Sunflower** | **18.05** | **0.74** | 1.50* | **30.30** | **1.24** | **0.27** | 21.88 | **0.68** | **0.60** |
| **BNARI 2011** | 13.61 | 1.56* | **0.29** | **33.36** | 1.68* | **0.19** | **25.09** | 1.61* | **0.13** |
| **BNARI 2012** | 13.58 | -0.06* | **0.21** | 24.07 | -0.02* | **0.08** | 21.21 | 0.06* | **0.20** |
| **KITASE 2012** | 13.92 | **1.27** | **0.17** | 26.52 | **1.17** | **0.18** | 22.27 | **1.15** | **0.15** |
| **KUMASI 2012** | **18.49** | **1.23** | **0.24** | **33.90** | **1.16** | **0.19** | **24.90** | **1.19** | **0.11** |
| **Overall mean** | **14.90** | | | **29.46** | | | **23.37** | | |
| **Heritability** | **70.09** | | | **78.75** | | | **82.69** | | |
| **PC1** | **63.29*** ** | | | **65.75*** ** | | | **73.24*** ** | | |
| **PC2** | **26.09*** ** | | | **18.26** ** | | | **16.48** | | |
| **B-test** | *** | | | *** | | | *** | | |

**[a] values in bold are higher than the overall mean; [b] values in bold are not significantly different from unity at P < 0.05 while those in red font are either smaller than or more than unity at P < 0.05; [c] values in bold are not significantly different from zero at P < 0.05; while those with *, are significantly different from zero at P < 0.005; [d]**, *** = Significant at 0.1% and 0.01% respectively; B-test = Barlett's test of homogeneity of variances; *Xi*= means for genotypes; $\beta_i$ = Regression slope; $S^2d_i$ = deviation from regression slope; ++ = Local check; ºº = elite check clone; Tsugars = Total sugar**

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### 5.3.4 Broad sense heritability estimates

Low heritability ($H^2$) estimate of 27% was obtained for total storage root yield (Table 5.19). Root quality traits on the other hand had high heritability estimates of 95.8%, 83.01%, and 99.0% for dry matter, starch and β-carotene respectively. For storage root sugars, values obtained were 70.09, 78.75%, 82.06, 84.34 and 86.92% for maltose, total sugars, sucrose, glucose and fructose respectively (Tables 5.20a and 5.20b). Heritability for sucrose equivalent was 82.69.

### 5.3.5 Phenotypic correlation between traits

Table 5.21 shows the phenotypic correlation values for the traits of interest. There were positive and significant correlation between storage root yield and the following; harvest index, individual storage root weight, number of roots per plant, weevil damage, fructose, glucose and total cooked sugars. Weak and negative associations were observed between storage root yield and dry matter ($P < 0.05$, $r = -0.18$) and between storage root yield and starch ($P < 0.05$, $r = -0.16$). Harvest index was positively associated with the number of roots per plant ($P < 0.0001$, $r = 0.32$). Significant and negative correlations were observed between individual storage root weight and β-carotene ($P< 0.01$, $r = -0.25$). Weevil damage had strong and significant correlations with all the storage root quality traits. The association between weevil damage and sugars was also strong and positive ($P< 0.000.$, $r = 0.0.37? – 0.75$) while negative associations were observed between weevil damage and starch ($P< 0.0001$, $r = -0.69$) and between weevil damage and dry matter ($P< 0.0001$, $r = -0.34$). Significant positive association ($P< 0.0001$, $r = 0.55$) between dry matter and starch was recorded while dry matter was significant but negatively associated with the sugars ($P < 0.0001$, $r = -0.34$ to $-0.58$) except maltose. There was also strong and negative correlation ($P< 0.0001$, $r = -0.78$) between dry matter and β-carotene. Associations between starch and the individual sugars, except maltose, were strongly negative (P

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< 0.0001, r = -0.69 to -0.93). With the exception of maltose, there was weak to strong correlations among the individual sugars ($P < 0.0001$, r = 0.37 to 0.84); between individual sugars and total sugars ($P < 0.0001$, r = 0.37 to 0.75); between maltose and total sugars ($P < 0.0001$, r = 0.75); between maltose and β-carotene ($P < 0.01$, r = -0.26); between total sugars and β-carotene ($P < 0.05$, r = 0.75). While glucose, fructose and sucrose correlated significantly with many other traits, maltose correlated strongly ($P < 0.0001$, r = 0.75) with only weevil damage. Sucrose equivalent was negatively correlated with dry matter ($P < 0.0001$, r = -0.48) and starch ($P < 0.0001$, r = -0.91 but correlated positively with all sugar types ($P < 0.0001$, r = 0.57 – 0.85) and β-carotene ($P < 0.0001$, r = 0.0.42).

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**Table 5. 21: Phenotypic correlation between recorded traits of the 11 genotypes evaluated in four environments**

| | RY | HI | Irtwt | NRplt | WED | RDM | Starch | FRU | GLU | SUCR | Maltose | Tscooked | SE |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **HI** | **0.26**** | | | | | | | | | | | | |
| **Irtwt** | **0.51*** | **0.19** | | | | | | | | | | | |
| **NRplt** | **0.47***** | **0.32***** | **0.42***** | | | | | | | | | | |
| **WED** | **0.27**** | **0.001** | **0.12** | **0.10** | | | | | | | | | |
| **RDM** | **-0.18*** | **-0.04** | **0.15** | **-0.001** | **-0.34***** | | | | | | | | |
| **Starch** | **-0.16*** | **-0.06** | **0.13** | **0.06** | **-0.69***** | **0.55***** | | | | | | | |
| **FRU** | **0.28**** | **0.08** | **0.06** | **0.19*** | **0.37***** | **-0.48***** | **-0.70***** | | | | | | |
| **GLU** | **0.24***** | **0.04** | **-0.03** | **0.04** | **0.53***** | **-0.58***** | **-0.88***** | **0.84***** | | | | | |
| **SUCR** | **0.15** | **0.04** | **-0.11** | **-0.06** | **0.61***** | **-0.54***** | **-0.93***** | **0.60***** | **0.82***** | | | | |
| **Maltose** | **0.05** | **-0.03** | **0.05** | **0.03** | **0.75***** | **0.05** | **-0.15** | **-0.16** | **-0.10** | **0.01** | | | |
| **Tscooked** | **0.27**** | **0.001** | **0.12** | **0.10** | **1.00***** | **-0.34***** | **-0.69***** | **0.37***** | **0.53***** | **0.61***** | **0.75***** | | |
| SE | **0.20*** | 0.11 | -0.04 | 0.00 | -0.06 | **-0.48***** | **-0.91***** | **0.57***** | **0.75***** | **0.85***** | **0.49***** | **0.44***** | |
| **BC** | **0.07** | **0.09** | **-0.25**** | **-0.07** | **0.18*** | **-0.78***** | **-0.56***** | **0.61***** | **0.64***** | **0.58***** | **-0.26**** | **0.18*** | **0.42***** |

***if P ≤ 0.05, ** if P ≤ 0.01, *** if P ≤ 0.001. Tsugar = total sugars in cooked roots; RY = root yield; HI = harvest index; Irtwt = individual root weight in kg; NRplt= number of roots per plant;; WED = weevil damage; RDM = root dry matter; FRU = fructose; GLU = glucose; SUCR = sucrose; TScooked = total sugars in cooked roots; BC = β –carotene; SE = sucrose equivalent. Values represent Pearson's correlation coefficients (r)**

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## 5.4 DISCUSSION

The AMMI and regression coefficients were used to analyze yield and its components as well as storage root quality traits of ten promising genotypes and one farmer check variety in four environments. AMMI analysis of variance revealed significant ($P<0.05 – 0.0001$) main effects due to genotype, environments and G x E interaction for most agronomic traits, which is consistent with previous studies (Abidin *et al.*, 2002; Manrique and Hermann, 2002; Grüneberg *et al.*, 2005; Chiona, 2009; Tumwegamire, 2011; Some, 2013). On yield and its components, the influence of G x E has also been documented (Tewe *et al.*, 2003; Abidin *et al.*, 2005; Tekalign, 2007; Tsegaye *et al.*, 2007; Chiona, 2009; Some, 2013). In the present study environment main effect was not significant for harvest index which is in contrast with the study by Tumwegamire, (2011) who found significant environment effects for harvest index.

Generally, environment effects and G x E effects were more important than genotype main effects for agronomic traits emphasizing the importance of environment and its interaction` with genotype in expression of yield and its components. The low estimate of heritability for yield attained in this study coupled with G x E effect could slow progress in selection and emphasizes the importance of G x E analysis. Higher heritability estimates for yield have however, been reported (Jones *et al.*, 1986a; Some, 2013). Diverse environments can have a profound effect on estimates of heritability (Falconer and Mackay, 1996) and the significant differences between the environments in the current study may have contributed to the low estimates for yield. The highest yielding environment was BNARI 2011 with a mean yield of about 3-9 times higher than yields for trials conducted in the minor season in 2012 under irrigation. Though the 2012 trials were irrigated, inconsistent water supply as a result of intermittent water shortages caused periods of water stress. This suggests that the clones in this study were very responsive to

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adequate water supply as well as water stress. High average yields in wet seasons have also been reported by Tewe *et al*. (2003) in IITA Ibadan where annual rainfall is about 1200 mm. The authors also documented the negative effect of very high rainfall (2100 and 2500 mm) and its associated poor soil conditions on yields in other locations. These findings and those of this study could imply that, below or above a certain threshold of water supply sweetpotato could suffer heavy yield losses. In a study to evaluate response of 8 genotypes to water stress, dry matter and root carbohydrates, including reducing sugars, total sugars, and starch were significantly affected by irrigation treatments (Ekanayake and Collins, 2004). Root dry matter however increased as water stress increased and was the most sensitive root quality trait. The current study seemed to follow a similar trend, where the most stressed environments; Kitase 2012 and BNARI 2012, attained the lowest β-carotene and sugars but had a slight increase in dry matter over that of the most favorable environment, BNARI 2011.

The local check variety Blue Blue had the highest mean yield across genotypes and locations demonstrating superiority in performance of locally adapted varieties (Abidin *et al.*, 2002; Abidin *et al.*, 2005). Judging by the SED value (0.93) for yield (Table 5.5), the mean yields of introduced clones; MD-807, MD-844, Pelican Processor and Yellow Sunflower however, had mean yields that were significantly lower than that of the local check variety. In the 2011 trial in BNARI where there was adequate rainfall, these imported clones out-yielded the local check variety probably because they were virus free or had better response to better growth conditions or both.

Root quality traits of interest to breeders have been found to be influenced by G x E effects (Manrique and Hermann, 2001; Holland *et al.*, 2003; Ndirigwe, 2005). In this study G x E were all highly significant ($p<0.01$ – $P<0.0001$) for all quality traits. However, in contrast to

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agronomic traits, where environment and G x E effects were more important, the genotype effect was more important to the observed variation for quality traits except for maltose for which GxE was more important. A similar trend was observed by Grüneberg *et al*. (2005) in which the authors found genetic variation for root quality traits including dry matter, starch and β-carotene to be more important than the G x E effect. It is worth noting however that both supporting and contrasting reports with regard to G x E influence on nutritional traits have been documented. For example, a study in Rwanda (Ndirigwe, 2005) recorded highly significant G x E effect on β-carotene.. Manrique and Hermann, (2000) and Grüneberg *et al*. (2005) reported low G x E influence on β-carotene which is consistent with the current study. However, some earlier reports have indicated that both environment and G x E interactions were not important for β-carotene content (Chiona, 2009; Tumwegamire, 2011; Some, 2013). Regarding dry matter no G x E interaction was found in as earlier study (Li, 1979). This is inconsistent with the findings of the current study and in other previous reports (Jones *et al.*, 1986a; Manrique and Hermann, 2002; Tekalign, 2007) where G x E was important. It appears therefore that the significance and magnitude of G x E effects on root quality trait may be dependent on the trait under study, the environmental conditions prevailing at the study site and the genotype.

This study revealed that sweetpotato sugars were highly influenced by G x E interactions. For example, while MD- 607 recorded the highest amounts of total sugars in BNARI 2011 and Kitase 2012 trials, MD- 844 recorded the highest amounts for Kumasi 2012 and BNARI 2012 trial. Variation in individual sugar type was highly significant ($P<0.001 – 0.0001$) across genotypes and environments. The large genetic variation compared to G x E effect in sugars, implies that alteration in sugar levels to meet consumer preferences can be achieved through breeding. Generally, the trial at BNARI in 2011 yielded the highest for sugars and β-carotene.

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Since BNARI 2011 trial was carried out in the major raining season, better water supply, high humidity, and lower temperatures might have been responsible for higher values for both sugars and β-carotene in 2011. The effect of these climatic factors on the variation in these traits however requires further investigation. The clone MD-607, obtained the highest mean for total sugar. This clone had the highest mean for fructose and maltose in cooked roots across environments. Since fructose is the sweetest sugar (about five times as sweet as sucrose) (Moskowitz, 1970; Shallenberger, 1993) clones with high amounts of fructose and higher hydrolysis of starch to maltose, will be among the sweetest clones. The SE values also confirm this, as MD-607 had the highest SE values. J/7-13, W-248, Blue Blue, Kadzie and Hi-Starch were the lowest sugar lines because, not only were they low in glucose, fructose and sucrose but were also lower in cooked root maltose. The large genetic component for sugars and the high estimates for heritability imply that substantial gains can be made when selecting for low sugars.

On yield stability, three genotypes namely Pelican processor and Yellow Sunflower and MD-844 were identified with high yields and average stability across environments. The local check variety and two introduced clones; MD-807, and MD 607 had specific adaptation to high performance environments. Most genotypes with low GEI effects were also low yielding. This seems to agree with the fact that yield stability could be expected from low yielding genotypes which do not take advantage of favorable environments (Yan *et al.*, 2000; Mbwaga *et al.*, 2007).

With respect to quality attributes, the most stable clones for dry matter, starch and β-carotene were Hi Starch and Blue Blue; Hi Starch, Kadzie, and Pelican Processor; and MD-807 respectively. MD-807, a genotype with high β-carotene can therefore be suitable for use in hybridization with the other listed yellow to white-fleshed clones to incorporate high β-carotene into their high dry matter genetic backgrounds. Earlier reports indicate that β-carotene is

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controlled by additive gene and has high heritability estimates and is quantitatively inherited. Hernandez et al. (1967) found that certain parents produced transgressive segregants. Thus with recurrent selection and heterosis breeding, significant progress can be made (Sakai, 1964; Hernandez *et al.*, 1967; Jones *et al.*, 1986a; Some, 2013). Testing of such genotypes should be carried out in favorable agro-climatic conditions, since the highest mean for β-carotene was observed in a high performance environment.

Regarding stability of sugars no genotype showed stability for sucrose. W- 248 and MD-607 showed stability for glucose; while MD-807 and MD-844, both β-carotene lines were stable for maltose production. Stability for total sugars was exhibited by Hi Starch, Yellow Sunflower, Pelican Processor and Kadzie. These were also among the least sweet clones and will be useful as parents for a low-sugar breeding program for sweetpotato.

The combined understanding of G x E interactions, genetic correlations and stability parameters for root yield and nutritional traits is needed for informed choice of appropriate breeding strategies for sweetpotato (Grüneberg *et al.*, 2005; Tumwegamire, 2011). In this study correlations between yield and yield components as well as between yield and nutritional traits were identified, which is consistent with recent reports (Grüneberg *et al.*, 2009a; Tumwegamire, 2011; Some, 2013). Root yield significantly correlated with harvest index, individual root weight and number of storage roots per plant. Selection for any of these traits will imply selection for high yields. Weevil damage was associated positively with yield. This could be due to early bulking of high yielding clones that provide an early source of food for weevil attack. The significant positive association ($P< 0.001$, $r = 0.37 – 1.0$) between weevil damage and storage root sugars; and negative association between weevil damage and dry matter ($P< 0.0001$, $r = -0.53$); weevil damage and starch ($P< 0.0001$, $r = -0.69$) probably indicates that high dry matter

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and starch were unappealing to weevils while sugars encouraged feeding. While glucose, fructose and sucrose correlated significantly with many other traits, maltose was only strongly correlated ($P< 0.0001$, $r = 0.75$) with weevil damage. Even though sugar analyses were based on cooked roots, this could probably be because the high β-carotene lines have higher sugar levels (in raw and cooked roots) and are early bulking. They may therefore have been exposed to weevil attack much earlier than the low sugar clones. There could also be a relationship between the underlying cause of maltose formation, which is amylase content and weevil damage. In other words, perhaps weevils are more attracted to higher protein sweetpotato. However, there was no correlation between weevil damage and total protein content in raw roots was detected (data not shown).

Glucose, fructose and total sugars were associated positively with yield while higher yields were negatively associated with starch and dry matter. This observation could be explained by the fact that genotypes with very high fresh yields may have accumulated a lot of water, resulting in lower dry matter and starch. The observation is especially true for the high yielding β-carotene lines namely MD-807, MD-844 and MD-607 which are very low in dry matter and starch. The significant positive correlation ($P< 0.0001$, $r = 0.545$) between root dry matter and starch indicates the accumulation of genes controlling high starch content will result in high dry matter content (Lebot, 2008). With the exception of maltose, all other sugars had negative and moderate to strong association ($r = -0.48 – -0.93$) with dry mater and starch. Significant negative correlations between starch and sugars has been documented (Lin et al., 2007). Selection for high dry matter and starch may therefore lead to direct selection for low sugars. Grüneberg *et al* (2010) reported moderate correlations between starch and β-carotene, in agreement with the current study. Breeding for low sugar, high dry matter/starch and high β-carotene may however

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require considerable length of time and recurrent selection due to the negative and significant correlation between β-carotene and dry matter (P< 0.0001 r = -0.78); and positive correlation between β-carotene and the sugars (P= 0.05 – 0.0001, r = 0.18 – 0.64). However, earlier reports indicate the existence of East African genotypes that combine these traits quite satisfactorily (Mwanga *et al.*, 2007b; Tumwegamire, 2011). Such types were not identified in the collection of Ghanaian germplasm evaluated in chapter 4 of this thesis, but due to the complex genetics of sweetpotato these types can be obtained through genetic recombination.

## 5.5 CONCLUSION

Genotypic, environmental and G x E effects were significant for most traits. Genotype by environment effect was larger than environment and genotyp main effect for agronomic traits while genotype effects were more important for quality attributes. Three genotypes namely Pelican processor, Yellow Sunflower and MD-844 were high yielding with average stability across environments. Yellow Sunflower was the most stable genotype for total sugars but Pelican processor, W-248, Hi Starch and Kadzie with close to average stability and lower total sugars, may be the most suitable clones for a low-sugar breeding activity. The most stable clones for dry matter were Hi Starch and Blue Blue ; while for starch they were Hi Starch, Kadzie and Pelican Processor; and for β-carotene it was MD-807.

Broad sense heritability ($H^2$) for yield was low (27 %) but root quality traits had higher $H^2$ values. The significant correlations between yield and yield components; yield and quality traits; as well as between individual quality attributes will aid in selection processes. Selection for high dry matter and starch may lead to direct selection for low sugars due to the negative association between sugars and starch and between sugars and dry matter. β-carotene negatively correlated with dry matter (P< 0.0001 r = -0.78); but positive correlated with sugars (P= 0.05 – 0.0001, r =

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0.18 – 0.64) suggesting that, improvement of β-carotene content in high dry matter genetic backgrounds will require recurrent selection. Selection gain may however be rapid as a result of the high $H^2$ estimates attained for the quality traits.

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# CHAPTER SIX

## 6.0 GENETIC ANALYSIS OF INHERITANCE OF SUGARS, DRY MATTER AND BETA-CAROTENE IN SWEETPOTATO

### 6.1 INTRODUCTION

Sugars play a central role in the sensory acceptability of sweetpotato. While countries like the USA prefer the root sweet, most countries in sub-Saharan Africa prefer high dry matter sweetpotato with little or no sweetness (Mwanga *et al.*, 2007). Information on the genetic control of sugars in the crop is however, limited. As with sugar levels, dry matter content in the storage roots is also an important trait that determines consumer acceptability in the tropics (Adu-Kwarteng *et al.*, 2001; Abidin *et al.*, 2002; Lebot, 2008; Cervantes-Flores *et al.*, 2011). Major components of sweetpotato dry matter are starch and sugars (Palmer, 1982; Picha, 1987). Starch content is apparently determined mainly by the additive effect of polygenes and accumulation of genes controlling high starch content is recommended for achieving high dry matter content (Lebot, 2008). Dry matter and starch content have been found to be negatively correlated with sugar content (Gasura *et al*., 2008; Lebot, 2008). Selecting for high dry matter and starch content will, therefore, have direct impact on selection for low sugar lines. High heritability estimates of 75-88% (Zhang and Li, 2004), 64% (Jones *et al.*, 1986a; Lebot *et al.*, 2009) and 69.84% (Tsegaye *et al*., 2007) have been reported for dry matter content. These suggest that rapid genetic gain can be realized when selecting for dry matter (Mok *et al*., 1997).

In much of West Africa, including Ghana, Vitamin A deficiency is a major health concern (Akoroda, 2009). Consumption of orange-fleshed sweetpotato with high levels of β-carotene can alleviate this problem. The white or yellow-fleshed clones that are predominant in Ghana have

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relatively high dry matter but low β-carotene levels. Therefore, incorporating the high β-carotene trait into the high dry matter genetic background of adapted varieties will be useful for the Ghanaian consumer. High heritability estimates for β-carotene have been reported (Hernandez *et al.*, 1967; Jones *et al.*, 1986a; Tsegaye *et al.*, 2007) and total carotene content also appears to be controlled by several additive genes (Hernandez *et al.*, 1967). It has been suggested that qualitative genes controlling the trait may have been duplicated due to the hexaploid nature of the crop (Cervantes-Flores, 2006; Cervantes-Flores *et al.*, 2008b). Eight QTLs have been identified as being involved in the variation of beta-carotene content in sweetpotato (Cervantes-Flores *et al*., 2011).

In chapter three of this study, farmers' indicated their preference for low-sugar and high dry matter content sweetpotato and acceptance of β-carotene cultivars which have the desired culinary attributes. The presence of wide genetic variability in dry matter (Lebot, 2008), sugars (Mclaurin and Kays, 1992; Kays *et al*, 2005) and β-carotene (Woolfe, 1992) levels opens up an opportunity to employ conventional breeding techniques to improve on these traits. The negative correlation between dry matter and β-carotene (Andrade *et al.*, 2009; Cervantes-Flores *et al.*, 2011) will however require long term efforts at recurrent selection to increase carotene gene frequencies in high dry matter sweetpotato (Andrade *et al.*, 2009).

For an efficient prediction of genetic gains that can be made through selection, heritability is estimated (Jones, 1986; Holland *et al.*, 2003; Smalley *et al.*, 2004). Heritability can be measured in the broad sense ($H^2$) or the narrow sense ($h^2$). Broad sense heritability is the fraction of total variation which is heritable and is represented by $H^2 = V_G/V_P$, where $V_G$ is the genetic variance and $V_P$ is the total variance or phenotypic variance. The genetic variance can be subdivided into additive variance ($V_A$), the dominant variance ($V_D$) and epistatic variation ($V_I$). While broad

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sense heritability gives an indication of genetic gains that can be made through breeding, it does not separate the components of genetic variance, such as dominance and epistasis - which are expressed very differently from additive variance and so have very different implications for breeding strategies to be used by breeders. Narrow sense heritability includes only the additive variance and is given as $h^2 = V_A/V_P$ (Simmonds, 1979; Holland *et al.*, 2003) . It is this form of heritability that is of utmost interest to breeders, because it is a direct measure of resemblance between relatives. For this reason breeding experiments are conducted to estimate and separate the components of genetic variance so as to determine heritability in the narrow sense. High $h^2$ indicates a lesser environmental influence and the presence of additive gene effects on the traits under consideration (Simmonds, 1979; Holland *et al.*, 2003).

Heritability can be determined through mating designs by essentially two methods. The first method is based on analysis of variance from breeding studies. From these crosses, phenotypic variation ($V_P$) can be partitioned into the variance components ($V_A + V_D + V_I + V_E$). The second uses regression and correlation to estimate heritability. This is known as the parent-offspring regression in which a specific trait is measured for both parent and the offspring and compared using regression (Harman, 1976; Jong, 1984; Jones, 1986; Holland *et al.*, 2003). The slope ($b_{op}$) of the regression of offspring on parents gives a measure of narrow sense heritability, symbolized by $b_{op} = VA/VP = h^2$. A major advantage of estimating heritability from parent offspring regression is that the sample of parents chosen does not have to be a random sample from the reference population, in contrast to all of the heritability estimates based on variance components (Holland *et al.*, 2003). Jones (1986) has reported 207 studies that estimated narrow sense heritability using parent-offspring regression in sweetpotato breeding. However the use of parent-offspring method may yield heritability estimates quite different from those obtained by

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using variance components (Jones, 1986). For new and emerging traits like sugars and β-carotene in sweetpotato, comparison of the two methods will be useful (Falconer and Mackay, 1996)

In addition to heritability, estimates of genetic advance help in the prediction of the potential gain in selection while phenotypic correlation between traits facilitates selection, in that, it allows positive or negative selection of a trait depending on whether it is positively or negatively correlated with another. General (GCA) and specific (SCA) combining abilities are also derived from mating designs and are estimated from genetic variance that are helpful for identifying the prevalence of additive and non-additive gene actions, necessary for determining the methods to be employed in selection for a particular trait. These designs even though developed in maize (Comstock and Robinson, 1948; Jinks and Hayman, 1953; Christie and Shattuck, 1992; Dudley *et al.*, 1997), a diploid, are routinely used in sweetpotato, a hexaploid with more complex genetics. They are the best tools currently available and have proved adequate over the years for genetic studies in sweetpotato (Mwanga *et al.*, 2002; Lin *et al.*, 2007; Grüneberg *et al.*, 2009a; Cervantes-Flores *et al.*, 2011; Todd, 2013)

**The objectives of this study were therefore to:**

1. estimate narrow sense heritability for sugars, dry matter and β-carotene in addition to yield
2. estimate genetic gain from selection
3. estimate General combining (GCA) ability and specific combining ability (SCA) components for the traits under consideration

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## 6.2 MATERIALS AND METHODS

### 6.2.1 Parental genotype selection

Based on the results of germplasm evaluation (Chapter 4) and G x E analysis (Chapter 5) an initial number of twenty genotypes were selected based on their sugar, dry matter and β-carotene levels. These included five local and fifteen imported genotypes. The local germplasm accessions consisted one orange-fleshed variety and four genotypes with dry matter content ranging from high to low and were yellow or white-fleshed. The exotic clones included non-sweet, low-sweet, sweet and high β-carotene lines, low in dry matter and orange-fleshed. An isolated crossing block was established in BNARI in January of 2012 under irrigation (Plate 6.1). Flowering began in March and continued through October. Upon trellising and grafting of non-flowering genotypes on to *Ipomoea setosa* root stocks, seven of these clones produced either very scanty or no flowers and were therefore eliminated from the crossing block. The only clone classified as non-sweet among the parents failed to flower.

**Plate 6. 1: Isolated crossing block with 20 genotypes established in BNARI**

### 6.2.2 Identification of cross compatible clones

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The genotypes that flowered were used in a 13 x13 diallel mating design with the aim of identifying cross compatible clones. A series of reciprocal crosses in all combinations were carried out between March and June 2012. After over 400 individual paired crosses, those that produced no fruits were classified as incompatible. Six females and five males were identified as compatible and used in subsequent hybridization.

### 6.2.3 Mating strategy

The six females identified included three local varieties that were cream or yellow fleshed, low to intermediate sweet and were high in dry matter. The remaining three were exotic clones from USDA germplasm repository. Two of these were also low sweet, cream and yellow fleshed with high dry matter content, while the third was orange-fleshed, sweet and intermediate dry matter. The male parents, W-248 was low sweet; J/7-13 was intermediate sweet while the remaining three were sweet, orange-fleshed and had low dry matter (Table 6.1). A second crossing block was established in April 2012. Each parent was replicated 5 times in large plastic pots in each crossing block. The plants were well irrigated and maintained properly to ensure good plant health and adequate flowering. They were subsequently mated in a 6 x 5 North Carolina mating design 2 (NCII) with the aim of generating 30 $F_1$ families.

Standard procedures for sweetpotato crossing were employed. The evening before making crosses, mature but unopened flower buds of both male and female parents were covered with short pieces of drinking straw to prevent open pollination. Crossing began from 6.00am and continued until 9.30am. Female flowers were emasculated before pollination. After pollination, flower corollas were tied to prevent natural pollination by insects. Every controlled cross was labeled with the female and male parent, the date of crossing and the initials of the breeder or technician who carried out the cross.

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**Table 6. 1: Characteristics and origin of parental genotypes involved in the NCII design at the BNARI green house research unit, Ghana**

| Female parents | code | origin | characteristics | Male parents | code | origin | characteristics |
|---|---|---|---|---|---|---|---|
| 1 Daak/08/007 | P2 | local | IS, HDM, YF | 1 J/7-13 | P4 | USDA | IS, LDM, ORF |
| 2 Kadzie | P9 | Local | LS, HDM, YF | 2 MD 807 | P7 | USDA | S, LDM, ORF |
| 3 Hi-starch | P12 | Released (introduced from Japan) | LS, HDM, CF | 3 MD-607 | P11 | USDA | S, LDM, ORF |
| 4 Yellow sunflower | P5 | USDA | IS, HDM, YF | 4 W-248 | P15 | USDA | LS, LDM, ORF |
| 5 Pelican processor | P20 | USDA | LS, HDM, YF | 5 MD-844 | P19 | USDA | S, LDM, ORF |
| 6 W-115 | P10 | USDA | S, LDM, ORF | | | | |

S = High sugar; IS = intermediate sugar: LS = low-sugar; LDM = low dry matter; HDM = high dry matter; Cf = cream fleshed; YF = yellow-fleshed; ORF = orange-fleshed

The various steps employed in sweetpotato hybridization are shown in Plate 6.2. Developing fruits from successful crosses were visible within two weeks after hybridization and matured between 4-5 weeks after hybridization (Plate 6.3). Due to incompatibility problems, one female line (Pelican processor) generated only two seeds in cross combination with the male line MD-807. These two seeds failed to germinate, resulting in 29 $F_1$ instead of 30 $F_1$ families.

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**Plate 6. 2: Steps involved in sweetpotato hybridization: 1 = Mature, ready to open bud; 2 = Mature buds covered with pieces of drinking straw; 3 = expanded and elongated buds ready for hybridization; 4 = emasculation of female parts; 5 = dusting of pollen on stigma; 6 = tips of pollinated flowers tied to prevent pollination by insects**

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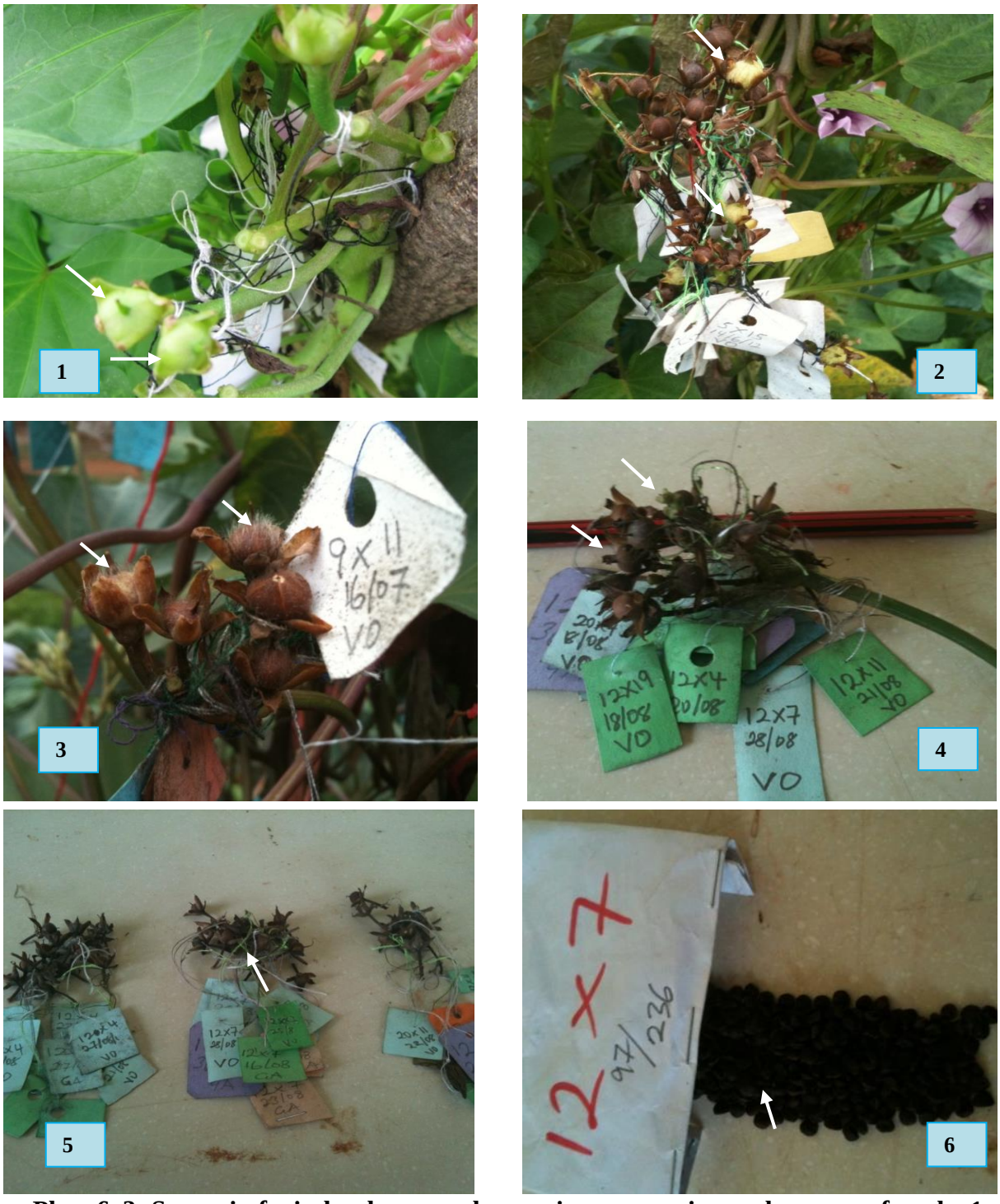


**Plate 6. 3: Stages in fruit development, harvesting, processing and storage of seeds; 1 = young developing fruits; 2 = 3-4 weeks old fruits; 3 = mature and dry fruits ready for harvest; 4 = Harvested dried fruits; 5. Harvested fruits sorted for hand threshing; 6 = seeds ready for packaging and storage**

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### 6.2.4 Seed processing and germination

Successful crosses were harvested between 28-35 days after crossing to prevent shattering. Capsules were hand threshed to extract seeds. Seeds were soaked in water with a drop of tween-20. Seeds that floated were discarded and those that sank were dried and stored in well-labeled envelopes containing naphthalene balls, until ready to use. Prior to germination, seeds were scarified with sand paper and sown directly in plastic trays containing a mixture of top soil and sawdust in a ratio of 3:1. There was 98-100 % germination within one week of sowing.


**Plate 6. 4: Germination and vine multiplication: 1 = seedlings at two weeks after germination in plastic trays; 2 = Seedlings at 4weeks of growth; 3 = transplanted seedlings in 6liter plastic bags; 4 = trellised plants at 3 months after germination.**

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After six weeks of growth in the plastic trays, seedlings were transplanted into 6 liter plastic bags in an irrigated screen house. Plants were trellised during vine multiplication to prevent spreading and for ease of identification of individual clones. Within three months after transplanting, each $F_1$ plant had produced enough vines for progeny evaluation trial (Figure 6.4).

### 6.2.5 Field evaluation

The trial was planted in March 2013, just before the onset of the major rains in two contrasting locations. In formation on geographic location, rainfall and soil is presented in Appendices 5.1, 5.2 and 6.1. The first location was in BNARI research farm in Greater Accra region; a coastal Savanna region, while the second was in the research field at the CRI in Kumasi; a moist semi-deciduous agroecology. In both locations the field was irrigated because the rains had delayed. Irrigation continued into the growth period due to poor rainfall in 2013. Twenty $F_1$ plants per cross were selected to represent each cross. Forty-two entries comprising the twenty-nine $F_1$ families, their 11 parents and two checks were planted in an α-lattice design. The entries were randomized within each block of the lattice and the check varieties were planted in each block to give a 10 x 5 lattice (Appendix 6.2). Locations were treated as replications for the purpose of statistical analysis in accordance with the accelerated breeding strategy developed by CIP (Grüneberg *et al.,* 2010). Each experimental plot was two 9 m row ridges with an inter-row spacing of 1 m and 30 cm between plants. Experimental plots were 1.5 m apart and contained the selected 20 $F_1$ progenies of a cross. Three vines per hill were planted for each individual. Hills were planted at a plant density of 33,000 plants per ha. No fertilizers or pesticides were applied but normal agronomic practices were observed.

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### 6.2.6 Data collection

At harvest, the following data were collected; storage root yield (RY), weight of individual storage roots (Irtwt), weevil damage (WED) and biomass yield. Harvest index was calculated as a ratio of commercial yield to total biomass. Storage root dry matter (DM) was determined as described in chapter 4. NIRS procedures for quantification of sugars and β-carotene are as described in Chapter 4. Cooked root sugars were determined after baking in an oven at 204 $^0$C for 60 minutes (Kays *et al.*, 2005).

### 6.2.7 Data analysis

Dry matter and β-carotene analysis were based on raw root data while analysis of sugars was based on cooked roots. General analyses of variance were performed with PROC GLM of SAS 9.3 for all yield and quality data of $F_1$s, their parents and checks for all the traits. Offspring means were regressed on mid-parent values using Genstat edition 12 to estimate narrow sense heritability as described by Holland *et al*. (2003). Standard errors for the slope were also estimated. Means were predicted using fixed model in Genstat while variance components were generated with the Restricted Maximum Likelihood (REML) tool in Genstat using random model. The generated variances were then used to estimate narrow sense heritability.

Genetic Advance (GA) was estimated as follows;

$$GA = ih^2GCV$$

Where i=1.76 (10% selection intensity), GCV= genotypic coefficient of variation estimated as $\sqrt{\sigma^2 g}/\ \overline{x}$; where $\sigma^2 g$ = genotypic variance, and $\overline{x}$ = mean and $h^2$ = narrow sense heritability estimate.

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Analyses of variance of NCII were conducted for offspring and parent values with PROC GLM of SAS. Main effects due to female and male parents are independent estimates of GCA while male x female interaction effects represent SCA variance. The ANOVA table for estimating GCA and SCA effects is shown below (Comstock and Robinson, 1948).

**Table 6.2: ANOVA table for NCII analysis**

| Source | df | Mean square | Expected MS |
|---|---|---|---|
| Rep | r-1 | MSr | $\sigma_e^2 + fm\sigma_r^2$ |
| $GCA_{Male}$ | m-1 | MSm | $\sigma_e^2 + r\sigma_{fm}^2 + rf\sigma_m^2$ |
| $GCA_{Female}$ | f-1 | MSf | $\sigma_e^2 + r\sigma_{fm}^2 + rm\sigma_f^2$ |
| SCA =Male x female | (m-1)(f-1) | MSmf | $\sigma_e^2 + r\sigma_{fm}^2$ |
| Error | mf(r-1) | MSe | $\sigma_e^2$ |

Where:

$\sigma_e^2$ = variance within full sibs = environmental variance

$\sigma_f^2$ = variance among females = GCAf variance

$\sigma_m^2$ = variance among males = GCAm variance

$\sigma_{fm}^2$ = variance due to interaction between females and males = SCA variance

$\sigma_r^2$ = variance due to replication (Location)

Standard errors (SE) for general and specific combining ability were calculated as follows;

SE females = (MSe /rm) ½

SE males = (MSe /rf) ½

SE females x Males = (MSmf /r) ½

Where: r = replication (two locations in this respect); f = number of females and m = number of males (Groz *et al.*, 1987)

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Critical difference (C.D) was calculated to test for significance of GCAs and SCAs as follows:

C.D = SE x t (tabulated).

If the absolute effect of GCA or SCA is greater than the C.D., it is considered significantly different from zero (Mohammed, 2009).

## 6.3 RESULTS

### 6.3.1 Mean performance of genotypes

#### 6.3.1.1 Mean performance of $F_1$ populations and their parents across the two locations

As shown in Table 6.3, significant differences were observed between the two locations (representing replications) with respect to all traits except glucose. The trial conducted in BNARI consistently had higher values for yield, yield components and weevil damage, but gave lower values for all root quality traits except starch and glucose.

In the case of yield, offspring yields were higher than those of both parents (Table 6.4). In terms of quality traits, offspring values were intermediate between that of female and male parents except for fructose where offspring had a lower mean and maltose where offspring mean was higher than both parents. The offspring value for yield was about 27% higher than the mid-parent value and was also about 0.14 % and 14 % higher than their parents for individual root weight and harvest index. Offspring recorded a reduction of 4 %, 29 % and 6 % for, weevil damage, fructose and β-carotene respectively in comparison to mid-parent values. Offspring however, had 12 %, 0.14 %, 10 %, 1.8 %, 10 % and 5 % higher levels for dry matter, starch, glucose, sucrose, maltose, and total sugars respectively, than the mid-parent values. Female parents were significantly ($P < 0.0001$) higher in, yield dry matter and starch but lower in sugars and β-

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carotene, while males were significantly (P< 0.001) higher in maltose, total sugars and β-carotene.

#### 6.3.1.2 Mean performance of the 11 parents involved in the NCII analysis

Table 6.5 shows mean performance of the 11 parents used in the NCII analysis. The boldened fonts indicate highest values recorded by females and males for all traits while green fonts represent lowest values for sugars. The highest yielding female and male were Pelican Processor and MD-844 with mean yields of 19.05 t/ha and 12.68 t/ha respectively. Mean yields for all genotypes were generally lower in this trial than the germplasm evaluation trial carried out in 2011(chapter 4). Rainfall in 2013 was poor compared to 2011(Appendix 5.2 and 6.1) and may have affected yield performance for all genotypes. Viral incidence by observation, was much higher (data not recorded) for the exotic clones, namel: W-115, MD-607, MD-807, MD-844, W-248 and J/7-13 and Yellow Sunflower, than the local varieties. This high incidence of viral infection may have further decreased the yields of exotic clones. Pelican Processor - an exotic female, however appeared healthier and yielded better than the others.

Kadzie was the highest for dry matter among the females with a mean value of 40.92 %, while male parent MD-807 had the highest dry matter of about 28.14 % among the males. The lowest means for fructose and glucose was recorded by the female lines Kadzie with an average of 0.03 % and 0.32 % respectively. Hi Starch and Kadzie recorded lowest amounts of sucrose with 12.54 % and 12.96 % respectively. These two varieties had the lowest means of 5.27 % and 9.70 % for maltose and were also the lowest for total sugars with means of 18.56 % and 25.31 % respectively. The female parent W-115 and male parents MD-807 and MD-607 were the highest for total sugars with a mean of about 42 % for W-115 and 44 % for both male parents. Among the males, the lowest mean for maltose was recorded by W-248, which was also the male line

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with lowest total sugars followed by male J/7-13. With respect to β-carotene the highest mean of about 32 mg/100 g dry weight occurred in the female line W-115 followed by the male line MD-607 with a mean value of 29.7 mg/100g dry weight respectively. The high coefficient of variation observed for some traits could be as a result of variable conditions in the two locations.

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**Table 6.3: Mean performance of 29 F1 populations and their 11 parents evaluated in 2013 in two locations in Ghana**

| | Agronomic traits | | | | | Quality traits | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **RY** | **Irtwt** | **Hi** | **WED** | **DM** | **Starch** | **Fru** | **Glu** | **Sucr** | **Malt** | **Tsugars** | **BC** |
| **BNARI** | 15.2 | 237.2 | 42.71 | 4.51 | 29.83 | 58.05 | 0.69 | 3.19 | 14.91 | 15.89 | 34.62 | 15.01 |
| **CRI** | 7.01 | 213.1 | 40.42 | 0.67 | 31.78 | 56.32 | 0..91 | 2.42 | 15.4 | 18.22 | 36.95 | 16.03 |
| **Grand mean** | 11.105 | 225.15 | 41.55 | 2.59 | 30.81 | 57.19 | 0.8 | 2.81 | 15.16 | 17.01 | 35.64 | 15.52 |
| **SED** | 0.87 | 7.05 | 1.07 | 0.23 | 0.27 | 0.81 | 0.03 | 0.25 | 0.38 | 0.38 | 0.48 | 1.87 |
| **CV %** | 39.11 | 22.01 | 18.82 | 67.83 | 6.05 | 3.05 | 30.25 | 66.26 | 13.88 | 16.25 | 10.23 | 20.45 |
| **LSD** | 1.83 | 5.2 | 2.03 | 0.93 | 1.93 | 1.71 | 0.34 | 0.98 | 1.21 | 1.21 | 1.36 | 2.68 |
| **Significance of entries** | *** | ** | * | *** | * | * | NS | NS | NS | *** | *** | NS |

***if P ≤ 0.05, ** if P ≤ 0.01, *** if P ≤ 0.001. RY = root yield (t/ha); Irtwt = individual root weight (g); HI = harvest index; WED = weevil damage; DM = root dry matter (%); Fru = fructose (%); Glu = glucose (%); Sucr = sucrose (%); Malt = maltose (%); Tsugar = total sugars in cooked roots (%); BC = β –carotene (mg/100g dry weight). All sugar values are from cooked roots**

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**Table 6.4: Comparison of mean performance of parents, their offspring and mid-parent values of the evaluation carried out in 2013 at two locations in Ghana**

| Generation | Agronomic traits | | | | Quality traits | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | RY | Irtwt | Hi | WED | DM | Starch | Fru | Glu | Sucr | Malt | Tsugars | BC |
| offspring | 12.95 | 225.40 | 42.26 | 2.46 | 33.23 | 57.35 | 0.63 | 2.75 | 15.16 | 16.85 | 35.19 | 15.02 |
| Female parent | 11.45 | 225.90 | 42.12 | 2.64 | 34.59 | 58.72 | 0.69 | 2.08 | 14.25 | 13.70 | 30.73 | 6.68 |
| Male parent | 8.92 | 224.26 | 40.26 | 2.50 | 24.64 | 55.51 | 1.08 | 2.90 | 15.51 | 16.74 | 36.24 | 25.36 |
| Mid-parent | 10.18 | 225.08 | 41.19 | 2.57 | 29.62 | 57.12 | 0.89 | 2.49 | 14.88 | 15.22 | 33.48 | 16.02 |
| % increase/mid parent | 27.20 | 0.14 | 2.5 | -4.28 | 12.21 | 0.41 | -29.05 | 10.44 | 1.86 | 10.70 | 5.10 | -6.24 |
| All entries | ** | ** | * | *** | * | * | * | *** | * | *** | *** | *** |

***if P ≤ 0.05, ** if P ≤ 0.01, *** if P ≤ 0.001. RY = root yield (t/ha); Irtwt = individual root weight (g); HI = harvest index; WED = weevil damage; DM = root dry matter (%); Fru = fructose (%); Glu = glucose (%); Sucr = sucrose (%); Malt = maltose (%); Tsugar = total sugars in cooked roots (%); BC = β –carotene (mg/100g dry weight). All sugar values are from cooked roots.**

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**Table 6.5: Mean performance for storage root yield and root quality traits of the 11 parents used in the NCII mating design and evaluated in 2013 in two locations in Ghana**

| | Yield traits | | | Quality traits | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **Parent** | **RY** | **Irtwt** | **DM** | **Starch** | **Fru** | **Glu** | **Sucr** | **Malt** | **Tsugars** | **BC** |
| **Females** | | | | | | | | | | |
| **W-115** | 5.17 | 212.23 | 24.02 | 54.81 | 0.84 | **2.70** | 15.02 | **24.07** | **42.63** | **32.10** |
| **HI Starch** | 13.12 | **255.67** | 33.13 | 60.89 | 1.01 | 2.06 | 12.54 | **9.70** | 25.31 | 1.28 |
| **Daak 07/008** | 13.06 | 226.15 | 35.15 | 59.65 | 0.58 | 1.83 | 14.45 | 11.71 | 28.57 | 1.56 |
| **Pelican Processor** | **19.05** | 239.38 | 35.56 | 58.13 | 0.57 | 2.08 | 15.20 | 13.98 | 31.83 | 2.15 |
| **Yellow Sunflower** | 7.56 | 168.95 | 38.76 | 52.69 | 1.11 | 3.51 | 15.35 | 17.47 | 37.44 | 2.88 |
| **Kadzie** | 11.12 | 253.01 | **40.92** | **66.15** | **0.03** | **0.32** | 12.96 | **5.27** | **18.58** | 0.15 |
| **Males** | | | | | | | | | | |
| **MD-607** | 6.72 | 237.63 | 21.31 | 57.56 | 0.84 | 2.32 | 14.58 | **26.52** | **44.26** | **29.70** |
| **W-248** | 5.32 | 208.30 | 24.95 | 58.76 | 1.01 | 2.36 | 13.78 | 11.71 | **28.86** | 24.42 |
| **MD-844** | **12.68** | **254.78** | 22.89 | **60.41** | **0.38** | **1.64** | **12.73** | 17.88 | 32.62 | 25.91 |
| **J/7-13** | 4.21 | 230.46 | 25.91 | 56.05 | 1.04 | 2.82 | 15.26 | 12.03 | 31.15 | 20.87 |
| **MD-807** | 15.70 | 190.11 | **28.14** | 44.78 | **2.15** | **5.34** | **21.22** | 15.58 | **44.29** | 25.89 |
| **SE** | **3.22** | **24.81** | **1.00** | **0.86** | **0.095** | **0.91** | **1.05** | **1.80** | **1.22** | **1.52** |
| **CV %** | **49.79** | **22.01** | **6.05** | **3.04** | **30.25** | **66.27** | **13.88** | **16.25** | **10.25** | |

**Note: Bolded fonts represent highest values for all traits for male and female groups while green fonts are the lowest values for sugar traits among females and males;RY = root yield (t/ha); Irtwt = individual root weight (g); HI = harvest index; WED = weevil damage; DM = root dry matter (%); Fru = fructose (%); Glu = glucose (%); Sucr = sucrose (%); Malt = maltose (%); Tsugars = total sugars in cooked roots (%); BC = β –carotene (mg/100g dry weight).**

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#### 6.3.1.3 $F_1$ family average performance for yield parameters and quality attributes

As depicted in Table 6.6, the families exhibited variability for the studied traits. Yield varied from as low as 5.03 t/ha for the W-115 x MD-607 family to as high as 26.52 t/ha for the Hi Starch x MD-844 family, which in case of the latter was much higher than the yield of both parents. Individual root weight ranged from 103.42 g for Yellow Sunflower x MD-807 family to 357.56 g for the Hi Starch x MD-844 family. Families that performed best were mostly from the hybrid families involving the female parent, Pelican Processor. Six $F_1$ families, namely Hi Starch x MD-844, Daak 07/008 x W-248, Pelican Processor x MD-607, Pelican Processor x W-248, Pelican Processor x J/7-13 and Kadzie x J/7-13, with yields between 19.54 and 26.52 t/ha, performed better than Pelican Processor whose yield was 19.05 t/ha

Dry matter ranged from 29.07 % in W-115 x MD-607 family to 37.21 % in Kadzie x W-248 family while mean starch ranged from 50.09 % for W-115 x MD-807 family to 62.88 % for Kadzie x J/7-13 family respectively. The highest mean offspring values for dry matter and starch were also higher than the parental means (Table 6.5 and 6.6). Six $F_1$ families namely Yellow Sunflower x MD-607, Yellow Sunflower x MD-844, Yellow Sunflower x MD-807, Kadzie x 607, Kadzie x W-248 and Kadzie x J/7-13, had above 35 % dry matter and exhibited mid-parent heterosis. Fructose levels for all families were relatively low compared to the other sugars, ranging from 0.28 % to 1.47 % for families Daak 07/008 x MD-807 and W-115 x MD-807 respectively. The lowest offspring mean for fructose was lower than fructose levels in both Daak 07/008 and MD-807 and the highest offspring mean was also higher than that of W-115 and MD-807 (Table 6.5 and 6.6). Most families had mean glucose levels ranging from 1 – 2 % but a high mean of 10.32 % was observed for Daak 07/008 x MD-844 family, a value much higher than that expressed in both parents. With respect to sucrose the lowest mean of 10.27 % was expressed by

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family Daak 07/008 x MD-844, while families W-115 x J/7-13, W-115 x MD-807, Daak 07/008 x MD-607 had the highest of about 17 %. The lowest offspring mean for sucrose was also lower than that for both parents while the highest offspring mean values were higher than for their parents. Maltose was the most abundant sugar in cooked roots and ranged from 10.30 % (lower than parental values) in family Yellow Sunflower x J/7-13 to 21.46% in family W-115 x MD-807, which was much higher than the parental values. The lowest mean for total sugars of about 26 % was observed in family Yellow Sunflower x J/7-13 while the highest mean of 45.57 mg/dry weight was from W-115 x MD-807. Eight $F_1$ families, namely; W-115 x MD-807, Daak 07/008 x J/7-13, Yellow Sunflower x W-248, Yellow Sunflower x MD-844, Yellow x MD-807, Yellow Sunflower x J/7-13, Kadzie x J/7-13 and Kadzie x W-248, exhibited mid-parent heterosis in the negative direction, in that their total sugars ranged from 26.13 % – 32. 95 % which was lower than the mid-parent value of 33.48 %. For β-carotene the range was from 8.75 mg/100g dry weight to as high as 29.14 mg/100 g dry weight in families Kadzie x J/7-13 and W-115 x J/7-13 respectively. No $F_1$ family obtained higher β-carotene levels than the best β-carotene parent (W-115) but 11 $F_1$ families were higher in β-carotene than the mid-parent value of 16.02 mg/100 g dry weight.

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**Table 6.6: Average performance for yield parameters and quality attributes of the 29 $F_1$ families evaluated in 2013 in two locations in Ghana**

| | Yield traits | | | Quality attributes | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **Family** | **Yield** | **Irtwt** | **Dry matter** | **Starch** | **Fructose** | **Glucose** | **Sucrose** | **Maltose** | **Tsugars** | **β-carotene** |
| **W-115 x MD-607** | 5.03 | 219.59 | 29.07 | 56.23 | 0.59 | 2.52 | 16.39 | 18.08 | 36.20 | 19.45 |
| **W-115 x W-248** | 5.22 | 189.31 | 33.34 | 56.13 | 0.70 | 2.84 | 15.80 | 14.20 | 32.95 | 19.19 |
| **W-115 x MD-844** | 12.09 | 257.51 | 30.30 | 51.36 | 1.12 | 4.25 | 16.90 | 17.76 | 39.44 | 25.28 |
| **W-115 x J/7-13** | 7.44 | 239.37 | 31.51 | 52.67 | 1.00 | 3.75 | 17.15 | **12.69** | 33.97 | **29.14** |
| **W-115 x MD-807** | 9.56 | 155.38 | 32.46 | 50.09 | **1.47** | 4.55 | 17.26 | **21.46** | **45.57** | 19.58 |
| **Hi Starch x MD-607** | 10.87 | 253.97 | 33.77 | 56.39 | 0.43 | 2.06 | 15.88 | 19.13 | 37.17 | 16.72 |
| **Hi Starch x W-248** | 13.29 | 206.26 | 32.91 | 54.86 | 0.80 | 3.07 | 16.07 | 16.70 | 35.47 | 16.00 |
| **Hi Starch x MD-844** | **26.52** | **357.56** | 32.55 | 57.44 | 0.71 | 2.65 | 14.79 | 19.22 | 37.66 | 19.11 |
| **Hi Starch x J/7-13** | 9.04 | 209.81 | **34.04** | 56.64 | 0.54 | 2.42 | 14.57 | 20.25 | 37.46 | 14.82 |
| **Hi Starch x MD-807** | 12.06 | 250.77 | 33.62 | 57.41 | 0.56 | 2.18 | 15.25 | 17.45 | 36.25 | 11.29 |
| **Daak 07/008 x MD-607** | 7.17 | 232.43 | 31.48 | 53.65 | 0.36 | 2.37 | **17.48** | 19.82 | 39.69 | 13.71 |
| **Daak 07/008 x W-248** | 19.92 | 241.66 | 31.09 | 54.15 | 0.52 | 2.44 | 16.68 | 18.43 | 39.25 | 14.03 |
| **Daak 07/008 x MD-844** | 17.93 | 225.75 | 30.24 | 53.31 | 0.94 | **10.32** | 10.27 | 19.12 | 41.33 | 16.19 |
| **Daak 07/008 x J/7-13** | 13.58 | 241.10 | **31.07** | 58.98 | 0.36 | 1.72 | 14.63 | **12.35** | **29.41** | 10.82 |
| **Daak 07/008 x MD-807** | 12.70 | 189.80 | **34.06** | 58.03 | **0.28** | 2.07 | 14.98 | 17.54 | 35.38 | 13.23 |
| **SED** | 3.66 | 10.4 | 3.94 | 3.74 | 0.68 | 1.96 | 2.42 | 2.42 | 2.72 | 5.36 |
| **CV %** | **49.78** | **22.01** | **6.05** | **3.04** | **30.25** | **66.27** | **13.88** | **16.26** | **14.38** | **20.47** |

**Note: Bolded fonts represent highest values for all traits while green fonts are the lowest values for sugar; IRWT = individual root weight**

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**Table 6.6 continued: Average performance for yield parameters and quality attributes of the 29 $F_1$ families evaluated in 2013 in two locations in Ghana**

| | Yield traits | | | Quality attributes | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **Family** | **Yield** | **Irtwt** | **Dry matter** | **Starch** | **Fructose** | **Glucose** | **Sucrose** | **Maltose** | **Tsugars** | **β-carotene** |
| **Pelican Processor x MD-607** | 21.54 | 254.57 | 32.03 | 54.47 | 0.72 | 3.01 | 15.26 | 21.30 | 38.92 | 16.49 |
| **Pelican Processor x W-248** | 21.78 | 190.88 | 32.87 | 57.27 | 0.56 | 2.27 | 14.83 | 16.81 | 36.79 | 14.91 |
| **Pelican Processor x MD-844** | 18.28 | 236.93 | **34.28** | 55.38 | 0.88 | 3.32 | 15.35 | 18.18 | 37.50 | 17.14 |
| **Pelican Processor x J/7-13** | 23.46 | **275.14** | 31.75 | 55.06 | 0.67 | 3.09 | 15.35 | 18.56 | 35.58 | 17.85 |
| **Yellow Sunflower x MD-607** | 9.28 | 200.37 | **35.00** | 56.54 | 0.62 | 2.43 | 15.49 | 16.20 | 33.73 | 12.03 |
| **Yellow Sunflower x W-248** | 5.79 | 177.84 | **35.31** | **60.64** | 0.50 | 1.80 | 13.98 | 12.77 | **28.10** | 10.78 |
| **Yellow Sunflower x MD-844** | 13.45 | 225.22 | **34.15** | **61.01** | 0.54 | 1.76 | 13.63 | 11.45 | **27.18** | 15.28 |
| **Yellow Sunflower x J/7-13** | 7.93 | 137.93 | 33.63 | **61.16** | 0.53 | 1.97 | 13.53 | **10.30** | 26.13 | 13.22 |
| **Yellow Sunflower x MD-807** | 6.58 | 103.42 | **36.61** | 59.30 | 0.73 | 2.25 | 13.60 | 14.67 | 30.87 | 10.34 |
| **Kadzie x MD-607** | 10.43 | 264.86 | **35.64** | 58.38 | 0.51 | 1.75 | 14.99 | 18.56 | 35.40 | 10.28 |
| **Kadzie x W-248** | 8.26 | 243.82 | **37.21** | **60.39** | 0.55 | 1.56 | 14.63 | 13.82 | 29.66 | 9.23 |
| **Kadzie x MD-844** | 12.61 | 225.72 | 32.85 | 56.54 | 0.56 | 2.12 | 16.44 | 18.58 | 38.71 | 10.59 |
| **Kadzie x J/7-13** | **19.54** | **279.43** | **36.97** | **62.88** | 0.25 | **1.31** | **12.41** | 14.25 | 27.69 | 8.75 |
| **Kadzie x MD-807** | 14.11 | 251.20 | 33.94 | 57.25 | 0.39 | 1.80 | 16.00 | 19.06 | 37.07 | 10.10 |
| **SED** | 3.66 | 10.4 | 3.94 | 3.74 | 0.68 | 1.96 | 2.42 | 2.42 | 2.72 | 5.36 |
| **CV %** | **49.78** | **22.01** | **6.05** | **3.04** | **30.25** | **66.27** | **13.88** | **16.26** | **14.38** | **20.47** |

**Note: Bolded fonts represent highest values for all traits while green fonts are the lowest values for sugar; IRWT = individual root weight**

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### 6.3.2 Estimation of genetic parameters

#### 6.3.2.1 Narrow Sense heritability estimates and genetic advance

Narrow sense heritability ($h^2$) estimates obtained from parent offspring regression was higher than those obtained from variance components for all agronomic traits except yield, while estimates from variance components were higher for all quality traits apart from sucrose (Table 6.7). Both methods gave moderate to high estimates for most traits except glucose. Harvest index had the highest heritability among agronomic traits with values of 0.62 and 0.55 respectively by regression and variance components methods. For yield, individual root weight and weevil damage, estimates of 0.27, 0.48 and 0.49 were obtained using regression, while 0. 51, 0.46 and 0.28 were obtained for variance components method respectively. For quality traits, very high heritability estimate of 0.80 was observed for β-carotene using variance method, while a moderate estimate of 0.40 was obtained using regression of offspring values on mid-parent values. Parent-offspring regression gave moderate estimates of 0.38, 0.40, 0.39, 0.24 and 0.36 respectively, for dry matter, starch, fructose maltose and total sugars respectively while relatively high estimates of 0.56, 0.53, 0.45, 0.59, and 0.48 respectively were obtained with variance components method. Regression based heritability estimates of 0.05 and 0.31 were obtained for glucose and sucrose but these were not significant.

As shown in Table 6.7, phenotypic coefficient of variation (PCV %) were higher than the genotypic coefficient of variation (GCV %) suggesting the importance of the contrasting environments used for evaluating the studied traits. Moderate genetic advance of 30.66 %, 12.5 %, 21.75 %, 10.67 and 17.54 % were obtained for yield, individual root weight, harvest index, fructose, maltose, total sugars and β-carotene respectively. Comparatively, dry matter, starch,

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glucose and sucrose had low genetic advance of 4.69 %, 3.7 %, 5.9 % and 1.15 % respectively. Genetic advance for weevil damage was 14.71 %

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**Table 6.7: Phenotypic and genotypic variances, phenotypic and genotypic coefficient of variation, heritability and predicted genetic advance for the different traits of the genotypes evaluated in 2013 at two locations in Ghana**

| | Agronomic traits | | | | Quality attributes | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Genetic Parameters** | **Yield** | **irtwt** | **Hi** | **WED** | **Dry matter** | **Starch** | **Fructose** | **Glucose** | **Sucrose** | **Maltose** | **Total sugars** | **β-carotene** |
| **$\sigma^2p$** | **42.025** | **2534.5** | **69.19** | **2.07** | **4.57** | **9.52** | **0.071** | **2.76** | **2.63** | **9.88** | **23.54** | **24.67** |
| **$\sigma^2g$** | **21.25** | **1175** | **37.73** | **0.58** | **2.55** | **5.05** | **0.03** | **0.401** | **0.41** | **5.84** | **13.7** | **19.68** |
| **$h^2$ from regression** | **0.27 ±0.18*****| **0.48 ±0.13*****| **0.62 ±0.09*****| **0.49 ±.09*****| **0.38 ±0.09*****| **0.40 ±0.11*****| **0.39 ±0.13*****| **0.05 ±0.45 ns** | **0.31 ±0.18 ns** | **0.24 ±0.08*****| **0.36 ±0.10*****| **0.40 ±0.08*****|
| **$h^2$ from variance** | **0.51** | **0.46** | **0.55** | **0.28** | **0.56** | **0.53** | **0.45** | **0.15** | **0.16** | **0.59** | **0.58** | **0.80** |
| **$\overline{X}$** | **13.38** | **223.7** | **42.21** | **2.58** | **33.26** | **59.71** | **0.66** | **2.81** | **15.16** | **17.01** | **35.54** | **15.02** |
| **PCV %** | **0.48** | **0.23** | **0.20** | **0.56** | **0.06** | **0.05** | **0.40** | **0.60** | **0.11** | **0.18** | **0.14** | **0.14** |
| **GCV %** | **0.34** | **0.15** | **0.15** | **0.30** | **0.05** | **0.04** | **0.27** | **0.23** | **0.04** | **0.14** | **0.10** | **0.12** |
| **Genetic Advance %** | **30.66** | **12.50** | **13.97** | **14.71** | **4.69** | **3.70** | **21.75** | **5.90** | **1.15** | **14.75** | **10.67** | **17.54** |

**Note: Heritability estimates generated from variance components were used to calculate genetic advance; *** = significant at P < 0.001; ns = not significant**

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### 6.3.2.2 General Combining Ability effects

The analysis of variance shown in Table 6.8 reveals significant GCA mean squares for most traits except for glucose, sucrose and weevil damage. Replication (which in this study represented two locations) was also significant for most characters with the exception of harvest index, starch, sucrose, glucose and β-carotene. The GCA effects were substantially greater than SCA effects, in that the ratio of variance of GCA to SCA ($\sigma_{gca}^2 / \sigma_{sca}^2$) effects were 7.4, 6.4, 8.7, 2.7, 8.9, 7.1, 6.1, 2.8, 2.8, 10.2, 9.3 and 21.8, for yield, individual root weight, harvest index, weevil damage, dry matter, starch, fructose, glucose, sucrose, maltose, total sugars and β-carotene respectively. In addition, with the exception of weevil damage, GCA variance for females were larger than for males, with ratios ($\sigma_f^2 / \sigma_m^2$) of 3.2, 1.5, 1.1, 0.2, 5.2, 5.9, 2.8, 1.03, 1.9, 1.1, 1.5 and 6.6 for yield, individual root weight, harvest index, weevil damage, dry matter, starch, fructose, glucose, sucrose, maltose, total sugars and β-carotene in that order.

The highest positive GCA effect for yield was expressed by female parent Pelican Processor followed by the male parent MD-844. The highest negative GCA effect for yield was expressed by female parent W-115 followed by female parent Yellow Sunflower. The highest positive and significant GCA effect for individual root weight was expressed by female parent Hi Starch followed by male MD-844. High positive but insignificant GCA effects were also expressed by Pelican Processor and Kadzie (both females) and MD-607 (male). Female parent, Yellow Sunflower and Male parent, MD-807 had the highest negative GCA effects for individual root weight among females and males respectively. For dry matter, GCA effect of all male lines was not significant. Females Yellow Sunflower and Kadzie had the highest and significant GCA effects for dry matter and starch. Male J/7-13 also contributed significantly to starch. The highest and significantly negative GCA effect of starch was displayed by female parent W-115. Only

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male parent MD-844 and female W-115 expressed positive and significant GCA effects for fructose. The others were either significant but negative or positive but not significant. The male parent MD-844 also had the highest positive GCA effect for glucose. With respect to sucrose and maltose female W-115 and male MD-607 expressed the highest positive GCA effects respectively. Female Yellow Sunflower and male J/7-13 gave the highest negative GCA effect for maltose. Again these two clones (J/7-13 and Yellow Sunflower) expressed the highest negative significant GCA effect for total sugars while W-115 showed the highest positive and significant GCA for the total sugars. Female W-115 displayed the highest significant positive GCA effect for β-carotene followed by male MD-844. The highest significantly negative GCA effects for β-carotene were displayed by females Kadzie and Yellow Sunflower.

#### 6.3.2.3 Specific Combining Ability effects

Even though SCA effects were not significant for most traits as revealed by the ANOVA (Table 6.8), a few hybrids showed significant SCA effects for some characters (Table 6.10). No hybrid showed significant SCA effect for yield. The Hi Starch x MD-844, displayed a high positive but insignificant SCA value of 8.30. This hybrid was the highest yielding among the $F_1$s (Table 6.6) and was also the only one that expressed significant positive SCA for individual root weight. The hybrid W-115 x MD-607 and Daak 07/008 x MD-807 had significant positive SCA effect for starch while W-115 x MD-807, Hi Starch x W-248 expressed significant negative SCA effects. For total sugars only hybrids W-115 x MD-807 showed significant positive SCA effects. The only hybrid with significant SCA for glucose and sucrose was Daak 07/008 x MD-844, which had positive SCA for glucose but negative effect for sucrose. Hybrid Daak 07/008 x MD-844 also had the highest mean of 10.32 % for glucose and the lowest mean of 10.27 % for sucrose (Table 6.6). No hybrid displayed significant SCA effect for maltose. Daak 07/008 x MD-844 had

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the highest mean for total sugars as well and displayed the highest and the only significant SCA effect for total sugars. W-115 x J/7-13 was the only hybrid with significant SCA effect for β-carotene.

### 6.3.3 Characteristics of 28 selected $F_1$ hybrids

Table 6.11 shows a list of 28 selected $F_1$ plants with desirable levels of yield, dry matter, starch, total sugars, maltose and β-carotene. Their yields ranged from 9 – 28 t/ha; dry matter ranged from 24 – 44 %, starch from 50 – 69 %, total sugars from 11 – 36 % and β-carotene from 10 – 30 mg/100 dry weights. Eight of these marked by '++', had high DM, high starch, and intermediate to high β-carotene. With the exception of Pelican Processor x MD-607 which had higher sugar levels than the lowest check variety (Blue Blue) for total sugars, the eight superior $F_1$ clones also had lower sugar levels than Blue Blue.

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**Table 6.8: Combining ability mean squares for females and males of the NCII mating design evaluated for agronomic and quality traits evaluated in 2013 across two locations in Ghana**

| | | Mean square for agronomic traits | | | | | Mean square for quality traits | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Sources** | **df** | **Yield t/ha** | **irtwt** | **Hi** | **WED** | **DM** | **Starch** | **Fructose** | **Glucose** | **Sucrose** | **Maltose** | **Tsugars** | **β-carotene** |
| **Rep/location** | **1** | **828.51*** ** | **14118.97*** | **14.64** | **212.02*** ** | **5.73ns** | **0.08ns** | **1.35*** ** | **8.60ns** | **3.48ns** | **78.79** ** | **178.81*** ** | **1.53** |
| **$GCA_f$** | **5** | **199.18** ** | **10112.49** ** | **255.36*** ** | **1.2ns** | **27.33*** ** | **57.72*** ** | **0.36*** ** | **6.86ns** | **7.66ns** | **42.62*** ** | **109.74*** ** | **188.50*** ** |
| **$GCA_m$** | **4** | **60.80ns** | **6759.31*** | **224.24** ** | **6.42ns** | **5.22ns** | **9.73*** | **0.13** ** | **6.69ns** | **3.95ns** | **38.27** ** | **73.59*** ** | **28.44*** |
| **$SCA_{mf}$** | **19** | **34.90ns** | **2619.46ns** | **55.17ns** | **2.80ns** | **3.64ns** | **9.50** ** | **0.08*** | **4.8ns** | **4.14ns** | **7.92ns** | **19.65ns** | **9.94ns** |
| **Error** | **28** | **41.55** | **2461.18** | **63.25** | **2.78** | **4.04** | **2.98** | **0.04ns** | **3.31** | **4.43ns** | **7.50** | **12.95** | **9.43** |
| **$\sigma_{gca}^2 / \sigma_{sca}^2$** | | **7.4** | **6.4** | **8.7** | **2.7** | **8.9** | **7.1** | **6.1** | **2.8** | **2.8** | **10.2** | **9.3** | **21.8** |
| **$\sigma_f^2 / \sigma_m^2$** | | **3.2** | **1.5** | **1.1** | **0.2** | **5.2** | **5.9** | **2.8** | **1.0** | **1.9** | **1.1** | **1.5** | **6.6** |
| **Total** | **57** | | | | | | | | | | | | |

***, **, *** Significant at P<0.05, P< 0.01 and p<0.001 respectively ; ns = not significant; $GCA_f$ = variation due to general combining ability of female parents, $GCA_m$ = variation due to general combining ability of male parents, SCA = variation due to specific combining ability.**

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**Table 6.9: Estimates of General Combining Ability (GCA) for agronomic and quality traits for males and females used for the NCII analysis in Ghana**

| | Yield | | Quality attributes | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **Females** | Yield | Irwt | DM | Starch | Fructose | Glucose | sucrose | Maltose | Tsugars | β-carot |
| **W-115** | **-5.079**** | -13.201 | -1.898 | **-3.380**** | **0.343**** | 0.836 | **1.540**** | -0.014 | **2.435**** | **7.509**** |
| **Hi Starch** | 1.409 | **32.238**** | 0.145 | -0.127 | -0.0249 | -0.270 | 0.154 | 1.697 | 1.610 | 0.570 |
| **Daak 07/008** | 1.312 | 0.713 | -1.645 | -1.053 | **-0.145**** | 1.036 | -0.350 | 0.599 | 1.822 | -1.423 |
| **Pelican Processor** | **8.318**** | 13.944 | -0.499 | -1.129 | 0.070 | 0.175 | 0.038 | 1.861 | 2.006 | 1.578 |
| **Yellow Sunflower** | **-4.340**** | **-56.480**** | **1.708**** | **3.052**** | -0.048 | -0.705 | -1.212 | **-3.775**** | **-5.989**** | **-2.687**** |
| **Kadzie** | 0.044 | 27.574 | **2.089**** | **2.411**** | **-0.182**** | -1.077 | -0.264** | 0.003 | -1.484 | **-5.231**** |
| **SE** | 2.038 | 15.688 | 0.636 | 0.546 | 0.061 | 0.575 | 0.666** | 0.866 | 1.138 | 0.971 |
| **C.D $_{0.05}$** | 4.175 | 32.136 | 1.302 | 1.118 | 0.125 | 1.179 | 1.363 | 1.774 | 2.330 | 1.989 |
| **Male** | | | | | | | | | | |
| **MD-607** | -2.228 | 12.198 | -0.401 | -0.734 | -0.095 | -0.392 | 0.755 | **1.996** | 1.659 | -0.238 |
| **W-248** | -0.569 | -17.139 | 0.554 | 0.566 | -0.030 | -0.416 | 0.173 | -1.397 | -1.487 | -0.995 |
| **MD-844** | **3.864**** | **29.347**** | -0.836 | -0.836 | **0.157** | **1.324**** | -0.594 | 0.532 | 1.779 | **2.246** |
| **J/7-13** | 0.555 | 5.027 | -0.072 | **1.222**** | -0.0768 | -0.371 | -0.551 | **-2.119** | **-3.483** | 0.747 |
| **MD-807** | -1.946 | **-35.322**** | 0.905 | -0.261 | 0.054 | -0.175 | 0.259 | 1.185 | 1.838 | **-2.113** |
| **SED** | 1.861 | 14.321 | 0.580 | 0.498 | 0.056 | 0.525 | 0.608 | 0.791 | 1.038 | 0.886 |
| **C.D$_{0.05}$** | 3.812 | 29.336 | 1.189 | 1.021 | 0.114 | 1.076 | 1.245 | 1.619 | 2.127 | 1.816 |

**** = significant at P < 0.05 level; C.D = critical difference; IRWT = individual root weight; DM = dry matter; Tsugars = total sugars; BC = β-carotene.**

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**Table 6.10: Estimates of Specific Combining Ability (SCA) effects of the 29 crosses from the 6x5 NCII mating design, evaluated in 2013 in two locations in Ghana**

| Crosses | Yield | IRWT | DM | Starch | Fructose | Glucose | sucrose | Maltose | Tsugars | β-carot |
|---|---|---|---|---|---|---|---|---|---|---|
| **W-115 x MD-607** | -0.609 | -4.839 | -0.401 | **3.665**** | **-0.290**** | -0.674 | -1.066 | -0.758 | -3.085 | -2.840 |
| **W-115 x W-248** | -2.082 | -5.782 | 0.554 | **2.272**** | -0.244 | -0.326 | -1.072 | -1.240 | -3.191 | -2.342 |
| **W-115 x MD-844** | 0.360 | 15.927 | -0.836 | -1.096 | -0.013 | -0.657 | 0.796 | 0.393 | 0.030 | 0.501 |
| **W-115 x J/7-13** | -0.980 | 22.109 | -0.072 | -1.849 | 0.095 | 0.541 | 0.998 | -2.025 | -0.168 | **5.868**** |
| **W-115 x MD-807** | 3.635 | -21.528 | **0.905**** | **-2.948**** | **0.443**** | 1.145 | 0.300 | 3.433 | **6.107**** | -0.836 |
| **Hi Starch x MD-607** | -1.260 | -13.901 | -0.401 | 0.572 | -0.079 | -0.025 | -0.191 | -1.417 | -1.287 | 1.373 |
| **Hi Starch x W-248** | -0.496 | -32.272 | 0.554 | **-2.252**** | 0.220 | 1.013 | 0.581 | -0.452 | 0.153 | 1.409 |
| **Hi Starch x MD-844** | 8.297 | **72.538**** | -0.836 | 1.728 | -0.054 | -1.147 | 0.076 | 0.134 | -0.923 | 1.273 |
| **Hi Starch x J/7-13** | -5.867 | -50.895 | -0.072 | -1.129 | 0.004 | 0.309 | -0.187 | 3.821 | 4.140 | -1.514 |
| **Hi Starch x MD-807** | -0.350 | 30.417 | 0.905 | 1.125 | -0.099 | -0.121 | -0.322 | -2.284 | -2.389 | -2.189 |
| **Daak 07/008 x MD-607** | -4.866 | -5.914 | -0.401 | -1.235 | -0.038 | -1.024 | 1.916 | 0.372 | 1.015 | 0.349 |
| **Daak 07/008 x W-248** | 6.235 | 32.648 | 0.554 | -2.042 | 0.056 | -0.930 | 1.698 | 2.380 | 3.729 | 1.430 |
| **Daak 07/008 x MD-844** | -0.198 | -29.740 | -0.836 | -1.477 | **0.289**** | **5.212**** | **-3.944**** | 1.132 | 2.537 | 0.352 |
| **Daak 07/008 x J/7-13** | -1.230 | 9.922 | -0.072 | 2.132 | -0.053 | -1.690 | 0.375 | -2.988 | -4.122 | -3.525 |
| **Daak 07/008 x MD-807** | 0.384 | -1.029 | 0.905 | **2.666**** | -0.264 | -1.538 | -0.088 | -1.094 | -3.465 | 1.747 |
| **SED** | 4.558 | 35.080 | 1.421 | 1.221 | 0.136 | 1.287 | 1.488 | 1.936 | 2.544 | 2.171 |
| **$C.D_{0.05}$** | 9.337 | 71.858 | 2.911 | 2.500 | 0.279 | 2.636 | 3.049 | 3.967 | 5.210 | 4.448 |

**** = Significant at P < 0.05 level; C.D = critical difference; IRWT = individual root weight; DM = dry matter; Tsugars = total sugars; BC = β-carotene.**

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**Table 6.10 continued: Estimates of specific combining ability (SCA) effects of the 29 crosses from the 6x5 NCII mating design, evaluated in 2013 in two locations in Ghana**

| Crosses | Yield | IRWT | DM | Starch | Fructose | Glucose | sucrose | Maltose | Tsugars | β-carot |
|---|---|---|---|---|---|---|---|---|---|---|
| **Pelican Processor x MD-607** | 2.504 | 2.992 | -0.401 | -0.339 | 0.109 | 0.477 | -0.695 | 0.592 | 0.060 | 0.131 |
| **Pelican Processor x W-248** | 1.084 | -31.359 | 0.554 | 1.160 | -0.117 | -0.232 | -0.538 | -0.504 | 1.083 | -0.692 |
| **Pelican Processor x MD-844** | -6.854 | -31.800 | -0.836 | 0.669 | 0.014 | -0.929 | 0.747 | -1.067 | -1.474 | -1.701 |
| **Pelican Processor x J/7-13** | 1.644 | 30.733 | -0.072 | -1.708 | 0.039 | 0.538 | 0.702 | 1.966 | 1.863 | 0.501 |
| **Yellow Sunflower x MD-607** | 2.900 | 19.216 | -0.401 | -2.458 | 0.131 | 0.776 | 0.689 | 1.126 | 2.865 | -0.060 |
| **Yellow Sunflower x W-248** | -2.243 | 26.022 | 0.554 | 0.347 | -0.053 | 0.171 | -0.241 | 1.086 | 0.386 | -0.553 |
| **Yellow Sunflower x MD-844** | 0.975 | 26.919 | -0.836 | 2.116 | -0.202 | -1.603 | 0.174 | -2.159 | -3.800 | 0.706 |
| **Yellow Sunflower x J/7-13** | -1.227 | -36.054 | -0.072 | 0.209 | 0.024 | 0.298 | 0.037 | -0.663 | 0.414 | 0.140 |
| **Yellow Sunflower x MD-807** | -0.080 | -30.216 | 0.905 | -0.170 | 0.091 | 0.386 | -0.702 | 0.413 | -0.171 | 0.119 |
| **Kadzie x MD-607** | -0.332 | -0.342 | -0.401 | 0.022 | 0.153 | 0.435 | -0.661 | -0.287 | 0.032 | 0.732 |
| Kadzie x W-248 | -4.163 | 7.955 | 0.554 | 0.741 | 0.124 | 0.268 | -0.436 | -1.642 | -2.561 | 0.432 |
| Kadzie x MD-844 | -4.244 | -56.633 | -0.836 | -1.714 | -0.048 | -0.910 | 2.143 | 1.194 | 3.228 | -1.447 |
| Kadzie x J/7-13 | 5.997 | 21.397 | -0.072 | 2.571 | -0.123 | -0.032 | -1.932 | -0.483 | -2.529 | -1.787 |
| **P9 x P7** | 3.065 | 33.510 | 0.905 | -1.577 | -0.115 | 0.269 | 0.842 | 1.021 | 1.523 | 2.422 |
| **SED** | 4.558 | 35.080 | 1.421 | 1.221 | 0.136 | 1.287 | 1.488 | 1.936 | 2.544 | 2.171 |
| **$C.D_{0.05}$** | 9.337 | 71.858 | 2.911 | 2.500 | 0.279 | 2.636 | 3.049 | 3.967 | 5.210 | 4.448 |

**** = Significant at P < 0.05 level; C.D = critical difference; IRWT = individual root weight; DM = dry matter; Tsugars = total sugars; BC = β-carotene.**

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**Table 6.11: Characteristics of the 28 clones with desirable combination of the studied traits, selected from the 29 $F_1$ families evaluated in 2013 across two locations in Ghana**

| | GENOTYPE | PLANT NO | RY (t/ha) | DM % | Starch (%) | Malt (%) | Tsugars (%) | BC mg/100 g dry wt |
|---|---|---|---|---|---|---|---|---|
| **1** | **Daak 07/008 x J/7-14** | **9** | 12.32 | **31.52** | **62.25** | 13.73 | **30.35** | **20.16** |
| **2** | **Daak 07/008 x J/7-14** | **2** | 10.99 | 29.92 | 52.71 | **6.82** | **27.46** | **16.61** |
| **3** | **Daak 07/008 x MD-807** | **6** | 9.66 | **33.02** | 54.63 | 19.19 | **36.67** | **24.07** |
| **4** | **Daak 07/008 x MD-844** | **11** | 14.99 | 30.14 | **61.28** | 13.87 | **29.35** | **17.13** |
| **5** | **Yellow Sunflower x MD-607** | **9** | 10.99 | **32.75** | 56.68 | **10.79** | **27.60** | 14.68 |
| **6** | **Yellow Sunflower x W-248** | **18** | 10.82 | **35.89** | **62.03** | 13.25 | **29.48** | 15.40 |
| **7** | **Yellow Sunflower x W-248++** | **10** | 9.99 | **40.06** | **61.65** | **1.80** | **14.26** | **18.74** |
| **8** | **Yellow Sunflower x W-248++** | **10** | 11.99 | **40.06** | **61.65** | **1.80** | **14.26** | **18.74** |
| **9** | **Kadzie x J/7-13** | **17** | **23.64** | **36.28** | **63.88** | 18.13 | **28.76** | 10.24 |
| **10** | **Kadzie x J/7-13++** | **16** | 13.32 | **38.82** | **61.33** | **10.28** | **19.18** | 14.92 |
| **11** | **Kadzie x J/7-13** | **13** | 13.32 | **35.54** | **62.23** | 19.80 | **33.37** | **17.43** |
| **12** | **Kadzie x J/7-13** | **10** | 12.32 | **34.73** | **63.17** | 15.47 | **28.78** | **17.47** |
| **13** | **Kadzie x MD-607++** | **7** | 11.66 | **34.83** | **63.91** | **8.74** | **19.50** | 12.67 |
| **14** | **Kadzie x MD-607** | **12** | 15.98 | **35.71** | **63.98** | 12.66 | **24.10** | 12.61 |
| **15** | **Kadzie x W-248** | **19** | 15.82 | **33.10** | 57.32 | **7.68** | **23.70** | **16.39** |
| **16** | **Kadzie x W-248** | **9** | 15.82 | **44.53** | **60.50** | **10.28** | **26.35** | 11.23 |
| | **SED** | | **0.87** | **0.27** | **0.81** | **0.38** | **0.48** | **1.87** |
| | **CV %** | | **39.11** | **6.05** | **3.05** | **16.25** | **10.23** | **20.45** |
| | **Mean for checks** | | **17.38** | **31.505** | **58.06** | **12.505** | **30.13** | **16.15** |

**** Blue Blue = local farmer variety used as check for dry matter and low sugar; Apomuden = released high β-carotene check; BC = β-carotene; Malt = maltose; Tsugars = total root sugars. Bolded fonts represents values that are above the mean of checks for dry matter, starch and β-carotene while green fonts represent values below the check means for the sugars; +++ The eight clones with combination of preferred quality attributes; ∞ = High DM and starch, high β-carotene but higher sugar than Blue Blue. (Table continued on next page)**

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**Table 6.11continued: Characteristics of 28 clones with desirable combination of the studied traits, selected from the 29 $F_1$ families evaluated in 2013 across two locations in Ghana**

| | GENOTYPE | PLANT NO | RY (t/ha) | DM % | Starch (%) | Malt (%) | Tsugars (%) | BC mg/100 g dry wt |
|---|---|---|---|---|---|---|---|---|
| **17** | **Kadzie x MD-844++** | **2** | **22.64** | 30.75 | **69.51** | **1.64** | **11.69** | **20.50** |
| **18** | **Kadzie x MD-844** | **3** | 9.99 | **31.09** | **63.07** | 15.17 | **27.98** | 10.32 |
| **19** | **W-115 x MD-607** | **8** | 12.32 | **32.69** | **58.08** | 15.60 | **29.55** | 14.87 |
| **20** | **W-115 x MD-607** | **8** | 12.32 | **32.69** | **58.08** | 15.60 | **29.55** | 14.87 |
| **21** | **W-115 x MD-844++** | **5** | **28.97** | **31.47** | **58.46** | **1.85** | **23.49** | **26.06** |
| **22** | **Hi Starch x MD-807** | **3** | 11.99 | **33.76** | 53.57 | **11.73** | **31.67** | 15.04 |
| **23** | **Hi Starch x MD-607++** | **11** | 9.99 | **38.55** | **63.01** | **6.51** | **20.36** | 11.07 |
| **24** | **Hi Starch x MD-607** | **19** | 11.32 | **35.61** | **60.34** | **14.04** | **29.35** | 14.09 |
| **25** | **Hi Starch x W-248** | **14** | 14.32 | **36.36** | **61.55** | **4.02** | **18.77** | 11.27 |
| **26** | **Hi Starch x W-248** | **19** | 9.66 | **32.88** | 57.27 | 12.65 | **29.18** | 12.51 |
| **27** | **Pelican Processor x J/7-13** | **3** | 11.99 | 24.18 | 54.62 | **9.45** | **29.46** | **30.55** |
| **28** | **Pelican Processor x MD-607++∞** | **10** | **18.32** | **39.06** | **63.29** | **18.19** | **28.44** | **27.90** |
| **29** | **Blue Blue**** | | **19.78** | **35.28** | **65.64** | **10.24** | **22.06** | **4.40** |
| **30** | **Apomuden**** | | 14.98 | 27.73 | 50.47 | 14.77 | 38.20 | **27.90** |
| | **Mean for checks** | | **17.38** | **31.50** | **58.06** | **12.50** | **30.13** | **16.15** |
| | **SED** | | **0.87** | **0.27** | **0.81** | **0.38** | **0.48** | **1.87** |
| | **CV %** | | **39.11** | **6.05** | **3.05** | **16.25** | **10.23** | **20.45** |

**** Blue Blue = local farmer variety used as check for dry matter and low sugar; Apomuden = released high β-carotene check; BC = β-carotene; Malt = maltose; Tsugars = total root sugars. Bolded fonts represents values that are above the mean of checks for yield, dry matter, starch and β-carotene while green fonts represent values below the check means for the sugars; ++ The eight clones with combination of preferred quality attributes; ∞ = High DM and starch, high β-carotene but higher sugar than Blue Blue.**

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## 6.4 DISCUSSION

Genetic diversity and heritability are the plant breeder's most powerful tools and form the basis of global breeding efforts in every crop. To modify sweetpotato quality characteristics so as to meet farmer and end-user preferences, it was important to obtain estimates of heritability and determine the genetic control of key attributes. This study was carried out to gain an understanding of the genetic control of selected traits of importance to consumers in Ghana, and to generating new genetic diversity which may be exploited to meet the needs of both growers and consumers of sweetpotato.

The significant mean square values for entries for the studied traits (Table 6.3) are indicative of genetic variation among parents and their families. Six out of the 29 $F_1$ families outperformed their parents in yield. This may be attributed to heterosis or transgressive segregation. In sweetpotato, transgressive segregation for desirable traits (e.g. beta-carotene, dry matter, starch content and yield) in which clones show either higher or lower values than either parents for particular traits have been reported (Gasura *et al.*, 2008; Cervantes-Flores *et al.*, 2011). However high viral incidence of exotic parental clones could be implicated for the much lower mean yields of parents compared to progeny yields, hence further investigation is required to ascertain the phenomenon of heterosis in this population. Transgressive segregants that result in higher values are useful for traits like yield, dry matter, starch and β-carotene where high offspring values are required. For the sugars, however, transgressive segregants with lower values are desirable. In the current study 8 $F_1$ hybrids had total sugar values below the mid-parent value; however, there were specific individuals within $F_1$ families', which had sugar levels below the lowest check variety. This is favorable as it has positive implications for low-sugar breeding. For dry matter and β-carotene, 7 and 11 $F_1$ families respectively had higher values than their mid-

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parent but lower than the best parents. This may be because parents involved in the study were divergent for dry matter, sugars and β-carotene.

Heritability estimated from mid-parent offspring regression was highly significant ($P < 0.001$) for most traits except for glucose and sucrose. Estimates from regression and variance components were moderate to high for most traits. Agronomic traits had values ranging from 0.27 – 0.62 while quality traits had values between 0.24 – 0.80. Glucose had low heritability of 0.05 and 0.15 from parent-offspring and variance methods respectively. With respect to yield, results of the current study are inconsistent with that by Todd (2013) who found low heritability for yield. However on quality attributes the findings of the current study agree with Todd (2013) who found moderate to high heritability for quality traits using either variance components from sib analysis or from parent-offspring analysis. Heritability enables breeders to select individuals based on their phenotypic performance and genetic advance gives an indication of the gene action involved in the expression of the trait (Tsegaye *et al*. 20007).

According to Tsegaye *et al*. (20007), high heritability estimates is not always associated with high genetic advance, therefore, estimates of heritability should always be considered simultaneously with genetic advance. In addition, additive gene action plays a major role when values for genetic advance are high while low values are reflective of non-additive effects. Heritability estimates are therefore reliable when associated with high genetic advance (Tsegaye *et al.*, 2007). Predicted genetic advance for the various traits evaluated in the current population were moderate to low. For attributes such as glucose and sucrose with low heritability and low genetic advance, gains in selection would be difficult to predict. Heritability estimates for yield, individual root weight and harvest index of this population was moderate to high, ranging between 0.27 and 0.62. These were associated with moderate predicted genetic advance of

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30.6%, 12.5% and 13.9% indicating that both additive and non-additive gene action were at play in the expression of yield and its related traits. This finding is in agreement with Jones (1986) and Grüneberg (2009) who obtained heritability of 0.44 and 0.50 respectively for yield. Some (2013), obtained both low genetic advance and low heritability for storage root yield and yield components. These results suggest that gradual progress can be achieved through recurrent selection for yield and its components. However, breeders may also take advantage of heterosis.

Storage root dry matter and starch also had moderate heritability of 0.38 and 0.40 respectively from parent-offspring regression and higher values of 0.56 and 0.53 respectively from variance components. These moderate heritability values were associated with very low genetic advance implying that, gain in selection could be slow but advances could be made through selection of transgressive segregants. Jones *et al*. (1986a) however obtained higher heritability of 0.65 for dry matter. Higher genetic advance for dry matter has also been reported (Tsegaye *et al.*, 2007; Some, 2013) and is at variance with the current findings. Results from the current study and those from previous studies seem to suggest the importance of both additive and non-additive gene actions in the control of dry matter. Previous studies however, have found inbreeding to be an effective method of increasing dry matter (Komaki *et al.*, 1998), suggesting that dry matter is primarily controlled by additive effects, as dominance effect would result in inbreeding depression.

Regarding sugars, moderate heritability associated with relatively moderate genetic advance was observed for fructose, maltose and total sugars. Heritability estimates for glucose and sucrose were low and not significantly different from zero and also associated with very low genetic advance. Heritability estimates obtained for sugars in this study seem to partly agree with those reported by Todd (2013) who obtained moderate heritability using variance method and much

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higher values using parent- offspring regression method. In Irish potato tubers, moderate to high heritability estimates for sugars have been reported (Grassert *et al*., 1984; Pereira *et al*., 1994), which corroborates the present findings. Low heritability estimates have also been reported for reducing sugars (fructose and glucose) in Irish potato while the non-reducing sugar (Sucrose) had moderate heritability (Regassa and Basavaraj, 2005). The results of the current study seem to suggest that low sugar breeding could be achieved through recurrent selection and by selection of transgressive segregants with much lower sugar values than their parents.

Beta carotene on the other hand, had moderate heritability from regression but a very high value from variance components. Heritability for β-carotene was also associated with moderate genetic advance. Some (2013) obtained high heritability for β-carotene using regression and very low genetic advance in contrast with the results of the current study where a moderate heritability and moderate genetic advance was predicted using regression. Chiona (2009) using variance components obtained low heritability estimate for β-carotene but in this study a high estimate was obtained with variance components. It has been suggested that β-carotene is controlled by several additive genes (Hernandez *et al*., 1967). Cervantes-Flores *et al*. (2006) reported the significant effect of eight quantitative trait loci (QTL) on variation in β-carotene in sweetpotato. It seems therefore that, both additive and non-additive factors may play significant roles in controlling the expression of this trait but additive effects seem more prominent than non-additive effects in the current population

Generally, the moderate heritability for the traits analyzed in this study could be attributed to the fact that environmental influence had a profound effect on the expression of the traits. This is depicted by the highly significant location effect and the very high phenotypic coefficient of variation relative to the genetic coefficient of variation for all studied traits. Twenty progenies

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per cross were used in this study. The small population size may have resulted in low gene frequencies which could also have influenced the heritability estimates (Falconer and Mackay, 1996).

General combining ability (GCA) for males and females were highly significant ($P < 0.001$) for most traits as also reported by others (Chiona, 2009; Todd, 2013). The presence of more significant GCA than SCA effects and the substantially greater GCA than SCA confirm the preponderance of additive over non-additive gene action as also suggested by the moderate narrow sense heritability estimates. The trend of greater variation explained by female than male GCA effects for all traits except weevil damage suggests that cytoplasmic or maternal effects probably influenced the expression of the traits. This however is inconclusive and should be interpreted with caution because of the unbalanced number of males and females used in the NCII analysis and also because the model did not test reciprocal differences. Notwithstanding, maternal effects have been found to influence a number of traits in sweetpotato (Lin *et al.*, 2007; Chiona, 2009)

Considering the GCA effect of individual parents, GCA of female (Pelican Processor) for yield was very high, positive and significant ($P < 0.05$). Pelican Processor was the best performing female in terms of yield and produced some of the best yielding hybrids. The male line MD-844 was the highest yielding male and had significant positive GCA effect for yield. This is indicative of the ability of Pelican Processor and MD-844 to transfer favorable alleles for yield to their offspring. MD-844 had highly significant positive GCA for individual root weight. GCA for Pelican Processor was positive but not significant. SCA for yield was however not significant for any of the hybrids, suggesting that, in this population, only additive gene effects may be important for yield. Heritability and estimates of genetic advance obtained in this study, however

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suggests both additive and non-additive effects were important. The female line Hi Starch also had significant and positive GCA effect for individual root weight and was the only one with significant positive SCA effect for individual storage root weight in cross combination with MD-844. Hi Starch may therefore exhibit partial dominance effect in addition to additive effects with regard to yield.

Regarding dry matter and starch, the female parents, Yellow Sunflower and Kadzie had significant positive GCA while only male J/7-13 had significant positive GCA for starch. No male parent expressed significant GCA effect indicating that males did not contribute significantly to dry matter content. Only female W-115 had a high negative and significant GCA for starch implying that while Yellow Sunflower and Kadzie (females) and J/7-13 males contributed genes in an additive manner to improve on starch content of their progenies, female W-115 contributed additive genes to decrease starch content in its progeny. However, SCA effect of the crosses W-115 x P11 and W-115 x P15 as well as Daak 07/008 x MD-807 were significant and positive indicating that dominant gene effects were more important in these crosses, considering the fact that the GCA effects for these parents were either insignificant or significant but negative for starch.

The female parents Daak 07/008, Kadzie and Yellow Sunflower with significantly negative GCA effects for fructose, glucose and sucrose respectively, suggest that genes from these parents acted additively to lower the levels of reducing and non-reducing sugars. In addition Yellow Sunflower had a high and significantly negative GCA for maltose making GCA effect for total sugars for Yellow Sunflower negative and significant. Among the male parent J/7-13 had negative and significant GCA effect for maltose and total sugars. This suggests that genes from parents Daak 07/008, Yellow Sunflower, Kadzie and J/7-13 acted in an additive manner to negatively impact

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on sugar levels. For example hybrid Daak 07/008 x J/7-13 had the lowest mean values for maltose and total sugars (Table 6.6) while crosses involving Yellow Sunflower and Kadzie produced hybrids that were among the families with the lowest amounts of total sugars. Daak 07/008 x MD-844 produced the lowest amount of sucrose and the highest amount of glucose (Table 6.6) due to the fact that Daak 07/008 x Kadzie was the only hybrid with highly significant negative SCA effect for sucrose and highly significant positive SCA for glucose. Dominant gene effects may have negatively influenced sucrose production but impacted positively on glucose production to compensate for the decreased levels of sucrose. SCA effect for maltose was not significant for any of the hybrid families, emphasizing the predominance of additive gene effects for maltose formation. Maltose formation has however been reported to be under the control of a single gene (β-amy), but due to the hexaploid nature of sweetpotato, perhaps even a qualitative trait such as this may have been duplicated and thus inherited quantitatively.

The only family with significant positive SCA for β-carotene was W-115 x J/7-13. GCA effect of W-115 for β-carotene was also significant and positive but that for J/7-13 was not significant. This suggests that additive and dominant genes effects from W-115 may have influenced the expression of β-carotene levels in this particular hybrid resulting in this hybrid being the highest for β-carotene content.

## 6.6 CONCLUSION

Most of the studied traits had moderate to high heritability estimates associated with low to moderate predicted genetic gains indicating the importance of both additive and non-additive gene action in expression of the traits. However, the presence of more significant GCA than SCA effects and the high ratio of GCA: SCA (ranging from 2.7 – 21.8) imply that additive gene action was more prevalent than non-additive gene effects for all characters. With the exception of

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weevil damage, the variance ratio of GCA of females to males ($\sigma_f^2$ / $\sigma_m^2$) was above unity (ranging from 1.1 – 6.6) for all characters, which probably is an indication of the presence of maternal effects. The highly significant GCA mean squares for the traits indicate the presence of sufficient genetic variation in the population for effective selection of each of the traits of interest except for glucose and sucrose. Good general and specific combiners in desirable directions for the various traits were identified. Pelican Processor and MD-844 were the best in terms GCA for yield. Hi Starch and MD-844 were the best general combiners for individual root weight while Hi Starch x MD-844 was a good specific combiner for storage root weight. The best female general combiners for dry matter and starch were Yellow Sunflower and Kadzie while for the males it was J/7-13. W-115 x MD-607, W-115 x W-248 and Daak 07/008 x MD-807 were good specific combiners for starch, while W-115 x MD-807 had the best SCA for dry matter. Good general combiners for low sugars were also identified. These included Yellow Sunflower, Kadzie and J/7-13. W-115 and MD-844 were identified as good general combiners for β-carotene while W-115 x J/7-13 exhibited good SCA for β-carotene. The good combiners also exhibited heterosis in that they out-performed their respective parents for their respective traits. Twenty eight clones with desirable combination of the preferred farmer traits namely; high dry matter, high starch, low sugars and moderate to high levels of β-carotene have been selected for further evaluation.

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# CHAPTER SEVEN

## 7.0 CONCLUSION AND RECOMMENDATION

Despite its great potential to alleviate food insecurity, malnutrition and poverty, sweetpotato has remained the untapped resource in many developing countries (Low *et al.*, 2009). In Ghana it is both a food and cash crop. Its importance as a cash crop is gaining momentum for farmers in rural areas and in big cities like Bawku in the Upper East region. A huge market exists in urban centers of the country for fried sweetpotato chips. However, in spite of its high energy, production levels and nutritive value, sweetpotato is yet to become a major staple in Ghana. Its limited use in local food cuisines is attributed to undesirable root quality characteristics. In this study, efforts were made to: 1) identify through PRA, farmers production constraints and preferences with respect to eating quality characteristics; 2) assess genetic diversity and select suitable parents for breeding; 3) assess the importance of G x E effects on the expression of root quality traits and 4) determine the genetic factors that control the expression of the traits of interest.

Production constraints identified by farmers can be classified into two main categories: a) factors limiting cultivation of the crop and 2) factors that directly relate to demand. Drought emerged as the most important constraint in the first category. Key factors identified in the second category determine the acceptability of the crop in traditional food preparation. These include low sugar, high dry matter and poundability. Sweetpotato lacks these quality traits and therefore, has low appeal as a staple. Low utilization in local cuisines and the lack of diversified use were therefore identified as major factors that constrain demand and production. The development of varieties with low sugar and high dry matter content is therefore necessary if sweetpotato is to become a

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staple. For sweetpotato to effectively enhance food and nutrition security in Ghana, it was also necessary to improve on the β-carotene content of staple type sweetpotato as the most stable way to alleviate the prevalence of vitamin A deficiency in the country.

For an initial step to incorporate farmers identified needs and preferences into a breeding initiative, it was necessary to characterize and evaluate available germplasm diversity so as to identify clones with the desirable agronomic and quality characteristics. One hundred and thirty clones made up of farmer varieties, germplasm collections within national programs and exotic clones from the USDA germplasm repository, were assembled and evaluated. Characterization based on morphological and quality traits revealed large variations within the 130 genotypes analyzed. Sugar, dry matter and β-carotene contents varied widely, offering an opportunity for selection and genetic improvement. The 9 morphological and eight root quality markers identified represent key phenotypic characters that are diagnostic for germplasm differentiation but root quality markers were the most useful in differentiating genotypes in the current study.

Genotype by environment analysis showed that genotype main effects, environment main effects and G x E effects were significant for most traits. Genotype by environment effect was larger than environment and genotype main effect for agronomic traits while genotypic effects were more important for quality attributes. The findings of this study agree with that reported by Grüneberg *et al*. (2005) on G x E interaction for sweetpotato yield and nutritional traits. For agronomic traits therefore, many more environments may be required for evaluation than for quality traits. Broad sense heritability estimates revealed low heritability estimate of 27% for yield and very high values ranging from 83% - 99% for storage root quality traits, which seem to suggest that improvement of quality traits may be based on phenotypic selection while yield improvement may be based on recurrent selection. Three genotypes were identified with average

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stability for yield. These were Pelican processor, Yellow Sunflower and MD-84. Pelican processor, W-248, Hi Starch and Kadzie were the most suitable clones for low-sugar breeding. Hi Starch and Blue Blue were most stable for high dry matter, while Hi Starch, Kadzie and Pelican Processor had stability for starch. MD-807 was identified as suitable for β-carotene breeding due its high β-carotene content.

Eleven compatible clones generated 29 $F_1$ families. The newly developed population was evaluated in two locations and narrow sense heritability, genetic advance, GCA and SCA parameters were estimated. The studied traits had low to high narrow sense heritability ($h^2$) estimates that associated with low to high predicted genetic advance, indicating the presence of both additive and non-additive mode of inheritance. According to Jones *et al.* (1986a) estimates over 0.60 are quite adequate for good selection advance but estimates as low as 0.30 by regression and 0.40 by variance-covariance could be considered favorable provided that the selection techniques have enough precision.With the exception of storage root yield, glucose and maltose where estimates by regression were lower than 0.30, all other traits exceeded 0.30 by regression. However, based on variance components almost all traits had estimates above or close to 0.40. For the traits with moderate to high $h^2$ and moderate to high predicted genetic advance (yield traits, fructose, maltose, total sugars and β-carotene) in this study, rapid genetic gain should be possible through selection. For those with low $h^2$ and low genetic advance (dry matter, starch, glucose and sucrose) progress in selection may be slow and may require recurrent selection over time to make significant progress.

The highly significant GCA mean squares for most traits indicate the presence of sufficient genetic variation in the population for effective selection. This could be attributed to the fact that parents used to develop the current population included both local and exotic germplasm. The

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newly developed population may therefore contain new alleles in various combinations, to provide a wider genetic base that may be of benefit to further improvement strategies. The more significant GCA variances than SCA variances corroborate the predominance of additive over non-additive gene action in controlling their expression. The variance ratio of GCA of females to males ($\sigma_f^2$ / $\sigma_m^2$) was above unity for all characters, which may be an indication of maternal effects. Previous studies on maternal effects have been reported for sweetpotato (Lin *et al.*, 2007; Chiona, 2009) however, since unbalanced number of females and males were used in this study and maternal effects were not tested, further studies are required to confirm the influence of maternal effects on these traits.

Clones with good general and specific combining ability in desirable directions for the various traits were identified. These included Pelican Processor and MD-844 for yield, Hi Starch and MD-844 for individual root weight, Yellow Sunflower, Kadzie and J/7-13 for dry matter and starch, Yellow Sunflower, Kaddzie and J/7-13 for low sugars and W-115 and MD-844 for β-carotene. The good specific combiners were; Hi Starch x MD-844 for storage root weight, W-115 x MD-607, W-115 x W-248 and Daak 07/008 x MD 807 for starch, W-115 x MD 807 for dry matter and W-115 x J/7-13 for β-carotene. Daak 07/008 x MD-844 had low SCA for sucrose.

Even though the hexaploid, self-incompatibility and heterozygous nature of the sweetpotato make inheritance studies very complicated, the presence of high level of heterozygosity and wide diversity among sweetpotato populations have also been valuable sources for favorable genes (Mcharo and La Bonte, 2007) whose dominant or epistatic effects can result in heterosis (Mcharo and La Bonte, 2007; Gasura *et al.*, 2008; Cervantes-Flores *et al.*, 2011). The good combiners in this study also exhibited heterosis in that they out-performed their respective parents for their

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respective traits. The clonally propagated nature of sweetpotatoes will allow this heterosis to be maintained through asexual propagation.

## 7.1 RECOMMENDATIONS

1. Drought resistance must be considered as another priority trait in sweetpotato improvement programs in Ghana
2. Further work is required to confirm the usefulness of sucrose equivalents as proxy for cooked taste. This may provide a quick method for eliminating clones so as to increase precision for sensory evaluation of sugars.
3. Further studies are required to assess the presence of maternal control on the expression of the studied traits
4. Future marker studies should focus on maltose as one of the main criteria for genotype classification
5. The 28 selected clones with the desirable yield and quality characteristics should be re-evaluated in multi-locational and on-farm trials linked with the process of official variety release.

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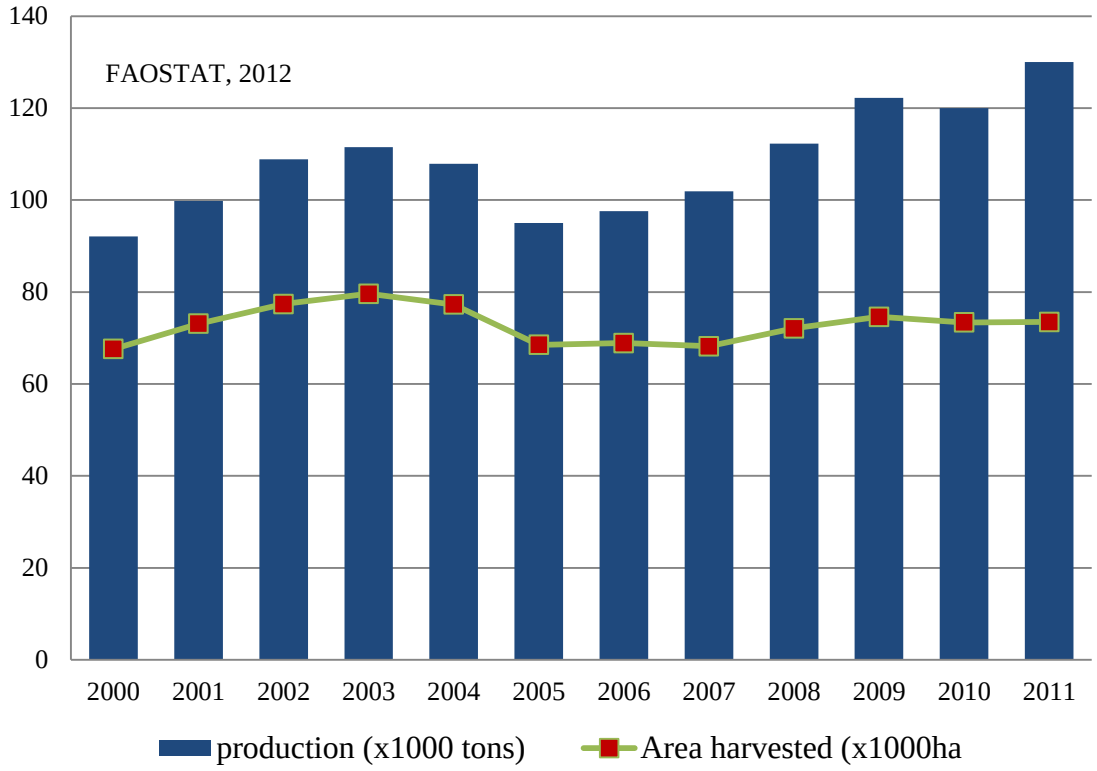
# APPENDICES

**Appendix 1.1: Sweetpotato production in Ghana from 2000 – 2011**



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**Appendix 3.1: Breeding staple type sweetpotato for Ghana**
**Questionnaire for Individual Sweetpotato Farmers**

1.0 **Demographic Data**
Name……
……..
Village……
……
District……
……
Age……
……
Sex Male ( ) Female ( )
Marital Status Married ☐ Single ☐

2.0 **What are the sweetpotato varieties grown? Please tick all that apply.**
**a)** Apomuden **b)** Otoo **c)** Ogyefo **d)** Hi starch **e)** Sauti
**e)** Faara **f)**Okumkom **g)** Santom pona **h)** Jukwa orange **i)** others (specify)

3.0 **Where do farmers obtain their planting material?**

| | **Sources of seed** | **Varieties** | **Reason** |
|---|---|---|---|
| **a.** | Self or Farm saved | | |
| **b.** | Neighbours/other farmers | | |
| **c.** | Agric officers | | |
| **d.** | Farmer Associations | | |
| **e.** | NGO's (Please specify) | | |
| **f.** | …… | | |
| **g.** | …… | | |

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**Appendix 3.1 continued: Breeding staple type sweetpotato for Ghana**
**Questionnaire for Individual Sweetpotato Farmers**

4.0 **Which of the following sweetpotato production constraints do you face? Rank in order the level of importance in severity. Assign the number one (1) to the most important; number two (2) to the second most important in that order etc.**

| | **production constraints** | **Please tick all that apply** | **Ranking** |
|---|---|---|---|
| **a.** | Unreliable rainfall | | |
| **b.** | Insect pests | | |
| **c.** | Diseases | | |
| **d.** | High input cost | | |
| **e.** | Land shortage | | |
| **f.** | Declining soil fertility | | |
| **g.** | Lack quality planting material | | |
| **i.** | Poor storageability | | |
| **j.** | High cost of seeds | | |
| **k.** | Low utilization/processing | | |
| **l.** | Weed control | | |
| **m.** | Lack of ready market | | |
| **n.** | Low prices | | |
| | **Others** (Please specify) | | |
| **o.** | …….. | | |
| **p.** | …… | | |
| **q.** | …… | | |

5.1 **Give the top three most important constraints that face sweetpotato production?**
**(1)**
……
……
**(2)**
……
……..
**(3)**
……
……..

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**Appendix 3.1 continued: Breeding staple type sweetpotato for Ghana**
**Questionnaire for Individual Sweetpotato Farmers**

**Please indicate your preferences for selecting a sweetpotato variety for growing in your farm**

| | Variety | Indicate yes(Y) or No(N) | Criteria |
|---|---|---|---|
| **1)** | Apomuden | | |
| **2)** | Otoo | | |
| **3)** | Ogyefo | | |
| **4)** | Hi starch | | |
| **5)** | Sauti | | |
| **6)** | Faara | | |
| **7)** | okumkom | | |
| **8)** | Santom pona | | |
| **9)** | Jukwa orange | | |
| **10)** | Others (specify) | | |

8.0 **Indicate your sources of information on new technologies for sweetpotato production**

| | Source | Tick all that apply | Type of information |
|---|---|---|---|
| **a)** | AEAs | | |
| **b)** | NGO's | | |
| **c)** | Local FM | | |
| **d)** | National radio | | |
| **e)** | Television | | |
| **f)** | Internet | | |
| **g)** | Field days | | |
| **h)** | On-farm demonstrations | | |
| **i)** | Other farmers | | |
| **j)** | Fact sheets | | |
| **k)** | No information | | |
| | ***Other (specify)*** | | |
| **l)** | | | |
| **m)** | | | |

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**Appendix 3.1 continued: Breeding staple type sweetpotato for Ghana**
**Questionnaire for Individual Sweetpotato Farmers**

9.0 **What characteristics of sweetpotato do you prefer for its market value?**

**a)** Flesh colour
(specify)……
……

**b)** Root colour
(specify)……
……

**c)** Tuber size
(specify)……
……

**d)** Maturity
(specify)……
……

**e)** Yield
……
……

**f)** Disease resistance
……
……

**g)** Pest resistance
……
……

**h)** Smooth or Rough textured
skin……
……

**i)** Storage
capacity……
……

**j)** Number of times produced in a
year……
……..

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**Appendix 3.1 continued: Breeding staple type sweetpotato for Ghana**
**Questionnaire for Individual Sweetpotato Farmers**

10. **Do you treat sweetpotato before storage? Indicate Yes (Y) or No (N)**

| | **Treatment Options** | **Indicate Y or N** | |
|---|---|---|---|
| **1.** | Storage chemical | | ***Specify***…… |
| **2.** | No treatment | | |
| | ***Other means of treatment*** | | |
| **3.** | | | ***Specify***…… |
| **4.** | | | ***Specify***…… |
| **5.** | | | ***Specify***…… |

11. **How do you store sweetpotato? Indicate all that apply.**

| | **Storage type** | **Variety** | **Reason** |
|---|---|---|---|
| **a)** | Sacks | | |
| **b)** | shelves | | |
| **c)** | soil | | |
| **d)** | Cribs | | |
| | ***Other means of storage*** | | |
| | | | |
| **e)** | | | |
| **f)** | | | |
| **g)** | | | |

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**Appendix 3.1 continued: Breeding staple type sweetpotato for Ghana**
**Questionnaire for Individual Sweetpotato Farmers**

12. **Indicate your sweetpotato preference for home consumption by rank order. 1 = the most preferred; 2 = the second most preferred in that order.**

| | Sweetpotato preference (home consumption) | Rank order |
|---|---|---|
| **a)** | Easy to cook and easily stored | |
| **b)** | High yielding | |
| **c)** | Tolerant to insect infestation | |
| **d)** | Tolerant to diseases | |
| **e)** | Early maturing | |
| **f)** | Large and unbroken tubers | |
| **g)** | Colour of cooked tubers | |
| **H)** | Taste | |
| **i)** | Easy to peel | |
| **j)** | Texture | |
| **k)** | Dry mouth feel | |
| **l)** | Low/no blackening on cooking | |
| **m)** | others | |
| **n)** | | |

14. **What should farmers' involvement in research in sweetpotato be? Please tick all that apply.**

15. **What other traits of sweetpotato should breeders incorporate in sweetpotato varieties for you now?**

a)……
……
b)……
……

c)……
……...
d)……
……

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**Appendix 3.1 continued: Breeding staple type sweetpotato for Ghana**
**Questionnaire for Individual Sweetpotato Farmers**

Gender activity calendar analysis (men and women will be separated and then mixed again for corroboration)

**Characteristics of the household heads interviewed during the survey**

| Description | frequency |
|---|---|
| Male | |
| Female | |
| Not Educated | |
| Educated up to primary school level | |
| Educated up to secondary school level | |
| Educated up to post-secondary level | |
| Have off-farm employment | |
| Have no off-farm employment | |

| **Land sizes and utilization / Area, acres** | **acreage** |
|---|---|
| Area devoted to homesteads and other farm structures | |
| Area devoted to livestock sheds | |
| Area for food crops | |
| Area for forage crops | |
| Total farm size | |

| **Gender and ages assisting in the farms** | **frequency** |
|---|---|
| Men 16-60 yrs | |
| Women 16-60 yrs | |
| Women >60 yrs | |
| Men >60 yrs | |
| Boys 0-15 yrs | |
| Girls 0-15 yrs | |

| **Distribution and utilization of water resources, %** | **Home** | **Livestock** | **Forages** | **Crops** |
|---|---|---|---|---|
| Streams | | | | |
| Piped | | | | |
| Rainfall | | | | |

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**Appendix4.1: Local names for farmers' germplasm, GPS location of collection sites, districts and farmers description of varieties**

| Local name | Code | | Community | District/Region | Latitude/longitude | Farmers description |
|---|---|---|---|---|---|---|
| Faara | VOTC 001 | CR | Garemore | KEEA/CR | 5.07/1.51W | |
| Santom fufuo | VOTC 002 | CR | Garemore | KEEA/CR | 5.07/1.51W | White-fleshed |
| Mpampro | VOTC 003 | CR | Garemore | KEEA/CR | 5.07/1.51W | Leaves like bamboo |
| Santom pona | VOTC 004 | CR | Garemore | KEEA/CR | 5.07/1.51W | Tastes like the yam variety called 'pona' |
| Ntiatia | VOTC 005 | CR | Garemore | KEEA/CR | 5.07/1.51W | Thin vines |
| Blueblue | VOTC 006 | CR | Garemore | KEEA/CR | 5.07/1.51W | Puple leaves young leaves |
| Santom kokoo/ Faara? | VOTC 007 | CR | Garemore | KEEA/CR | 5.07/1.51W | Looks like Faara |
| TIS 2 | VOTC 010 | CR | Garemore | KEEA/CR | 5.07/1.51W | Purple leaves, may be TIS 2 |
| Santom kokoo (Faara?) | VOTC 011 | CR | Kuful | KEEA/CR | 5.07/1.51W | Purpleskined, may be Faara |
| Santom fufou | VOTC 008 | CR | Dahia farm 2 | Cape coast | 5.24/1.31W | White-fleshed |
| Local yellow | VOTC 009 | CR | Dahia farm 2 | Cape coast | 5.24/1.31W | Yellow-fleshed, may be TIS 2 |
| Local 1 | VOTC 012 | CR | Station 4 | Komenda/CR | 5.06/1.50W | |
| Local 2 | VOTC 013 | CR | Station 4 | Komenda/CR | 5.06/1.50W | |
| Local 3 | VOTC 014 | CR | Station 4 | Komenda/CR | 5.06/1.50W | |
| Local 4 | VOTC 015 | CR | Station 4 | Komenda/CR | 5.06/1.50W | |
| Star | VOTC 016 | CR | Station 4 | Komenda/CR | 5.06/1.50W | Star-like leaves |
| Local white | VOTC 001 | VR | Have Fiakpokope | Akachi/VR | 6.28/0.74E | Whit-fleshed |
| Local red | VOTC 002 | VR | Have Fiakpokope | Akachi/VR | 6.28/0.74E | Red-skined |
| Kadzie | VOTC 003 | VR | Avevlime | Ketu North/VR | 6.16.0.91E | Tasty, resistance to cylas, not as high yielding as shashango, stores well |
| Shashango | VOTC 004 | VR | Avevlime | Ketu North/VR | 6.16.0.91E | High yielding, but not very tasty, darkens, low market value, does not store well |

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**Appendix4.1 continued: Local names for farmers' germplasm, GPS location of collection sites, districts and farmers description of varieties**

| | | | | | | |
|---|---|---|---|---|---|---|
| Worleworme | VOTC 005 | VR | Avevlime | Ketu North/VR | 6.16.0.91E | Profuse and beautiful flowers. Red-skined, white-flesh |
| Local (Sauti?) | VOTC 006 | VR | Devego | Ketu North/VR | 6.12/0.90E | Looks like Sauti |
| Nagodzie | VOTC 007 | VR | Devego | Ketu North/VR | 6.12/0.90E | |
| Trotroyeye | VOTC 008 | VR | Ohawu | Ketu North/VR | 6.13/0.89E | Means change has come, one of preferred variety. Red skin, white-flesh |
| Nchidzitor | VOTC 009 | VR | Ohamu | Ketu North/VR | 6.13/0.89E | |
| Trotroyeye 2 (Sauti) | VOTC 010 | VR | Kporkuve | Ketu North/VR | 6.33/0.85E | Mostly preferred due to High yielding, early maturing, tasty. Red skin, white-fleshed |
| Naanunono | UE 001 | | Nimbasinia | KNE/UE | 10.90/1.04W | High yielding |
| Naanunasingo | UE 002 | | Nimbasinia | KNE/UE | 10.90/1.04W | High yielding, orange-fleshed |
| Kabisuba | UE 003 | | Tekuru | KNE/UE | 10.92/1.05W | Red-skined, yellow-fleshed |
| Tchichare | UE 004 | | Tekuru | KNE/UE | 10.92/1.05W | Orange flesh |
| Naanopongo | UE 005 | | Tekuru | KNE/UE | 10.92/1.05W | White-flesh, not tasty |
| Tuatibaro | UE 006 | | Manchuru | KNE/UE | 10.92/1.05W | Means in-law of the termites i. e susceptible to termites |
| Bonagayele | UE 007 | | Manchuru | KNE/UE | 10.92/1.05W | Red skin, white-flesh |
| Local orange flesh | UE 008 | | Manchuru | KNEUE | 10.92/1.05W | Orange fleshed |
| Local white | UE 009 | | Manchuru | KNE/UE | 10.92/1.05W | |
| Local white | UE 010 | | Kandiga Bambisi | KNW/UE | 10.93/0.95W | |
| Nyuzile | UE 011 | | Kandiga Bambisi | KNW/UE | 10.93/0.95W | Means egg yolk, orange fleshed, too sweet |
| Nyumegre | UE 014 | | Kandiga Bambisi | KNW/UE | 10.93/0.95W | Real potato |
| Yiyaripongo | UE 015 | | Nyangua | KNW/UE | 10.93/1.07W | Means don't sell your goat. Early maturing |
| Naanuveo | UE 012 | | Nyangua | KNW/UE | 10.93/1.07W | Very sweet, orange fleshed |
| Bonaganapongo | UE 013 | | Nyangua | KNW/UE | 10.93/1.07W | Means leaves like donkey hoofs |
| Dankle Dze | N(UE) 016 | | Kukobila | SND/NR | 10.92/1.08W | Red skin, orange flesh |
| Dankle piele | N(UE) 017 | | Kukobila | SND/NR | 10.92/1.08W | White-fleshed, white skin |

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## Appendix 5.1: Description of the three sites for the GxE analysis conducted in 2011 and 2012 in Ghana

| | | | | Annual rainfall | | Annual temperature | |
|---|---|---|---|---|---|---|---|
| **Sites** | **Latitude/longitude** | **Agroecologies** | **Elevation in meters above sea level** | **Min** | **Max** | **Min** | **Max** |
| **BNARI (Accra)** | **5º 40´ 65 N / 0º 12´ 23´´W** | **Coastal Savannah** | **61m** | **1000mm** | **1100mm** | **27ºC** | **28 ºC** |
| **Kitase** | **5º 49´ 00 N / 0º 11´ 0´´W** | **Moist deciduous rain forest** | **306m** | **1100mm** | **1200mm** | **26 ºC** | **27 ºC** |
| **Kumasi (CRI)** | **6º 41´ 53 N / 1º 32´ 19´´W** | **Semi-deciduous rain forest** | **246m** | **1400mm** | **1500mm** | **26 ºC** | **27 ºC** |

## Appendix 5.2: Soil characteristics, rainfall and temperature for the four environments for GxE analysis conductedin 2011 and 2012 in Ghana

| **Soil Characteristics** | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | **Soil Nutrition** | | | | | | **Particle size** | | | |
| **Environments** | **%Nitrogen** | **Phosphorus (ppm)** | **%potassium** | **%carbon** | **% organic matter** | **pH 1:1 $H_2O$** | **% Sand** | **% Silt** | **% Clay** | **Rainfall** |
| **BNARI 2011** | **0.39** | **5800** | **0.48** | **4.21** | **6.82** | **6.4** | **71** | **9** | **20** | **2200mm** |
| **BNARI 2012** | **0.29** | **4600** | **0.35** | **3.54** | **6.10** | **6.2** | **69** | **16** | **15** | **933.3mm** |
| **Kitase 2012** | **0.17** | **244** | **0.092** | **2.79** | **4.81** | **6.47** | **80** | **10** | **10** | **980mm** |
| **Kumasi 2012** | **0.08** | **2100** | **0.16** | **0.75** | **1.30** | **5.42** | **78** | **12** | **10** | **739mm** |

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**Appendix 6.1: Soil characteristics, rainfall and temperature for the four environments for GxE analysis conductedin 2011 and 2012 in Ghana**

| Environments | Soil Nutrition %Nitrogen | Phosphorus (ppm) | Particle size %potassium | %carbon | % organic matter | pH 1:1 $H_2O$ | % Sand | % Silt | % Clay | Rainfall |
|---|---|---|---|---|---|---|---|---|---|---|
| BNARI 2013 | 0.28 | 4650 | 0.33 | 3.50 | 6.12 | 6.2 | 69 | 16 | 15 | 650mm |
| Kumasi 2013 | 0.08 | 2100 | 0.16 | 0.75 | 1.30 | 5.42 | 78 | 12 | 10 | 599mm |

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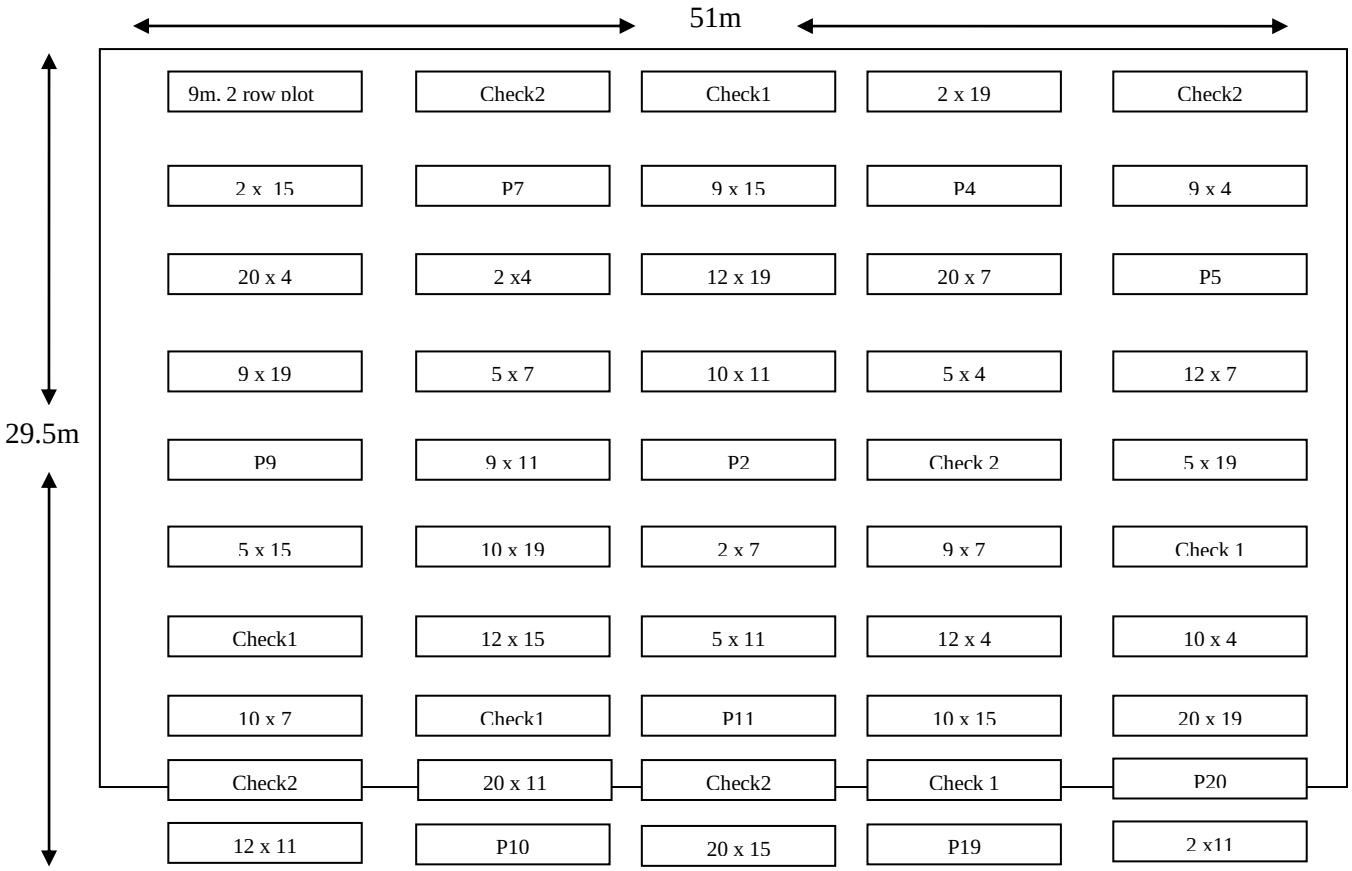
**Appendix 6.2: Field layout of the10 x 5 Alpha lattice showing randomization of the 42 entries**




**P2 = Daak 07/008; P4 = J/7-13; 3 P5 = Yellow Sunflower; P7 = MD-807; P9 = Kadzie; P10 = W-115; P11 = MD-607; P12 = Hi Starch; P15 = W-248; P19 = MD-844; P20 = Pelican Processor; Check 1 = Blue Blue; Check 2 = Apomuden; female x male crosses are represented by e. g., 2 x 4, which is a cross between P2 and P4.**

Note:

1. Each rectangle represents a plot that is made up of two rows. The length of a row is 9m with inter row spacing of 1m
2. Between plot spacing is 1.5m