Towards enhancement of β-carotene content of high dry mass sweetpotato genotypes in Zambia

By

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Thesis Abstract

The enrichment of β-carotene, a precursor to vitamin A, in the local sweetpotato (*Ipomoea batatas* L.) cultivars is an attractive option in order to improve vitamin A intake in Zambia. The study was conducted to: 1) identify sweetpotato genotypes high in β-carotene content and high root dry mass (RDM) and to determine their combining ability, as measured through their progeny performance; and 2) screen progeny for root characteristics, yield, β-carotene content, and RDM. Firstly, a participatory rural appraisal (PRA) was conducted to determine the consumer preferences for sweetpotato. These preferences would form the basis for selecting desirable genotypes. Secondly, five selected parents were crossed in a full diallel for genetic variance studies. A selected subset of the diallel progeny were evaluated in three environments. Thirdly, 15 polycross progeny were evaluated for stability in five environments using additive main effect and multiplicative interaction (AMMI). The PRA revealed that consumers preferred high RDM combined with high fresh root yield. The diallel crosses recorded significant general combining ability (GCA) and specific combining ability (SCA) effects for β-carotene, RDM, harvest index (HI) and root fresh yield (RFY). The ratios of GCA to SCA variances were large (0.68-0.92). Two high β-carotene parents exhibited positive high GCA effects, indicating that additive gene effects were predominant in the inheritance of β-carotene. Reciprocal mean squares were not significant for RDM but they were significant (p=0.01) for β-carotene content. The estimate of narrow sense heritability of RDM (76.3%) was high; but heritability of β-carotene (20.9%), HI (29.1%) and RFY (34.9%) were much lower. These results suggest that rapid genetic gains should be possible with mass selection breeding techniques based on the phenotype of the parent for RDM but progress will be slow for β-carotene content HI, and RFY. The AMMI analysis identified progeny G2 (β-carotene content = 5.0 mg 100 g^{-1} and RDM = 37%), G6 (β-carotene content = 4.7 mg 100 g^{-1} and RDM = 37%), and G8 (β-carotene content = 4.7 mg 100 g^{-1}, RDM = 35%) from the polycross as stable across environments for both β-carotene content and RDM. Genotype G3 was best suited to one of the test environments and had the highest β-carotene content (9.421 mg 100 g^{-1}) and a high RDM (35.47%).

Declaration

I, declare that:

(i) The research reported in this thesis, except where otherwise indicated, is my original research.

(ii) This thesis has not been submitted for any degree or examination at any other university.

(iii) This thesis does not contain other persons' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from those persons.

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As research supervisors we agree to submission of this thesis for examination:

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Dedication

To all who endeavour to dream and see visions. To those who have progressive ideas but cannot influence decisions.

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Abbreviations

CIP	International Potato Centre
CIAT	International Centre for Tropical Agriculture
CGIAR	Consultative Group of International Agricultural Research
CIMMYT	International Maize and Wheat Improvement Centre
F_1	First filial generation or the first hybrid generation after fertilisation
FAO	Food and Agricultural Organization of United Nations
FSR	Farming system research
GCA	General combining ability
GRZ	Government of the Republic of Zambia
H	Broad sense heritability
h^2	Narrow sense heritability
ha	Hectare
HI	Harvest index
IITA	International Institute of Tropical Agriculture
IRRI	International Rice Research Institute
masl	Meters above sea level
MOH	Ministry of Health
NFNC	National Food and Nutrition Commission
OFSP	Orange fleshed sweetpotato
PPB	Participatory plant breeding
PRA	Participatory rural appraisal
RDM	Root dry mass
RFY	Root fresh yield
RRA	Rapid rural appraisal
SCA	Specific combining ability
t	Tonnes
VAD	Vitamin A deficiency
VFY	Vine fresh yield
WHO	World Health Organization
ZARI	Zambia Agriculture Research Institute

General introduction

Vitamin A deficiency (VAD) is one of the major public health problems in the world, affecting over 70 countries. In 1976, the World Health Organization (WHO) indicated that about 228 million children had severe or moderate levels of VAD (WHO, 1976). In 1995, WHO further estimated that over 78 million children less than five years of age are vitamin A deficient, putting their health and survival at risk (WHO, 1995). The current estimates indicate that 45 and 122 countries have a VAD of public health significance based on the prevalence of night blindness and biochemical VAD (serum retinol concentration <0.70 µmol/l), respectively, in preschool-age children (WHO, 2009). Humphrey *et al.* (1992) reported that between 1.3 and 2.5 million deaths could be averted each year by improving vitamin A status.

The problem of VAD is rampant in most developing countries where the poor live mainly on starchy staples to which they add small quantities of nutritious foods as money and availability allow. The quantities of nutritious foods consumed are often not sufficient to affect the limited nutritional value of the staple. The staple crop, whether wheat (*Triticum aestivum* L.), rice (*Oryza sativa* L.), maize (*Zea mays L*.), millet (*Eleucine coracana* L.) or almost any other grain, does not on its own provide adequate vitamins and minerals. In addition, the staple is likely to contain phytates that inhibit the absorption of iron, compounding the problem (Layrisse *et al.*, 1997).

Vitamin A deficiency is a serious public health problem in Zambia and the existing means for addressing the problem are inadequate. The problem is manifested especially in young children and lactating mothers (FAO, 1993; Luo and Mwela, 1997). A 1985 survey of VAD in 4 275 children 6 to 72 months old in the Luapula Valley estimated that the prevalence of xerophthalmia (clinical eye lesions leading to nutritional blindness) was 1.9%, almost twice the WHO cut-off point (GRZ, 1985). Corneal scarring, which is responsible for about 70% of blindness among children in Africa, occurred in 0.7% of the children. In Ndola, in the Copperbelt Province, night blindness rates were even higher: 5% in rural areas, with subclinical deficiency in 13.6% of 6 to12 year olds (WHO, 1995).

Efforts to combat VAD in Zambia began in 1990, with a commitment to provide vitamin A supplements to vulnerable population groups. By 1992, the government of Zambia

began distributing vitamin A capsules to children 6 to 72 months old and lactating mothers in drought-affected areas; then it extended the distribution to health centres throughout the country, targeting these same groups (NFNC, 1996).

The 1996 Zambia Demographic Health Survey indicated that deficiency levels in vitamin A might still be high (Luo and Mwela, 1997). The survey found that Zambia had an infant mortality rate of 107.5 and under-five mortality rate of 192.3 per thousand live births despite good immunisation coverage. It was suggested that some of this mortality was related to VAD as a result of impaired immune status. As a result, a National Survey on VAD in Zambia was conducted in 1997. The survey confirmed that VAD levels were severe and that the supplementation programme was not reaching enough of the population to address the problem. The report stated that 66% of Zambian children were deficient in vitamin A. In addition, the survey found that vitamin A supplementation had reached only 28.4% of the under-five children and 13.5% of postpartum mothers.

At the inception of the supplementation programme, food fortification was considered as a complementary effort. In 1996, the food fortification programme was not well developed though it had started about 10 years earlier. Margarine had been fortified in Zambia since 1978, but the fortification contributed little to vitamin A levels in the population due to low margarine consumption levels, especially among the poor (MOH, 2000). The country has, since 1998, fortified sugar; however, rural consumption levels have not risen as expected. Though the commodity is available, very few rural people have the purchasing power (WHO, 1976; Van den Wijngaart, 1999).

As explained above, a number of solutions to alleviate VAD have been proposed and tried but have been inadequate owing to a number of limitations. The means for distributing vitamin A supplements have been inadequate to reach all the intended beneficiaries. Food fortification has also had its own limitations. Each potential solution has made a necessary but insufficient contribution. However, satisfactory results in reducing VAD could be achieved by an equivalent consumption of β-carotene-vitamin A-rich foodstuffs as the safest and most appropriate long-term approach to controlling VAD (Rahmathullah *et al.,* 1990). Therefore, the bio-fortification of commonly consumed foods such as maize, millet, sorghum (*Sorghum bicolor* L.), yam (*Dioscorea* spp.), bean (*Phaseolus vulgaris* L.), cassava (*Manihot esculenta* L.), sweetpotato (*Ipomoea batatas*

L.), banana (*Musa* spp.), cowpea (*Vigna unguiculata* L.), groundnut (*Arachis hypogaea* L.), and lentil (*Lens culinaris* L.) could potentially make a significant contribution in alleviating VAD.

Research on bio-fortification by both conventional plant breeding methods and molecular techniques is already in progress in some CGIAR centres such as IRRI in the Philippines, CIMMYT in Mexico, CIP in Peru, and CIAT in Colombia. As a result, bio-fortified foods could be on the market in the next few years. The prime beneficiaries of this research would be populations with limited access to supplements or commercially marketed foods (Graham et. al. 2004).

Sweetpotato is an important candidate for bio-fortification to address low levels of Vitamin A in Africa. It is a herbaceous dicot, belonging to the family Convolvulaceae, that is widely grown throughout the tropics and warm temperate regions of the world between latitudes 40°N and 40°S of the equator and between sea level and 2300 m altitude (Hahn, 1977; Bourke, 1985). It is ranked among the seven most produced food crops in the world (FAOSTAT, 2004). The FAO statistics (FAOSTAT, 2004) indicate that 95% of production is in developing countries. It is grown in more than 100 countries and in more than half it ranks among the five most important crops. Scott and Maldonado (1999) have reported that sweetpotato is grown in more countries than any other root and tuber crop. In developing countries, sweetpotato is a major staple crop that mitigates against hunger during times of famine (Horton, 1988). It has various uses such as cooking fresh roots and leaves for human consumption, the manufacture of candy and food colour. Sweetpotato is also used for processing into animal feed (Posas, 1989; Backer *et al.*, 1980), for starch extraction and for the production of alcohol (Collins, 1984). It can substitute wheat in bread and cereals and can be used in many tasty, nutritious recipes. Its tremendous yield potential has resulted in the use of the crop to produce novel plant products and/or nutriceuticals in different parts of the world (Kays and Kays, 1998; Yoshimoto, 1998). Scott *et al.* (2000) predicted that, by 2020 more than two billion people in Asia, Africa, and Latin America will depend on root and tuber crops, among which is sweetpotato, for food, feed, and income. In addition, they projected the annual growth of world sweetpotato production at 1.45%.

Sweetpotato has been receiving attention in part because it grows on soils with limited fertility, is relatively drought tolerant, provides good ground cover, and is often cultivated without fertilizer or pesticides (Ewell, 1990). These qualities are attractive to agriculturalists and ecologists interested in developing sustainable food production systems in the tropics where most resource poor farmers are found.

Sweetpotato is an important staple in Africa for its supply of carbohydrates, vitamin A and C, fibre, iron, potassium and protein (Woolfe, 1992). It produces more edible energy per ha per day than wheat, rice or cassava. It can provide carotene, a precursor for vitamin A, to adults and children, hence can ward off VAD in children and lactating mothers. Children, the group most at risk of VAD, particularly like the crop (Low *et al.*, 1997). The orange-fleshed sweetpotato (OFSP) contains high counts of β-carotene which is largely responsible for the orange colour of the flesh (Simonne *et al.*, 1993; Takahata *et al.,* 1993). Tsou and Hong (1992) reported that the ratio of 4:1 to 8:1 is used to estimate the conversion of β-carotene into retinol as not all β-carotene can be converted to vitamin A in the body. They also indicated that 100-120 g of yellow flesh sweetpotato containing 2500 µg 100 g^{-1} fresh mass of β-carotene was adequate to meet the daily requirement of vitamin A. Mukherjee and Ilangantileke (2002) reported that a regular intake of about 100 g of OFSP roots per day provides the recommended daily amount of vitamin A for children, and it protects them from blindness.

Of the 129 million t sweetpotato produced annually in the world, Africa produces about 9 million t, most of which is consumed by humans (FAOSTAT, 2004). Cultivars that are widely consumed, however, have white or pale yellow flesh and contain very little β-carotene (Ameny and Wilson, 1997). OFSP storage roots, high in carotenoids and vitamin A-active β-carotene are eaten less because they are watery (have less dry mass) (Hagenimana *et al.*, 1999). Hence, the challenge is to develop cultivars that are both high in β-carotene and dry mass.

Though sweetpotato has all these advantages, it is not without problems. Among the sweetpotato constraints in Zambia are low yields resulting from lack of planting materials and improved cultivars. The roots store poorly and most of the roots are not marketable due to the weevil problem and bad root shape. Available genotypes take long to mature and most do not do well under drought stress (Chiona, 1998).

However, the disadvantages notwithstanding, sweetpotato, a cheap source of carbohydrates, is readily available and with all the advantages mentioned earlier offers a good alternative means of addressing the VAD if it can contain high levels of Vitamin A.

Not all sweetpotato have high levels of β-carotene but wide genetic variability for vitamin A occurs naturally in sweetpotato (Woolfe, 1992). This means that conventional breeding techniques can be employed to incorporate β-carotene into sweetpotato by crossing local cultivars with introductions that have high β-carotene. Therefore, the purpose of this research was to enhance β-carotene content in high dry mass sweetpotato, which are preferred by the farmers. This was done to contribute to reducing the prevalent VAD in Zambia.

The objectives of this research were to:

a) identify high β-carotene and high dry mass germplasm and determine their heritability estimates in 2006;
b) cross at least five high β-carotene parents with at least five high dry mass parents to produce a segregated progeny population to be screened by end of 2007;
c) screen for root traits, yield, β-carotene, dry mass, pests and diseases by 2008;
d) carry out organoleptic tests to determine the acceptability of the cultivars by 2008.

The assumptions made for this research thesis were that:

a) Sweetpotato landraces found in Zambia and CIP materials were cross compatible and had high heritability values for dry mass and β-carotene.
b) β-carotene could be increased in high dry mass sweetpotato without compromising the quality of the end product.

The thesis is structured as follows:

1. A review of the literature relevant to the research process (Chapter 1);
2. Identifying grower and consumer preferences for orange-fleshed sweetpotato genotypes in three districts in Zambia (Chapter 2);

3. Evaluation of sweetpotato germplasm for yield, yield components and β-carotene (Chapter 3).
4. Diallel analysis of sweetpotato for β-carotene content, root dry mass, and yield (Chapter 4);
5. Evaluation of G x E interaction of sweetpotato genotypes for high β-carotene content, high RDM and high yield (Chapter 5)
6. A general, summary discussion of the research.

Chapters 2 – 5 are written as discrete research papers. Therefore, there is some overlapping of content and references.

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CHAPTER 1: Literature Review

1.1 Introduction

Sweetpotato (*Ipomoea batatas* (L) Lam.) is a member of the morning glory family, Convolvulacea, characterised by its succulent, edible, storage roots (Purseglove, 1972). It is accepted that cultivated sweetpotato originated in Central America or tropical South America. Nishiyama (1971) and Martin and Jones (1972) suggested Mexico as the centre of diversity of the *batatas* section of *Ipomoea*.

Approximately 900 different species of Convolvulacea in 400 genera have been identified around the world. Yen (1974) and Austin (1978, 1988) recognised 11 species in the section *batatas*, which includes sweetpotato. The closest relative of the sweetpotato appears to be *Ipomoea trifida* that is found in the wild in Mexico, and *Ipomoea tabascan* also found in Mexico in a single site in the state of Tabasco (Austin *et al.,* 1991). Sweetpotato has a chromosome number of 2n = 6x = 90. Since the basic chromosome number of the genus *Ipomoea* is 15, sweetpotato is considered to be hexaploid. Most sweetpotato cultivars are self-incompatible, which means that when self pollinated, they cannot produce viable seeds. Some cultivars are cross-incompatible (Martin, 1967; Naskar and Varma, 1985).

This literature review examines areas of knowledge relevant to the implementation of the research objectives: environmental conditions for growing sweetpotato; sweetpotato flowering and pollination; breeding methods of sweetpotato; heritability of characters in sweetpotato; inheritance of root flesh colour in sweetpotato; increase of β-carotene and other traits in sweetpotato and consumer acceptability tests.

1.2 Environmental conditions for growing sweetpotato

Sweetpotato is widely grown between latitudes 40°N to 40°S and at altitudes as high as 2500 masl (Hahn and Hozyo, 1984). These geographical limits relate to the optimal temperatures for growing sweetpotato. They grow well where the average temperature is 24°C (Kay, 1973). Cool weather, including cool nights, significantly retards growth and storage root production. At temperatures below 10°C, growth is severely retarded. The

crop is damaged by frost, and this restricts the cultivation of sweetpotato in the temperate regions to areas with minimum frost-free period of 4 to 6 months. Even where the frost-free period is sufficiently long, it is still essential that temperatures are relatively high during much of the growing period. In the tropics, yield declines with increased altitude, as do the number of roots and the proportion of roots that are marketable. Increasing altitude also delays maturity (Ngeve *et al.*, 1992).

Sekioka (1964) reported yields to be five to six times higher at 25/20℃ than at 15/13℃ (day/night), and higher at a soil temperature of 30℃ than 15℃. In contrast, Young (1961) found that high night temperatures, by increasing carbon loss through respiration, are deleterious with yields substantially lower at 29/29℃ than at 29/20℃. Seasonal plantings in north-western Argentina suggest that flower and seed production are best with daily maximum temperatures between 23 to 24℃ and minimum temperatures between 13 to 19℃ (Folquer, 1974). In Puerto Rico, flowering in a greenhouse did not occur above 27℃ (Campbell *et al.*, 1963). From these arguments, it is clear that there is an optimum day and night temperature for sweetpotato development and flowering that still needs to be established. However, it appears from the evidence given that the optimum may be around 20℃ for night and around 25° C for day temperatures.

Growth of sweetpotato is closely related to the availability of sufficient moisture. Sweetpotato performs best in regions with 750 - 1000 mm rainfall per annum, with about 500 mm falling during the growing season. Water and adequate aeration are particularly important during the establishment of the cutting. The crop does not tolerate water deficit during root initiation that occurs in the first few weeks of growth. The roots become lignified and will not enlarge (Hahn, 1975). Hahn and Hozyo (1984) suggested that at other times it may have tolerance to drought.

Sweetpotato is intolerant of water logging, particularly during root initiation (Wilson, 1982; Hahn and Hozyo, 1984) so good drainage is essential. Where the water table is high, the crop is planted on mounds or ridges. Sweetpotato grows best on sandy-loam soils and does poorly on clay soils. Soil with high bulk density or poor aeration tends to retard root formation and results in reduced yields (Watanabe *et al.*, 1968). Wet soil conditions at harvest lead to an increase in root rot and adversely affect yield, storage life, nutritional and baking quality (Ton and Hernandez, 1978).

1.3 Sweetpotato flowering and pollination

The flowers of sweetpotato are born solitarily or on cymose inflorescences that grow vertically upward from the leaf axis (Purseglove, 1972; Onwueme, 1978). Each flower has five united sepals and five petals joined together to form a funnel-shaped corolla tube. The tube is usually lavender coloured and is the most conspicuous part of the flower. Five stamens, varying in height, are attached to the base of the corolla tube. In most cultivars the two longest stamens are about the same length as the style. The filament is white and hairy; the anther is also white and contains numerous rounded pollen grains on the surface. The ovary consists of two carpels, each of which contains one locule. Each locule contains two ovules, so that there is a maximum of four ovules in each ovary (Onwueme, 1978).

Most sweetpotato cultivars are daylength sensitive. Short days promote flowering and storage root growth (Lam *et al.*, 1959; Porter, 1979; Martin, 1988). Cultivars differ in this respect. Some flower readily at any season. Others only when days are short. Still others do not flower under any normal conditions. Those that do not flower readily can often be induced to flower by grafting on other *Ipomoea* species. A simpler technique is to train the vines to trellises during the season of short days (Dai *et al.,* 1994). Lack of flowering may be a severe impediment to use of a particular sweetpotato as a parent in controlled crosses. Hence, it may be advisable to do a check for incompatibility at the start of the hybridisation programme.

The flower opens before dawn on a particular day and closes in the afternoon the same day. The length of time the flower remains open is slightly longer if the weather is cool and cloudy. It is easy to emasculate and cross-pollinate by hand. Pollination is by insects, particularly bees. The physiology of the sweetpotato flower is complex: Firstly, the formation of the flower is subject to environmental control, especially photoperiodic control; secondly, the flower is open and receptive only for several hours; thirdly, incompatibility complexes exist; fourthly, the existence of variation in stamen length with respect to the style introduces a further morphological hindrance into the pollination mechanism. All these features make seed production difficult (Onwueme, 1978).

The sweetpotato fruit is a capsule 5 to 8 mm in diameter. A false septum, formed during fruit development, may divide each of the two locules into two, thereby creating four chambers in the mature fruit. Each chamber may contain a seed, but usually one or two chambers in each fruit contain any seed. The seed is black and about 3 mm long. It is flat on one side and convex on the other. The micropyle is located in a hollow on the flattened side. Endosperm is present in the seed in addition to cotyledons. The testa is very hard and almost impermeable to water or oxygen. For this reason, the seed germinates with difficulty. Germination can be improved by scarifying the seed either by mechanically clipping the testa, or by treating it with concentrated sulphuric acid for about 45 minutes. Freshly harvested seeds will germinate if scarified, since the only dormancy mechanism present is the impermeable testa (Purseglove, 1972; Onwueme, 1978). Scarification of sweetpotato seed by sulphuric acid is a standard practice (Steinbauer, 1937; Wang, 1982). Germination of scarified seed occurs in 1 to 2 days.

1.4 Difficulties in breeding sweetpotato

The sweetpotato is almost always self-incompatible (Martin, 1967); however, it is possible to observe self-compatibility (Tumana and Kesavan, 1987). The self-incompatibility and other sterility causing processes have adversely limited the understanding of the breeding system of sweetpotato. Nevertheless, a clear interpretation has been achieved.

The system of self-incompatibility in *Ipomoea* is that of the sporophytic multiple allelic type. A series of alleles at one locus controls the genotype of the parent. The incompatibility reaction of each plant is determined by the interaction of the alleles at a locus and all pollen grains exhibit the same incompatibility phenotype (Martin, 1968). Based on the knowledge of the incompatibility system in a diploid, it is possible to interpret the incompatibility of the sweetpotato on the assumption that the incompatibility locus has been doubled or tripled (Martin, 1968).

Even when a cross is compatible, serious physiological problems, which occur mainly as post-pollen germination barriers to fertility, often impede seed production. Martin and Cabanillas (1966) have demonstrated how pollen tube growth and embryo development fail at various times after pollination. Thirteen detectable failures in sweetpotato

reproductive process were outlined by Martin (1982). Problems of incompatibility and sterility impede controlled pollination in sweetpotato. Some crosses are not possible, and practically all crosses produce much less than the potential four seeds per capsule.

Methodologies developed for cross-pollinated crops are of limited application to sweetpotato breeding because of factors affecting sweetpotato such as: heterozygosity of the crop which is compounded by shy flowering habits and low fertility of blossoms; hexaploidy with 90 chromosomes; cytological abnormality (Warmke and Cruzado, 1949); and self- and cross-incompatibility. Hybridization between desirable parents is difficult due to cross-incompatibility. To overcome crossing barriers, desired genotypes can be given an equal opportunity in a nursery to cross with each other by means of natural pollinators. This type of breeding is called polycross breeding and has been used extensively by different workers (Jones, 1965; Jones *et al.,* 1969; Martin, 1984; Tumana and Kesavan, 1987; Yoon *et al.,* 1987; Freyre *et al.,* 1991; McLaurin and Kays, 1992; Kamlam, 1994; Naskar and Ghosh, 2002). It is also practised with forage grasses to develop high yielding genotypes as well as obtain genetic information (Nguyen and Sleper, 1983; Kölliker *et al.*, 2005). However, controlled pollinations are still employed in sweetpotato breeding (Hernandez *et al.,* 1967; Nishiyama *et al.,* 1975; Dai *et al.,* 1994; Mwanga *et al.*, 2002;).

1.5 Breeding methods for sweetpotato

The breeding methodologies of sweetpotato have had to be adapted to the constraining traits of the crop.

1.5.1 Polycross method of breeding sweetpotato

Jones (1965) was the first to use the polycross method for genetic studies and improvement of sweetpotato. Stuber (1980) defined the term polycross as a mating arrangement for interpollinating a group of cultivars or genotypes using natural hybridisation in an isolated crossing block. He noted that the polycross was used frequently for forage grasses, legumes, sweetpotato, and sugarcane (*Saccharum* spp.). Further, he termed it as a mating design.

The main purpose of a mating design in genetic studies is to generate progeny of known relationships so that the phenotypic components of variances can be equated with the covariances (Becker, 1967). Therefore, progeny from each entry have a common parent in the polycross design and result in half-sib families that are frequently used for evaluating general combining abilities. The polycross method was developed in order to produce progeny that are cross-compatible in outbreeding crops.

A relatively large number of parents of diverse genetic backgrounds are placed together in an isolated nursery to cross with one another in order to determine their combining ability. In sweetpotato polycrosses, the number of parents is usually less than, or about, 30, and insect pollinators are used. The seeds from the polycross nursery may be used in a further general combining ability test of the female parents or may enter a clonal evaluation procedure from where the new cultivars may be selected (Tysdal and Crandall, 1948).

The variance component procedure, as described by Becker (1967), may be used in polycrossing to derive various phenotypic and genotypic components of variance. The procedure is based on the fact that the mean performance of the progeny of any one female parent in a polycross gives a basis for measuring the general combining ability of that female parent. Plant breeders use variance components to select the breeding strategy, given the predominant genetic mechanism controlling the trait to be improved. Since the polycross mating design generates half-sibs, the phenotypic variance component due to differences among half-sibs is equal to the covariance within half-sibs. Based on expected mean squares, the covariance between half-sibs from a polycross mating design is a quarter of the additive genetic variance, assuming no epistasis among additive genes. General combining ability reflects the additive genetic component of variance (Falconer and MacKay, 1996).

Various researchers have further developed the polycross methodology. Wellensiek (1952) explained the genetic basis of the polycross as a means of recognising the desirable genotypes of the female parents by studying their individual progeny following open intercrossing. Shaepman (1952) proposed two ways of designing the polycross test. As used in genetic studies, one of the assumptions of the polycross test is that all

other genotypes grown in the same polycross seed production nursery randomly pollinate each genotype. Several suggestions have been made to ensure randomisation in pollination. Hittle (1954) suggested that polycross seeds must be produced from a relatively large number of replications (10 or more) of single randomised plants to minimise differential pollen effects.

It is necessary that flowering of all the parents be synchronised if crossing is to occur freely within the polycross nursery. There are various ways of achieving this, including short day treatment, grafting, wounding, girdling and phyto-hormone treatment (Miller, 1937; Ahn *et al.*, 2004). Cleft grafting has been used with some success at Asian Vegetable Research Development Centre (AVRDC). The parents are arranged in the field according to a pre-established statistical design that ensures a maximum amount of random mating. Plants are staked and trained and about 40 days after anthesis, the fruits are harvested and the seeds removed (Yoon *et al.*, 1987).

Wit (1952), while working with perennial ryegrass, concluded that polycross progeny provided a more reliable test of the genotype than open-pollinated progeny. Another study with sweetclover found that polycross progeny yields were highly correlated at approximately equal magnitudes with open-pollination and first generation inbreds (Johnson and Hoover, 1953).

1.5.2 Polycross mating designs

Olesen and Olesen (1973) proposed the polycross pattern formula. From the formula, they deduced the following properties of the pattern: the pattern is a latin square, and every genotype has any other genotype as its nearest neighbour and has only one nearest neighbour in each of the four directions, namely: North, South, East and West. The formula holds true for n genotypes where $n+1$ is a prime number. Olesen (1976) indicated that the polycross pattern formula of Olesen and Olesen (1973) was balanced with respect to nearest neighbours in any of the four main directions (i.e. in the North, South, East, or West position). However, with respect to nearest neighbours in the intermediate directions, the pattern was not balanced.

Therefore, Olesen (1976) presented a completely balanced polycross design. This design requires *n* polycross designs, each of size *n* x *n,* and balanced in both main and intermediate directions. He indicated the properties with respect to nearest neighbour as follows: “In anyone of the four main directions, namely: North, South, East, and West, every genotype has any other genotype as nearest neighbour. In any of the intermediate directions, namely: Northeast, Southeast, Southwest, and Northwest, every genotype has any other genotype as a nearest neighbour exactly *n-2* times, and itself as a nearest neighbour exactly *n-1* times”. He also cited the work of Wright (1965) who had given ready-to-use field plans for a systematically designed polycross of any possible size from 6 x 6 to 46 x 46.

Later, Morgan (1988) extended the result of Olesen (1976) in two ways:

a) He demonstrated that a completely balanced polycross design in *n* Latin squares of side *n* may be obtained for any even *n* (dropping the restriction that *n+1* be prime); and
b) That the same neighbour balance properties may be obtained for odd *n* in *n* x *n* squares which are not Latin.

Other workers have used a randomised complete blocks design with four or more replications for their polycross nurseries (Tumana and Kesavan, 1987; Saladaga, 1989). Although the use of the randomised block design may not be as efficient as the Latin square proposed above it can be used to achieve the specified objectives where resources are limiting.

1.5.3 Other mating designs for sweetpotato

Various designs have been used in sweetpotato breeding programmes for different purposes. Ahn *et al.* (2004) used a full diallel cross for examination of cross-incompatibility in Korean cultivars. Similar studies using full diallels have been reported by other workers (Hernandez and Miller, 1963; Martin, 1968).

Kriegner *et al.* (2003) have used what was termed a pseudo-testcross, after Grattapaglia and Sederoff (1994), which they have used to generate a linkage map of sweetpotato based on amplified fragment length polymorphism. On the other hand, Komaki *et al.*

(1998) in Japan and Ma *et al.* (1999) in China, have used the pedigree method with inbreeding and backcrossing for breeding high starch content and high dry mass in sweetpotato.

1.5.4 Recurrent selection of sweetpotato

Pedigree methods of plant breeding have been useful but are labour intensive. Apart from the complex inheritance of sweetpotato, it is propagated vegetatively and pedigree records are much less useful than in crops where there is a need to reproduce a particular genotype.

Sweetpotato is hence best suited to mass recurrent selection procedures (Jones, 1965). Mass recurrent selection consists of selecting 20 or more individuals with the best expressions of the trait required, stimulating them to flower in a polycross block and crossing by honey bees. Seeds produced are germinated for the next round of selection, and the process is repeated. This results in rapid accumulation of major dominant genes, and slower accumulation of minor and recessive genes (Martin, 1988). Jones *et al.* (1969) suggested that simultaneous mass selection of several characters should prove effective.

Saladaga (1989) indicated that breeders are faced with situations of selecting alternative strategies for selecting progeny after making crosses. He gave an example of a breeder with 60 000 to over 100 000 seeds who must choose between two alternatives as follows:

a) He could grow all these seeds into seedlings and clonally propagate each until sufficient materials are available for replicated tests before selection is done; or
b) He could apply either slight or immediately intense selection pressure directly on the seedlings grown from sexual seeds.

Saladaga (1989) reasoned that these alternatives exist because the sweetpotato is highly heterozygous and highly cross-pollinated. As a result, sweetpotato produces seeds that can be grown into plants distinctly different from each other because of the genetic recombination that has taken place in the sexual reproduction process. Natural

vegetative propagation, which is possible in sweetpotato, enables the breeder to maintain each of the 60 000 – 100 000 recombinants for vegetative multiplication without any segregation until replicated tests are possible. If a certain level of selection is attained at an early stage, however, the selection should be done right then to reduce the bulk of material to be handled.

This view is in opposition to Jones (1965) who had 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. The period allowed before selection would allow for the break-up of the relatively long linkage blocks. Indeed, a decade later, Jones *et al.* (1976) demonstrated that the sixth generation had high frequencies of flowering and seed set, attractive root shape, orange flesh, thin cortex, root specific gravities of about 1.02, acceptable yield, and resistance to fusarium wilt (*Fusarium oxysporum* f. sp. *batatas* (Wr.) Snyd. and Hans.) and other pests and diseases. Such could be the choice that the breeder has to make. A breeder's intuition coupled with his best interpretation of data on the mode of inheritance, heritability values of particular characters in his germplasm materials, and other quantitative genetic data are his resources for making the best choice.

At Louisiana State University the practice of imposing selection or screening on greenhouse grown, 4 - 5 month old seedlings from sexual seeds, was adopted. The procedure was later modified. Thus seeds are sown in seed boxes in the greenhouse and vine tips are planted in the field (after 2 - 3 months) following the standard practice, except that the plants are spaced 60 cm between hills. This reduces interplant competition and allows each genotype to express itself. At harvest, roots are dug and piled by hill. Selection is then made based on traits of high heritability values and those of importance to the specific breeding objectives. Subsequent clonal tests progressively use characters having lesser heritability values applied only in replicated traits as selection criteria (Saladaga, 1989).

1.6 Heritability of traits in sweetpotato

Genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an effective breeding programme (Dudley and Moll, 1969). Narrow-sense heritability estimates are useful for predicting the phenotypes of offspring during selection procedures; the closer h^2 is to 1.0, the more accurate is the prediction of the phenotype of the offspring based on the knowledge of parental phenotypes (Klug and Cummings, 2005).

1.6.1 Heritability estimates of traits from a polycross

The theoretical basis for the quantitative genetics of the sweetpotato was developed by Jones *et al.* (1976) and he and others have calculated the heritability estimates of economic traits (Table 1.1), using several different methods. The formal heritability estimates suggest that progress is possible in the selection for any trait that is dominant and can be defined. However, sweetpotato heritability estimates are usually intermediate in magnitude, further suggesting that progress in selection will be slow. This is not surprising when the high number of chromosomes of the sweetpotato is considered.

The higher heritability for yield and component characters in the first and second cycles is of particular interest to breeders as it increases response to selection (Nanda *et al.,* 1990). High narrow sense heritability estimates indicate that either the environment has less influence on the traits under consideration, or fewer genes are involved. High heritability estimates could also mean the characters are controlled by additive genes.

Parent-offspring regressions are calculated using the replicate means of measurements of traits of interest. From these regression coefficients (b), heritability estimates (h^2) are calculated as $h^2 = 2 \times b = V_A/V_P$ where V_A = additive variance and V_P = total phenotypic variance applicable to the half-sibs of polycrosses (Simmonds, 1979).

Table 1.1 Narrow sense heritability estimates of important economic traits in sweetpotato (Martin, 1988)

Character	**Heritability estimates %**
Root mass	25, 41, 44
Growth cracking	37, 51
Flesh colour	53, 66
Flesh oxidation	64
Dry mass	65
Fibre	47
Skin colour	81
Sprouting	37, 39
Vine length	60
Leaf type	59
Flowers/inflorescence	50
Fusarium wilt resistance	50, 86, 89
Nematode egg mass index	57, 69, 75
Insect complex resistance	45
Flea beetle resistance	40
Weevil resistance	84

As mentioned earlier, the variance component procedure of Becker (1967) may be used in estimating genetic variance and heritability in sweetpotato from a polycross design. The procedure involves conducting an analysis of variance (ANOVA) and deriving the phenotypic variance components from the expected mean squares (Table 1.2).

Table 1.2 Analysis of variance with expected mean squares (Falconer and Mackay, 1996)

Source of variation	**Degrees of freedom**	**Mean square**	**Expected mean squares**
Between parental groups	$g - 1$	MS_g	$\sigma_\omega^2 + \sigma_g^2$
Within parental groups	$\Sigma n_i - g$	MS_w	σ_ω^2
Total	$\Sigma n_i - 1$		

Note: Σn_i = number of all I; g = number of parent groups; σ_g^2 = component of variance due to differences among parent groups; and σ_ω^2 = component of variance due to differences within groups or error.

The statistical model for the ANOVA of the polycross mating design is:

$Y_{ij} = \mu + \alpha_i + \varepsilon_{ij}$

Where: Y_{ij} = j^{th} observation within the i^{th} group;

μ = overall mean;

α_i = effect of i^{th} group; and

ε_{ij} = residual error.

The component of variance resulting from differences between parental groups, σ_g^2, is estimated as:

$\sigma_g^2 = (MS_g - MS_w) / k$;

where MS_g and MS_w are the mean squares between and within parental groups, respectively; and k = approximate average number of progeny per parent group.

For sweetpotato where selfing is negligible, the relationship between progeny within a female parent is mostly half-sib. Therefore, the genetic meaning of the phenotypic variance component is as follows:

σ_g^2 = covariance of half-sibs; and

$\sigma_g^2 = ¼ V_A$ (assuming negligible additive epistasis) where V_A = additive genetic variance component.

The heritability (h^2) in the narrow sense is therefore calculated as follows:

$h^2 = 4 \sigma_g^2 / (\sigma_\omega^2 + \sigma_g^2)$.

A study of the inheritance of 10 root traits in sweetpotato by Jones *et al.* (1969) demonstrated that the additive component of genetic variance was relatively more important than the non-additive for all traits except veining and number of edible roots. The results of these workers illustrated that the development of a randomly intermating population with improved flowering and seed production makes it possible to undertake a quantitative genetic study of a crop species such as sweetpotato.

General combining ability analysis is used to understand the relative importance of additive (general combining ability) and non-additive (specific combining ability) gene action in the inheritance of the characters. In a polycross, the emphasis of the estimation of combining ability is on GCA only since only the maternal parent is known and the paternal parent could be any of the other genotypes in the polycross. Progeny with high GCA may be exploited to isolate desirable segregates in sweetpotato.

1.6.2 Heritability estimates generated from a diallel analysis

Estimates of additive and dominance genetic variance components and the resulting estimate of h^2 are obtained from a diallel analysis through equating specific mean squares in the ANOVA to cross covariances such as full-sib covariances (Kempthorne, 1956). The method of Jinks and Hayman (1953) emphasises the analysis of the genetic variances from diallel crosses of homozygous parents. Dickson and Jinks (1956) have extended the method of Jinks and Hayman to diallel crosses involving heterozygous parents. Hence, diallel analysis can be applied to crosses of heterozygous sweetpotato parents enabling the derivation of genetic variance components from the expected mean squares which can then be used to calculate h^2. Hohls (1994) provides a comprehensive review of the various diallel cross analyses.

1.7 Inheritance of root flesh colour in sweetpotato

Carotenoids, especially β-carotene, are the determinant of the orange flesh colour in crops including sweetpotato storage roots (Purcell, 1962; Purcell and Walter, 1968; Takahata *et al.*, 1993). The depth of the colour is mainly a function of all-trans-β-carotene (Simonne *et al.*, 1993; Hagenimana *et al.*, 1999a).

Carotenoids represent the most widespread group of naturally occurring pigments in nature. They are primarily of plant origin and β-carotene predominates. β-carotene serves as an important nutritional component in foods. As a major precursor of vitamin A, it provides pleasant yellow-orange colours to foods (Simon, 1997). The colour intensity of the flesh differs from one cultivar to another, and is correlated with carotenoid content (Lauber *et al.*, 1967).

Sweetpotato exhibits a diverse range in flesh colour of the storage roots. The genepool contains a wide range of colour types that can be selected relatively easily (Kays, 1985). Typical cultivars exhibit white, yellow and orange pigmentation (Kays and Horvat, 1984). While all the pigments found in the sweetpotato genepool have not been fully identified, the prevalent pigments in the yellow and orange types are the carotenoids, predominantly β-carotene (Ezell and Wilcox, 1946; Yen, 1974; Hernandez *et al.,* 1967; Kays, 1985). Interest in increasing the concentration of β-carotene, the precursor of vitamin A, has resulted in a high selection pressure being placed on the trait.

Work done by Jones *et al.* (1976) indicated high heritability estimates for sweetpotato root flesh colour when the selection pressure for acceptable orange flesh decreased from 26% to 50%. These results confirmed work done earlier (Jones *et al.*, 1969) as expected. In the paper of Jones (1977), he also associated light orange root flesh colour with high dry mass. Similar results were obtained earlier by Hernandez *et al.* (1967).

Hernandez *et al.* (1967) indicated that orange root flesh colour (total carotenoid pigments) was controlled by several genes, most likely six, that are probably additive in effect. They concluded that inheritance of root flesh colour was a quantitative character. In addition, they found that certain parents transmitted high carotenoid content to a greater degree than others and crosses between certain parents produced transgressive segregants.

1.8 Increasing β-carotene content and other traits in sweetpotato

Success in developing orange-fleshed breeding lines and cultivars with multiple resistance to insects and diseases was recorded by the sweetpotato breeding programme at the U.S. Vegetable Laboratory (Jones *et al.*, 1986; Collins *et al.*, 1991;

Schalk *et al.*, 1991). In addition, several dry-fleshed cultivars with excellent resistance to wireworms and moderate resistance to sweetpotato weevil have been developed at the same laboratory (Jackson *et al.*, 1999; Bohac *et al.*, 2001). Consequently, similar conventional breeding techniques could be applied to develop new sweetpotato breeding lines that are high in β-carotene and dry mass and are resistant to major pests and diseases.

Sakai (1964) reported that additive gene effects controlled root dry mass (RDM) content and dominant gene effects controlled total storage root yield. He also concluded that the best method to develop new cultivars with high RDM content and high storage root yield was the development of high RDM inbred lines accompanied by crosses among them or with leading cultivars. Beta-carotene content appears to be controlled by several genes that are additive, as the pigment is readily transferred to the progeny (Hernandez *et al.,* 1967). A similar method to that suggested by Sakai (1964) can be employed to make progress in the incorporation of β-carotene in sweetpotato genotypes in addition to the polycross.

1.9 Consumer acceptability tests on new sweetpotato genotypes

For consumers to accept a cultivar, it needs to have good flavour. The flavour of sweetpotato is formed mainly during cooking and comprises both taste and aroma (Kays *et al.*, 1999). Taste is a sensation assessed through the contact of water-soluble compounds with oral chemoreceptors. Of the four primary taste sensations (sweet, sour, salty and bitter), sweetness is the dominant sensation in cooked sweetpotato. Sweetness is derived from endogenous sugars present in the raw root (principally sucrose, glucose and fructose), and maltose that is formed via starch hydrolysis during the cooking process (Sun *et al.*, 1994).

The characteristic aroma of sweetpotato is formed via thermal reactions during the cooking process and a cross-section of volatile compounds has been identified (Purcell *et al.*, 1980; Kays and Horvat, 1984; Tiu *et al.*, 1985; Horvat *et al.*, 1991; Sun *et al.*, 1993; 1994; 1995). Hence, screening for flavour must form part of the research targeted toward improving the amount of β-carotene in cultivars.

Cultivars that are widely consumed in parts of West, Central, and East Africa are high in RDM, have white or pale yellow flesh, and contain very little β-carotene (Ameny and Wilson, 1997). OFSP storage roots, high in carotenoids and vitamin A-active β-carotene are eaten less because they are watery (have less dry mass) (Hagenimana *et al.*, 1999b). Therefore, screening for RDM and consumer acceptability of newly developed OFSP is integral to the success of the breeding project.

1.10 Conclusion

Since sweetpotato genotypes are released as highly heterozygous F_1 progeny which are vegetatively propagated, a breeder must take advantage of the occurrence of transgressive segregation and additive gene action by utilizing mass recurrent selection as a breeding strategy. The variance component procedure is based on the fact that the mean performance of the progeny of a female parent in a polycross gives a basis for measuring the general combining ability of each female parent. Classical quantitative genetics interprets the genetic component of general combining ability as mostly due to additive effects. Hence, derived heritability estimates would be very useful in determining the intensity of selection to be imposed in a breeding programme. This information would be important in guiding selection strategies for simultaneously informing β-carotene content and RDM in sweetpotato.

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Chapter 2: Identifying grower and consumer preferences for orange-fleshed sweetpotato genotypes in three districts in Zambia

Abstract

Sweetpotato is the second most important root crop grown in Zambia. It is used for food security especially during periods of drought and famine. It has been recognised as a potential crop for alleviating vitamin A deficiency as some of the genotypes contain high levels of β-carotene as recognised by the orange colour of the root flesh. However, most of the genotypes grown in the country are white fleshed roots and are hence low in β-carotene. A breeding programme to incorporate β-carotene into high dry mass local genotypes has been initiated at Mansa Research Station in Zambia. It was deemed appropriate to involve farmers in developing the selection criteria for the programme. Consequently, a survey was conducted to better understand farmer and consumer preferences for orange fleshed sweetpotato in three districts of Zambia. An interdisciplinary team used participatory rural appraisal tools to collect data from 10 households in each of three agricultural camps in each district. Pairwise comparisons were employed for ranking preferred products or attributes. The respondents provided a number of preference related attributes. The most common preference among farmers was the sweetness of the roots which accounted for about 35 % of the respondents followed by yield at 23%. The joint third common reasons for preference were early maturity and good storability at 9%. The other attributes that were prominent still related to taste, and storage of both roots and vines. Some of the other selection criteria identified in the survey relate to good root storage, good taste, less fibrous, high dry mass, leaves that make a good vegetable and resistance to pests and diseases. All these criteria, that apply to sweetpotato in general, will have to be taken into account as new orange fleshed sweetpotato cultivars are developed for consumers.

2.1 Introduction

Sweetpotato is an important staple crop in Africa because of its supply of carbohydrates, vitamin A and C, fibre, iron, potassium and protein (Woolfe, 1992). It produces more edible energy per ha per day than wheat, rice or cassava (Woolfe, 1992). It can provide carotene, a precursor for vitamin A, to adults and children, hence can ward off vitamin A deficiency (VAD) in children and lactating mothers. It has various uses such as cooking the fresh roots and leaves for human consumption, processing into animal feed, starch, flour, candy, alcohol and food colouring. It can substitute wheat in bread and cereals and can be used in many tasty, nutritious recipes.

Sweetpotato is highly adaptable to various environments. It tolerates high temperatures, low fertility soils, and can grow in areas with low annual rainfall. It is easy to propagate and maintain, and yields well in adverse conditions.

Though sweetpotato has all of these advantages, it is not without problems. Among the sweetpotato constraints in Zambia are low yields resulting from lack of improved planting materials and improved cultivars. The roots store poorly and are often not marketable due to weevil damage and bad root shape. Many of the cultivated genotypes take long to mature and most do not do well under drought stress (Chiona, 1998).

However, the disadvantages notwithstanding, sweetpotato offers a good alternative means of addressing VAD if the roots can contain high levels of Vitamin A precursors. The orange-fleshed sweetpotato (OFSP) contains high amounts of β-carotene which is largely responsible for the orange colour of the flesh (Simonne *et al.,* 1993; Takahata *et al.,* 1993). Tsou and Hong (1992) reported a range of ratios (4:1 to 8:1) that are used to estimate the conversion of β-carotene into retinol as not all β-carotene can be converted to vitamin A in the body. These authors also indicated that 100-120 g of yellow flesh sweetpotato containing 2500 µg 100 g $^{-1}$ fresh mass of β-carotene was adequate to meet the daily requirement of vitamin A. Mukherjee and Ilangantileke (2002) reported that a regular intake of about 100 g of OFSP roots per day provides the recommended daily amount of vitamin A for children, effectively protecting them from blindness.

Not all sweetpotato have high levels of β-carotene but there is wide genetic variability for vitamin A occurring naturally in sweetpotato (Woolfe, 1992). This means conventional breeding techniques can be employed to incorporate β-carotene into sweetpotato by crossing local cultivars with introductions that have high β-carotene levels. Efforts are underway in Zambia to cross local cultivars with introduced OFSP to improve the β-carotene content of local cultivars. However, to help with the selection process of the progeny, there is a need to establish what consumers of the cultivars demand so their preferences could be used as selection criteria for new genotypes. Participatory Rural Appraisal (PRA) tools were employed to gather the required information.

PRA is an active research tool that involves community members in defining and working to solve local concerns. Most PRAs stress local knowledge, empowerment, and sustainability in addressing natural resource, agricultural, health, social, or other issues (Chambers 1997), although many forms have emerged over the past several years (Pratt, 2001). PRA has been extremely popular among international NGOs and certain government agencies operating in developing countries over the past decade (Cornwall *et al.*, 2001).

PRA is often confused with Rapid Rural Appraisal (RRA). PRA is an “approach and method for learning about rural life and conditions from, with, and by rural people” (Chambers, 1992; Dunn, 1994). The key elements of RRA and PRA are quite similar, with the main difference being that RRA generates information for planners and PRA shifts the “presentation and analysis of information to community members”. Another key difference between RRA and PRA is that in PRA “rushing is replaced by relaxation” and there is a strong rapport with community members (Chambers, 1992).

PRA methods continue to evolve. There exist many PRA methods to help the practitioner involve various sectors and groups of a community in expressing their views, engaging with other community members, and empowering themselves. Among PRA methods is the Participatory Plant Breeding (PPB) method. PPB can be a powerful tool to meet the needs of sweetpotato consumers appropriately. PPB is actually based on a set of methods that involve close farmer-researcher collaboration. The interaction between farmers and researchers/breeders can be various and depends on: 1) the stage of the breeding process at which farmers interact with breeders; 2) the location where

selection and testing of germplasm takes place; and 3) the design and management of the germplasm evaluation process (Morris and Bellon, 2004). PPB recognizes that, regardless of whether the breeder likes it or not, it is the farmers who ultimately decide whether or not to adopt a new cultivar. It reduces the chances of developing cultivars that, for reasons unknown or overlooked by the breeder, are not acceptable to farmers (Ceccarelli *et al.*, 2003)

Against this background, a study was conducted among sweetpotato farmers in three districts of Zambia to assess the importance of sweetpotato in the diets of the people in relation to other crops. Also, PRA tools were used to obtain from farmers input on the traits that determine their choices of sweetpotato genotypes to use for specific purposes. This activity was carried out to add value to the breeding programme as the data would provide benchmarks for genotype selection.

2.2 Materials and Methods

2.2.1 Description of study areas

Due to limited resources, it was not possible to sufficiently cover all the representative areas in Zambia. However, an effort was made to select areas that would not impair the extrapolation of results to other areas of the country. Three representative districts were selected: Samfya is predominantly a cassava production and consumption area; Solwezi is a predominantly sweetpotato growing area; and Mazabuka is an area where cassava and sweetpotato are being introduced (Figure 2.1).

Samfya District
Altitude: 1171 masl
Latitude: 11° 21' 0" S
Longitude: 29° 33' 0" E

Mazabuka District
Altitude: 1102 masl
Latitude: 15° 52' 0" S
Longitude: 27° 46' 24" E

Solwezi District
Altitude: 1386 masl
Latitude: 12° 11' 0" S
Longitude: 26° 24' 0" E

Figure 2.1: Map of Zambia depicting the districts where the survey was conducted

2.2.2 Participants

A multidisciplinary research team was constituted with participants representing the different disciplines as follows: communities – these are the major stakeholders whose participation was indispensable to the success of the development facilitation; an agronomist/breeder; three research technicians; and an extension or community worker. Each participant brought unique experiences to the team. This was essential for capturing as much information as possible that would ensure the successful data collection.

The survey was conducted in September 2006 in Mazabuka and Solwezi when the communities were relatively free from the field work. The survey was done in May 2007 in Samfya just before crop harvesting.

2.2.3 Participatory rural appraisal method

In addition to informal rapport building, more structured information about community resources and opinions was required. Toward this end, primary data was collected via face-to-face exploratory interviews with community members. Two types of exploratory

interviews were carried out to collect information from community members. The surveys were conducted over the course of one week in each district by teams of two interviewers (Figures 2.2 and 2.3) and one or two community members depending on the day. The same agronomist/breeder and technicians conducted the research throughout the period. One or two different community members were selected each day to assist with the interviews. A conscious effort was made to minimize bias by choosing volunteers from different demographic backgrounds. Community volunteers who helped conduct the interviews varied in age from 14 to 65, and the group consisted of males and females, married and unmarried. Questions for the surveys consisted of open-ended and closed-ended questions, and limited probing and iteration were permitted.

Figure 2.2: Interviewing a sweetpotato farmer and his family in Mazabuka district

Figure 2.3: Some members of a focus group for an exploratory interview

All interviews were conducted in the homes of community members or in fields or work sites close to their homes. The interviewees were randomly selected. Due to cultural norms, respondents were predominantly male heads of household; however, often the male head of the household was not at home or available and the female head of household or older children answered questions. Due to cultural norms, children under the age of 15 were permitted to answer questions only if their input was reiterated or affirmed by the primary respondent. The first interview consisted of questions posed to a representative of a household in the community. This approach was chosen to ensure 100% community input and create a direct connection between the research team and every household. This interview was designed to collect socio-demographic information and to assess attitudes about sweetpotato and problems related to sweetpotato within the community.

The second exploratory interview was designed to gather information through both direct observations of the researchers and verbal responses of interviewees. Through this interview approach the research team gathered information regarding the quality and types of household resources for the construction of a community profile.

Three agricultural camps from each district were randomly selected using a simple procedure (Kerlinger, 1985). For each agricultural camp 10 farm families were targeted. However, farmers in the surrounding villages were invited to confirm some of the information. At times, it was challenging to reach the sampled farmers (Figure 2.4).

Figure 2.4: Interview team pondering how to cross the stream in Solwezi district

2.2.4 Data analysis

The data obtained was entered and analysed in Statistical Package for Social Scientist (SPSS) version 15. Cross tabulations were used in the analysis, and the percentages of respondents were calculated and represented graphically where applicable.

2.3 Results

2.3.1 General information about the districts surveyed

Samfya district is situated in Luapula Province in the northern part of Zambia. People are heavily dependant on cassava and sweetpotato for food. Besides subsistence

farming, fishing is the main occupation for the people. Sweetpotatoes are either sold for cash in the fishing camps or exchanged for fish, which is later sold to urban areas.

Solwezi district is situated in the North Western Province and produces significant quantities of sweetpotato roots and vines for home consumption and sale. The most widely grown sweetpotato variety in Zambia, Chingovwa, is named after one of the production sites. Meheba Refugee Camp which hosts refugees from the Democratic Republic of Congo, Angola, Rwanda and Burundi is located in Solwezi. The camp and the surrounding areas are known for sweetpotato production that is sold even beyond the borders of Zambia.

Mazabuka district is situated in the Southern Province of Zambia and is prone to droughts. The area is traditionally a maize production site, but with persistent droughts and removal of subsidies on agricultural inputs, farmers are turning to cassava and sweetpotato production for assured household food security. The potential for sweetpotato production is high as there is a ready market in the nearby urban centre, Lusaka.

2.3.2 Number of farmers interviewed

A total of 87 farmers were interviewed in three districts (31 in Mazabuka, 30 in Samfya and 26 in Solwezi), of which 45% were women and 55% men (Table 2.1). More females were interviewed in Mazabuka (65%) because the crop was considered to be a woman's concern. In contrast, more males were interviewed in Solwezi (77%) because in this area males are not allowed to talk to a married woman without the husband's consent. Overall the interviewees were predominantly male.

Table 2.1 Gender distribution among farmers in three districts of Zambia

District	Total	Percentage of Farmers	
		Female	Male
Mazabuka	31	65	35
Samfya	30	43	57
Solwezi	26	23	77
Total	87	45	55

2.3.3 Years of experience with sweetpotato

To assess the years of experience with growing sweetpotato, the farmers were classified into 1 - 2 years, 3 - 5 years, 6 - 10 years, 11 - 20 years and above 20 years experience in growing sweetpotato: the range being from 1 to 37 years. Seven men and three women could not indicate the specific length of time they had been growing sweetpotato. Since they simply said they had been growing it for many years, they have not been included in the analysis.

Almost half (47%) of the respondents had grown sweetpotato for five years at most. Very few farmers (six respondents) had grown sweetpotato for more than 20 years. The difference between males and females in each experience class was minimal (Table 2.2).

Table 2.2 Distribution of farmers' experience by sex in three districts of Zambia

Experience Class	Number of respondents*		
	Female	Male	Both
1-2 years	3	4	7
3-5 years	15	14	29
6-10 years	10	16	26
11-20 years	6	6	12
Above 20 years	2	1	3
Total	36	41	77

*Three female and seven male farmers are excluded as they could not specify their period of experience.

2.3.4 Source of income

All the respondents interviewed have farming as their livelihood. Their income is generated mainly from the sale of crops. A pairwise comparison was performed for the most important crops for income generation in each district and six of their preferred crops are recorded (Table 2.3). Sweetpotato, though not regarded as a cash crop in the country, appears to be playing a significant role in generating income for farmers in Solwezi and Samfya. Also, it has appeared on the Mazabuka list indicating it is becoming a significant contributor to income generation there as well.

Fishing is the other main source of income in the off-season in Mazabuka and Samfya. In Solwezi, farmers are involved in beekeeping which is being promoted by Keeper Zambia, an NGO promoting the sale of honey. Otherwise, farmers are involved in various kinds of trading to supplement their incomes.

Table 2.3 Crops for income generation in three districts, numbers generated from pairwise comparison

Rank	Mazabuka		Samfya		Solwezi	
	Crop	**Number of respondents**	**Crop**	**Number of respondents**	**Crop**	**Number of respondents**
1	Cotton	27	Cassava	22	Maize	17
2	Sunflower	16	Maize	20	Sweetpotato	12
3	Maize	13	Groundnuts	19	Beans	11
4	Groundnuts	11	Sweetpotato	15	Groundnuts	8
5	Cowpeas	5	Beans	4	Sorghum	4
6	Sweetpotato	3	Bambaranuts	3	Cassava	3

2.3.5 Most important food crops

Farmers were asked to indicate their most important staple crops. Maize emerged as the most important in Mazabuka (all respondents) and Solwezi (26 respondents). In both cases, sweetpotato was second with 10 and 9 of the respondents, respectively, indicative of its status as a complementary staple crop. In contrast, farmers in Samfya indicated that cassava was the most important staple crop with 29 respondents mentioning it whereas sweetpotato (with 9 respondents) was second (Table 2.4).

Table 2.4 Importance of crops for food in three districts of Zambia

Rank	Mazabuka		Samfya		Solwezi	
	Staple Crop	**Complementary crop**	**Staple Crop**	**Complementary crop**	**Staple Crop**	**Complementary crop**
1	Maize (31)*	Sweetpotato (10)	Cassava (29)	Sweetpotato (25)	Maize (22)	Sweetpotato (9)
2		Sorghum (6)	Maize (4)	Maize (17)	Cassava (7)	Cassava (7)
3		Irish potatoes (2)		Fingermillet (3)	Sweetpotato (1)	Sorghum (4)
4		Cassava (1)				Millet (2)
5						Irish potato (1)
Total [a]	31	31	30	30	26	26

*() = Number of respondents
[a]Total = Number of respondents possible

2.3.6 Prevalence of cultivars in the surveyed districts

Forty one names of cultivars were mentioned with Chingovwa being the dominant cultivar grown in Solwezi and Samfya. Mukakabbolo is dominant in Mazabuka. Further investigations revealed that the variety referred to as Kapiri, in Mazabuka is actually Chingovwa. This implies Chingovwa, a released cultivar in Zambia, is becoming a dominant cultivar even in Mazabuka. It was noted that in most cases a variety is named either after the person who brought it to the area or after a place where it came from. A considerable number of respondents (64) did not know the names of particular cultivars they were growing (Table 2.5).

2.3.7 Source of planting vines

Most of the sweetpotato planting material is obtained from within the districts. Only one farmer from each district mentioned having sourced planting vines from outside the district. Materials were sourced from Kapiri Mposhi, Chingola and Kitwe for Mazabuka, Solwezi and Samfya, respectively. As indicated earlier, the dominant cultivar in Kapiri Mposhi is Chingovwa hence its nickname of Kapiri by the people of Mazabuka. The majority of respondents kept their own planting material (26%) while others got it from Kaleya Agricultural Station (11%), friends (10%) and other local sources (17%). Only two people got the seed from research stations (Table 2.6). The remainder of the sources can all be referred to as local vine sources. Hence the local seed sources are very important for sweetpotato production with recycled seed playing a major role (Figure 2.5).

Table 2.5 Names of cultivars grown by farmers and the number of times they were mentioned in each district

No.	Cultivar	Meaning of Cultivar/Remark	Number of respondents*
1	Changachanga	-	3
2	Chapatala	-	4
3	Chingovwa	Released variety	54
4	Chishinde	-	1
5	Chiyinyela	-	1
6	Chumbu mukalamba	The big sweetpotato	1
7	Ifyumbu	Name of sweetpotato in Bemba	1
8	Imbata	-	6
9	Kabalenge	-	1
10	Kabolo	-	3
11	Kabompo	Came from Kabompo	1
12	Kakemba	-	1
13	Kakonko	-	4
14	Kalukuluku	-	1
15	Kalyabalumi	Reserved for the husband	10
16	Kambwalimbwali	-	4
17	Kapasaka	-	1
18	Kapataka	-	1
19	Kapiri	Came from Kapiri	28
20	Kapokola	Brought by a policeman	4
21	Kasimpabasilu	Grown by mad people	1
22	Kasompe	-	4
23	Katendeleka	-	1
24	Konto	-	1
25	Kyapatala	-	4
26	Matembele	-	1
27	Matuwa	-	5
28	Mukahali	Brought by wife to Harry	1
29	Mukakabbolo	Brought by wife to Kabolo	27
30	Mukamanda	Brought by wife to Manda	1
31	Mukamfwilwa	Brought by a widow	1
32	Muntubangezhi	Grown by newcomers	1
33	Munwe umo	Has one finger (referring to leaves)	1
34	Muswete	Light skinned	1
35	Namacushi	Poverty striken	1
36	Namambwe	Mrs Mambwe	1
38	Selumuna	-	7
39	Syanga umbone	Plant and you will see	4
40	Zambezi	Released variety	2
41	Zimbabwe	From Zimbabwe	1

*64 respondents did not know the names of the cultivars they were growing

Table 2.6 Sources of sweetpotato cultivars in three districts of Zambia

Source variety	Percent respondents within district			Total
	Mazabuka	Solwezi	Samfya	
Local	19.4	26.9	6.7	17.2
Kaleya Agricultural Station	32.3	-	-	11.5
Neighbours	6.4	-	-	2.3
Nanga Research Station	3.2	-	-	1.2
Kapiri Mposhi	6.4	-	-	2.3
Friends	9.7	3.9	16.7	10.3
Own seed	19.4	38.5	23.3	26.4
Chibalala	-	-	3.3	1.2
Samfya	-	-	16.7	5.8
Katanshya	-	-	3.3	1.2
Luapula river	-	-	3.3	1.2
Lubwe		-	3.3	1.2
Agriculture	-	-	3.3	1.2
Kitwe	-	-	3.3	1.2
Mwewa	-	-	3.3	1.2
Chesembe	-	-	3.3	1.2
Relatives	-	-	3.3	1.2
Chingola	-	3.9	3.3	2.3
PAM	-	3.9	3.3	2.3
Mansa Research	-	7.7	-	2.3
Maheba	-	11.5	-	3.5
Mumena	-	3.9	-	1.2
N/a	3.2	-	-	1.2
Total	100	100	100	100

Figure 2.5: Plot of sweetpotato seed being maintained in a farmer's yard in Mazabuka

2.3.8 Source of orange-fleshed sweetpotato and traits preferred by consumers

Respondents that had OFSP cultivars were asked where they got vines from. They indicated that they had bought (4 respondents), got from friends (19 respondents) or obtained the materials from Research Stations (3 respondents) (Figure 2.6). Furthermore, the same respondents were asked to comment on what they did not like about the OFSP. The majority indicated poor storage, followed by bad smell (6 respondents) and not good as a vegetable (6 respondents). Wateriness and being fibrous came third and fourth, respectively (Figure 2.7). Poor storage was associated with weevil infestation whereas bad smell referred to the aroma after boiling.

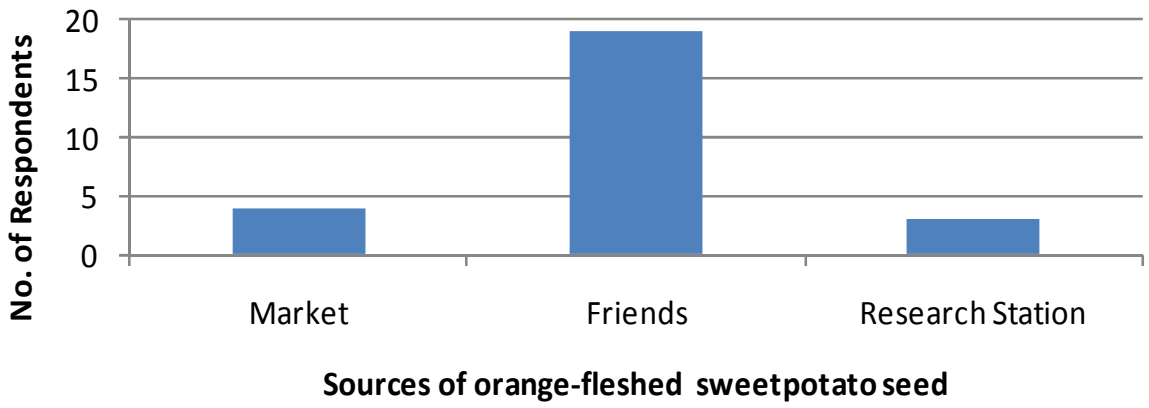

Figure 2.6: Sources of orange-fleshed sweetpotato seed in three districts of Zambia

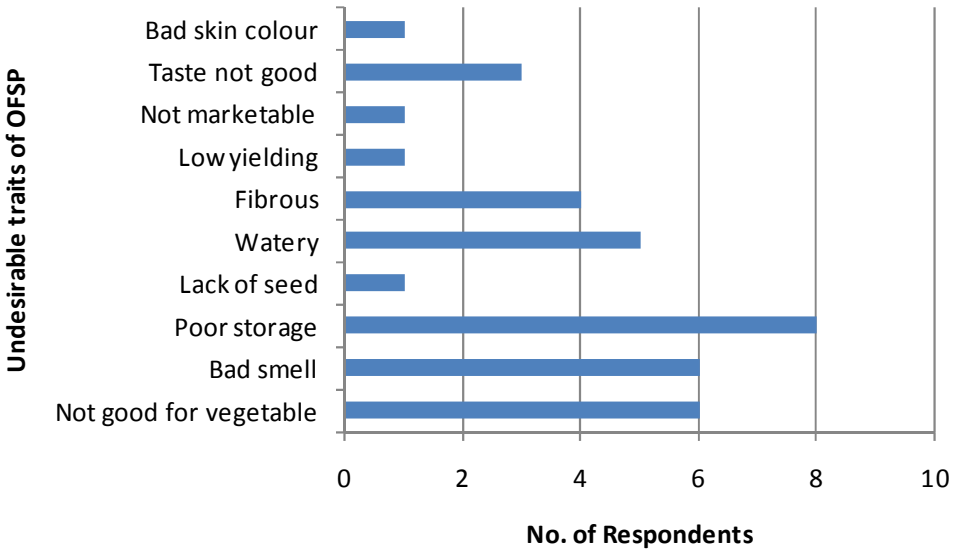

Figure 2.7: Undesirable traits of orange fleshed sweetpotato in three districts of Zambia

2.3.9 Preferred cultivars

Farmers were asked to indicate the variety they preferred most as well as the reason(s) for their preference. Chingovwa is the most favoured cultivar in all districts by 67% of the respondents, followed by Mukakabolo at 20% (Figure 2.8).

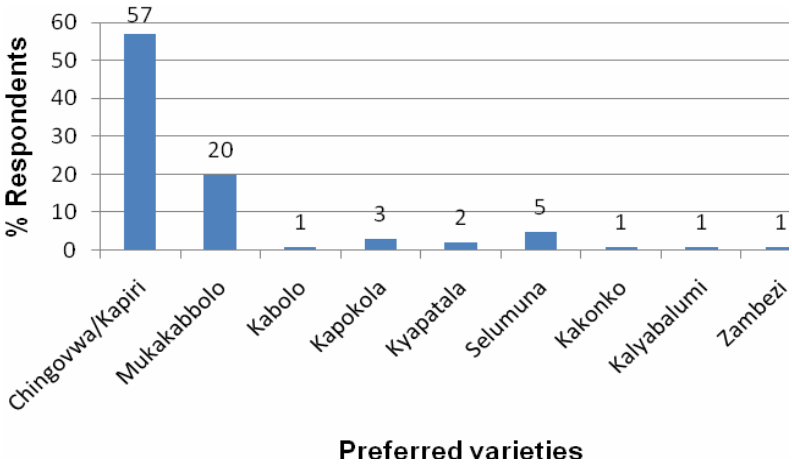

Figure 2.8: Farmers' preferred cultivars in three districts of Zambia

According to the results of the survey, the reasons for variety preference by the farmers in all the three districts were as described below (Figure 2.9). The most common preference among farmers was the level of sweetness of the roots which accounted for about 35 % of the respondents followed by the yield of variety at 23%. The joint third common reasons for preference were early maturity and good storage at 9% each.

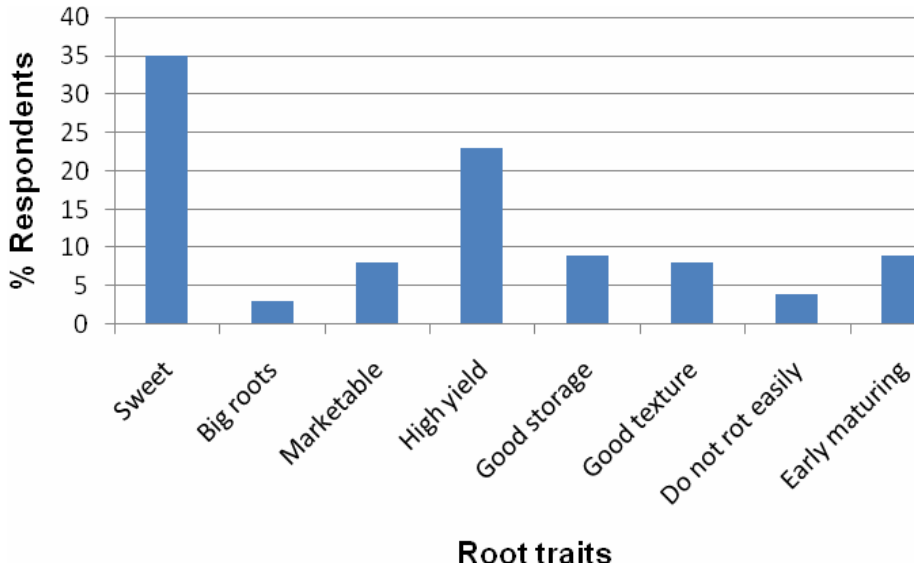

Figure 2.9: Farmers' preferences for sweetpotato roots in three districts of Zambia

2.3.10 Preferences of children and reasons for preference as perceived by their parents

The cultivar preference among children (age 5 and below) also confirms that Chingovwa is most favoured variety by 72% of respondents followed by Mukakabbolo at 16% (Figure 2.10). Varietal preferences are similar to that of adults (Figure 2.9).

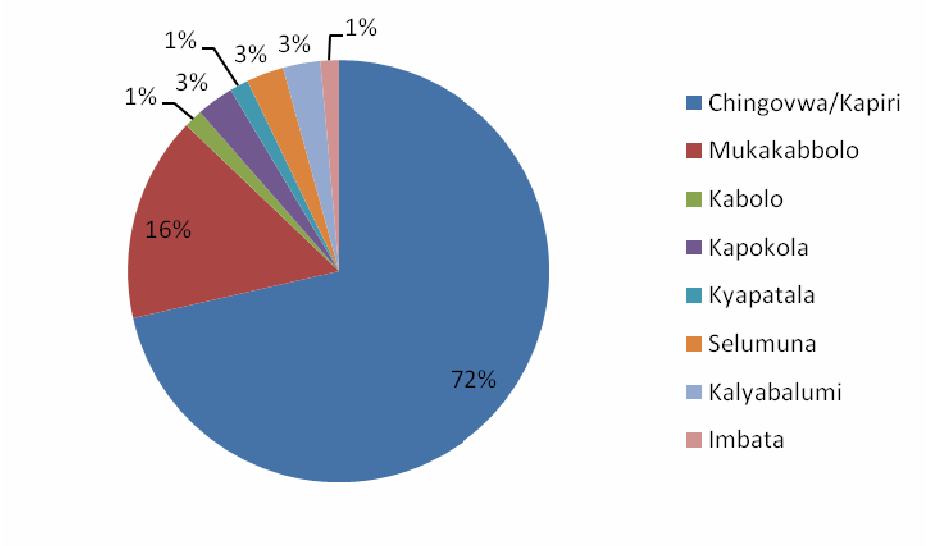

Figure 2.10: Cultivars preferred by children in three districts of Zambia

However, unsprisingly children based their preferences mainly on attributes related to eating as opposed to agronomic traits. The most favoured trait by children was the good taste of the variety at 32% of the respondents and colour of the variety at 10% of the respondents. The other traits preferred by children included availability of a variety for 8% of the respondents. The following attributes were at par with 6% of the respondents giving a preference for high yield, high dry mass composition and sweetness (Table 2.7).

Table 2.7 Reasons for preference of sweetpotato cultivars by children as perceived by adults

Reasons for preference	Frequency	Percent	Rank
Used to colour	9	10	2
Readily available colour (Common)	7	8	3
Good for marketing	2	2	6
High yield	5	6	4
Trying new colour	1	1	7
High dry mater content	5	6	4
Good storage	2	2	6
No stomach problem	1	1	7
Very soft	1	1	7
Early maturity	5	6	4
Easy to grow	1	1	7
Good taste	28	32	1
Sweet	5	6	4
Contain Vitamins	3	3	5
Learn about OFSP	1	1	7
Good shape	1	1	7
No response	5	6	4
Need for food	1	1	7
Looks good	1	1	7
Good texture	2	2	6
Attracts customers	1	1	7
Total	87	99	

2.3.11 Farmers who changed cultivars

Farmers were asked if they had recently changed cultivars, and the results indicate that a number of the farmers (39% in total) had actually changed cultivars. The percentages of respondents who changed cultivars within districts were 41.9% in Mazabuka, 42.3% in Solwezi and 33.3% in Samfya (Figure 2.11). The survey results illustrate that the main

reason(s) some people had not changed variety especially in Samfya may be attributed to non availability of alternative cultivars as most of them were growing Chingovwa.

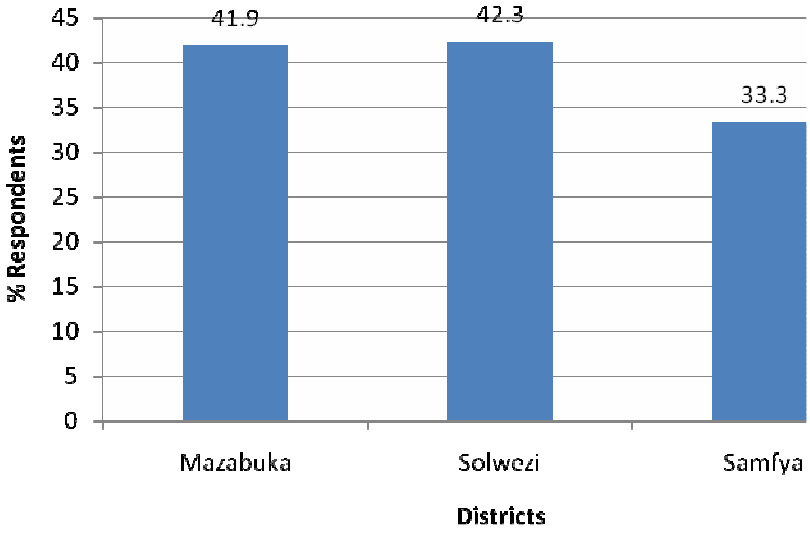

Figure 2.11: Percentage of farmers who changed cultivars within three districts of Zambia

The reasons for farmers changing cultivars were various (Figure 2.12). In Mazabuka, 16% of the respondents indicated that they changed cultivar because the old ones were low yielding while others (10%) indicated that the cultivars they were growing were of late maturity. Twelve percent of the respondents gave various reasons which included lack of planting material (3%), cause heart diseases (3%), small root size (3%) and because new cultivars taste better (3%).

Nineteen percent of respondents changed cultivars because the cultivars they were growing were low yielding while others (15%) indicated that the cultivars they were growing had small root size. Others (8% of the respondents) said they changed cultivars because the cultivars they were growing had no market.

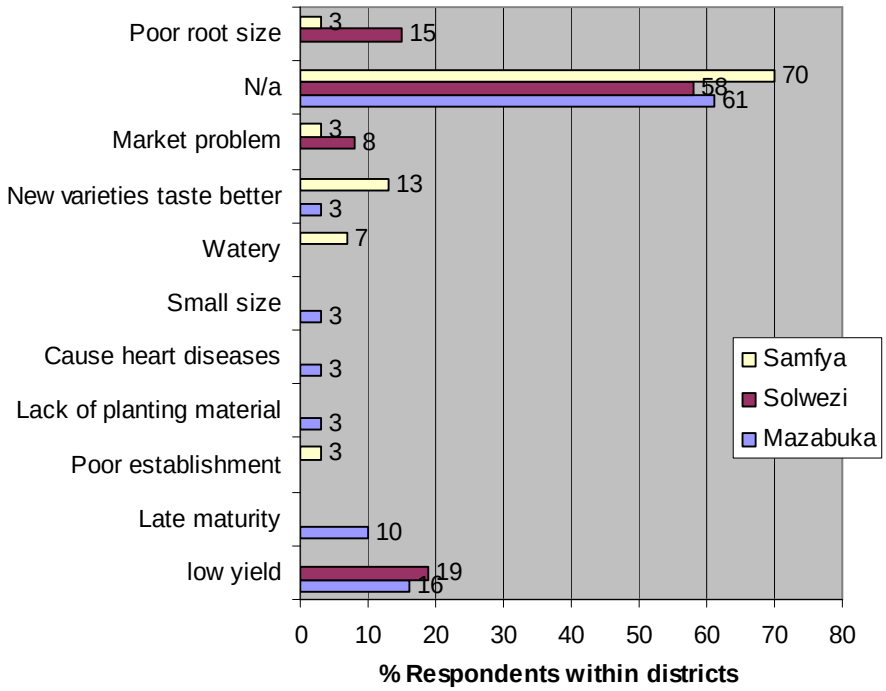

Figure 2.12: Reasons for abandoning sweetpotato cultivars in three districts of Zambia

2.3.12 Occurrence of malnutrition in families

Respondents were asked to indicate whether they had had incidences of malnutrition in their families. Malnutrition incidences were low in Solwezi (7.7%) and Samfya (6.7%). More than half of the respondents (51.6%) in Mazabuka had experienced some form of malnutrition (Figure 2.13). Fifty nine percent of respondents indicated they had no access to supplementary feeding to mitigate against malnutrition. Mazabuka, which had the highest number of people who reported malnutrition in families (51.6%), had the highest percentage (77.4%) of people accessing supplementary feeding (Figure 2.14).

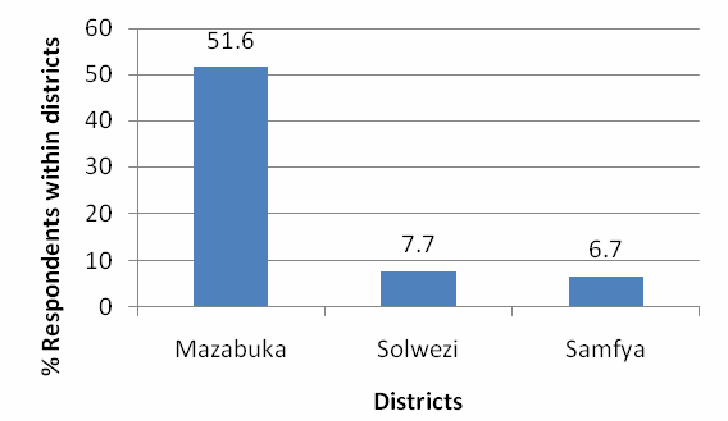

Figure 2.13: Malnutrition incidences in three districts of Zambia

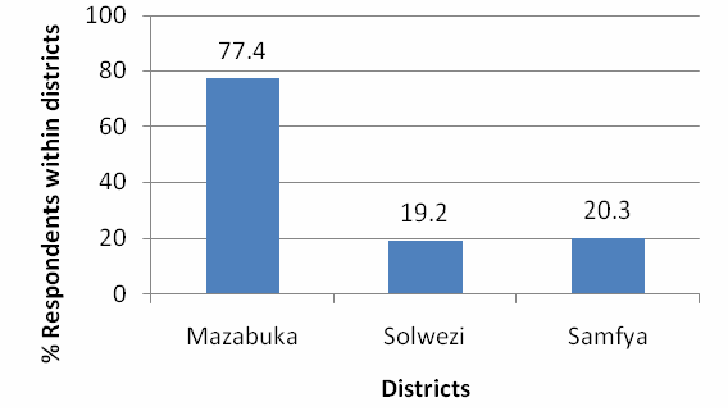

Figure 2.14: Farmers having access to supplementary feeding in three districts in Zambia

Farmers were asked about their knowledge on the importance of vitamin A and consuming food which met vitamin A requirements. In Mazabuka and Solwezi districts, most farmers (58% and 77%, respectively) expressed ignorance on the benefits of vitamin A, whereas in Samfya a larger percentage of the farmers (66.7%) had some knowledge on the benefits of vitamin A (Figure 2.15).

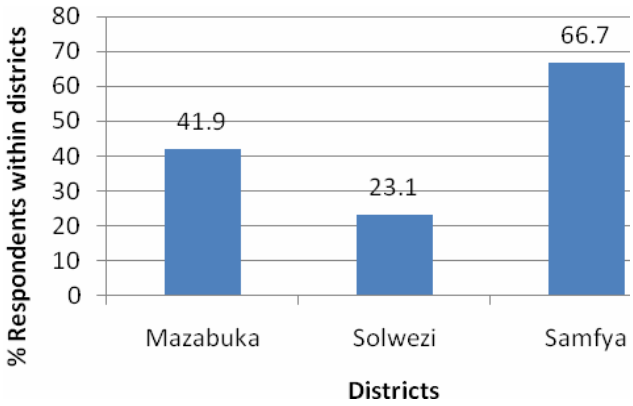

Figure 2.15: Farmers with knowledge of the benefits of vitamin A in three districts of Zambia

2.4 Discussion and conclusion

A high incidence of malnutrition was recorded in Mazabuka with more than half of the respondents having experienced it in one form or another. This result was corroborated by the high percentage of respondents accessing supplementary feeding from health institutions to alleviate malnutrition. This result demonstrates that resources are channelled first to where the greater need is. Rarely has it been reported that Solwezi and Samfya received food relief whereas it is reported almost every year that Mazabuka district receives food relief. In addition, results from the survey (Figure 2.15) indicate more farmers in Solwezi and Samfya are aware of the benefits of vitamin A than Mazabuka. This lack of knowledge may explain Mazabuka respondents reporting a high incidence of malnutrition. Therefore, the introduction of high β-carotene cultivars to mitigate VAD will be particularly pertinent to the people in Mazabuka.

Sweetpotato is one of the most important crops in large parts of Zambia. Its significance in the diets of people can be attested by the fact that sweetpotato has been grown for more than 20 years in all the districts surveyed. Its low profile in the food basket of the Zambian people is due to the fact that the crop is still considered insignificant to warrant gathering information on it. The Central Statistical Office in Zambia does not collect information on sweetpotato. However, this survey indicates that it contributes significantly to the diet and income generation in many of the households. Since

sweetpotato is already contributing significantly to income generation in the three districts, the endeavour to reduce VAD by improving the β-carotene content of sweetpotato will be successful. The genetic variation among local landraces indicates potential for selection of high β-carotene containing OFSP. However, with the predominance of popular cultivars like Chingovwa this genetic diversity may be lost. Hence, there will be need to release more diverse genotypes so as to conserve the remaining genetic diversity and conserve the genes still available with the farmers.

The released variety, Chingovwa, has been used by more than 90% of the respondents and has a considerable share of the land under sweetpotato cultivation. At the moment, it is the most preferred variety in the districts surveyed. This indicates that when a variety is good, its diffusion will take place without much effort from the developers. About 40% of the respondents reported having changed cultivars. The change may have resulted due to the release of Chingovwa which is being grown by the majority of farmers in the surveyed areas. It appears that Chingovwa is generally being distributed without its name being changed as normally is the case. This trend would help in tracking the spread of the new genotypes in future. Chingovwa was selected as SPN/O in Tanzania, released in Malawi in 1986 and named Kenya. In Zambia, it was released in 1993.

Sweetpotato vines are obtained from various sources within a district. Predominant among these sources are own, friends and relatives. It appears that whatever the source of planting material, once farmers have obtained a particular cultivar, they multiply it on-farm. Hence, buying has not featured as a source of planting materials. However, in the case of OFSP, few farmers (four only) reported having bought the planting materials. Sharing of planting materials among friends and relatives may be an indication that farmers are particular about the sources of their planting materials and the traits they posses. They are more likely to believe a relative than an outsider concerning the attributes of the planting material. There is an opportunity for a multiplication system to be created in these districts to supply planting materials to the farmers at the beginning of the rainy season. Most farmers did not have adequate irrigation facilities to multiply enough seed to fully plant their fields at the beginning of the planting season.

The majority of farmers chose sweetpotato cultivars based on the organoleptic properties of the variety, yield and storage. The organoleptic properties included root

fibre content, aroma, texture, wateriness and colour of the flesh. Traits related to yield included number of roots, root size, vegetable production and time of maturity. Storability referred to resistance to pests such as weevils, and diseases causing rots. By implication, the disliked attributes will need to be selected against if new cultivars are to be accepted by farmers and consumers in these areas; though the small sample size of the survey must be borne in mind in terms of full representation of all farmers and consumers.

In this PRA, an assessment of the importance of sweetpotato in the diets of the people in relation to other crops was done. Also, an attempt was made to obtain the respondents' input on the traits that determine farmers' choices of sweetpotato genotypes for specific end-uses. This study was carried out to add value to the breeding programme as the data has provided benchmarks for genotype selection.

Some of the selection criteria identified in this study relate to root storability, taste, fibrousness, dry mass percentage, leaves that make a good vegetable and resistance to pests and diseases. All these attributes will be used as selection criteria in the breeding programme.

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Chapter 3: Evaluation of sweetpotato germplasm for yield and β-carotene based on farmer preferences

Abstract

Sweetpotato is cultivated across a wide range of agroecological conditions. The objective of this study was to collect and evaluate sweetpotato germplasm for yield traits i.e., storage root yield, biomass, and harvest index (HI) and nutritional traits (i.e., root dry mass (RDM) and β-carotene content) in order to select parents for a β-carotene breeding programme. Sixty four germplasm accessions collected in four districts of Luapula Province in Zambia were evaluated and compared at Mansa Research Station in an 8 x 8 triple lattice experimental design. Genetic variation was detected for the traits of interest indicating that improvement was possible. Based on a selection index for HI, RDM, and good storability, 10 best performing accessions were selected for further evaluation and possible release and use as parents in a polycross. Mean root dry mass composition of the 10 selected parents was 32%, which was higher than the 28% of the popular cultivar Chingovwa. The HI of the selected parents was more than 80% and their mean root fresh yield was 3 t above the grand mean 8.86 t ha^{-1}. The selected parents have since been incorporated in a polycross.

3.1 Introduction

With the importance of maize (*Zea mays* L.) declining both in area and productivity in Zambia, production of other crops such as sweetpotato has been increasing. For example, between 1989 and 1999, the total area planted to sweetpotato increased by 54% (FAO/WFP, 2002). According to WHO (1995), vitamin A deficiency (VAD) is a problem of public health significance in Zambia. Subclinical VAD is significant, with a prevalence rate of 13.6% among 6 to 12 year olds. A survey reported in this thesis (Chapter 2) indicated a considerable number of respondents expressing ignorance on the benefits of vitamin A. Therefore, increasing the levels of vitamin A precursors in the human diet through increased consumption of orange-fleshed sweetpotato (OFSP) will make a significant contribution to improved health. It has been estimated that

consumption of bio-fortified OFSP in countries such as Uganda could reduce the burden of VAD by 40 to 66% as measured by the disability-adjusted life years[1] (Yanggen, 2005).

Sweetpotato is currently the second most important root crop in Zambia. Economic pressures that resulted from the Structural Adjustment Programme that was implemented by the government of Zambia in the late 90's and the beginning of this century caused food deficits, especially in urban areas (Simatele, 2006). As a coping strategy, many urban households turned to sweetpotato as an alternative food, especially for breakfast. Small-scale farmers in rural areas and some urban households have taken advantage of the situation and are now growing sweetpotato as a cash crop for sale to urban dwellers. Sweetpotato is more widely grown in the country than cassava, albeit on smaller plots per producing household. It is traded widely in the country and demand is increasing. It is assumed that sweetpotato will also directly substitute for maize nation-wide, thus further reducing the national maize requirements (FAO/WFP, 1998).

Though sweetpotato has all these advantages, it is not without problems. Among the constraints in Zambia are low yields resulting from lack of planting materials and improved cultivars. The roots generally have poor storability and most of the roots are not marketable due to weevil damage and unacceptable root shape. Available genotypes take long to mature and most do not do well under drought stress (Chiona, 1998).

The Zambian sweetpotato breeding programme is at a rudimentary stage. The genotypes under evaluation are mainly introductions or crosses of introductions from the International Potato Center through their Sub Saharan Africa Regional Office in Kenya. Among these introductions are OFSP genotypes with a low dry mass (Hagenimana *et al.,* 1999) which are less desirable (Chapter 2). To widen the genetic base of the breeding lines and to facilitate selection of parents for a β-carotene breeding programme, a collection of germplasm was undertaken. The germplasm collected was evaluated in a preliminary trial and selections made based on the agronomic traits.

[1] Daily-adjusted life years combines the years of life lost to death and the years of life spent with disability to give an overall estimate of the burden of disease.

3.2 Materials and Methods

3.2.1 Sweetpotato germplasm collection

Sweetpotato germplasm was collected in the Mwense, Kawambwa, Nchelenge, and Samfya districts of Luapula Province in Zambia in June and July 2006 (Figure 3.1). The collecting teams were organized to include two agricultural research workers and one extension worker. The extension workers interviewed the farmers to obtain indigenous knowledge and contextual data. Agricultural research workers collected germplasm and carried out the preliminary morphological characterisation.

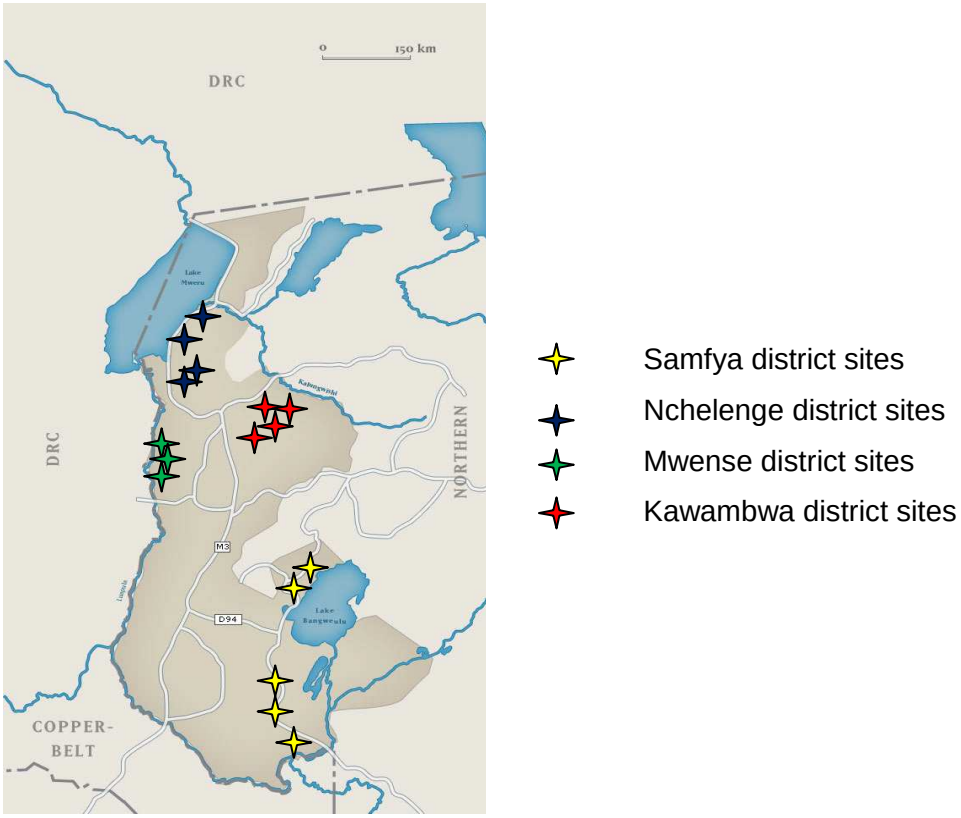

Figure 3.1: Sites of collecting sweetpotato germplasm in Luapula Province of Zambia

To select target areas for germplasm collection, the production statistics from each agricultural district office were reviewed. Sweetpotato production is for both human (roots and leaves) and animal (leaves) consumption in the four districts. Therefore,

cultivars that produce high quantities of vines along with the good storage-root production are the preferred genotypes in these areas. Collections in Mwense and Kawambwa districts were concentrated on the plateau (S 10° 25' 0", E 29° 0' 0"; Altitude 1175 masl) as this is where most sweetpotato is grown in these districts of Zambia. For Nchelenge district, most samples were collected in the valley area (S 9° 0' 0", E 29° 0' 0"; Altitude 919 masl). In Samfya, collection was concentrated in the Katanshya, Tuta road and Lubwe (Mwewa) areas.

At least three vine cuttings were obtained for each accession. The vines were easier to collect and less bulky to transport than roots. The cuttings were wrapped in a moist tissue paper and placed in transparent plastic bag that had aeration holes punched in them. Preliminary morphological characterization of leaf, vine and storage root was done at the collecting site, using Huaman's (1991) "Descriptors for Sweetpotato". This characterization was useful for obtaining preliminary data and for separating accessions that had been accidentally mixed up. Each accession was carefully labelled and given a code identifying the district and the farmer providing the accession. Additional information about the accessions was collected using a simple passport data sheet, to help understand why the farmers keep the cultivars. Farmers' knowledge helped to classify the accessions according to traits such as taste, sweetness, and quality after cooking. Information on special usage, such as weaning food was also obtained.

3.2.2 Germplasm screening and evaluation

Seventy accessions were collected and were multiplied at Mansa Research Station (11° 14'S and 028° 57'E), Mansa, Zambia. Multiplication involved planting three to four node cuttings vertically at a spacing of 10 x 10 cm in nursery beds 1 m wide. Two-thirds of the cutting was inserted into the soil. However, six accessions did not produce sufficient planting material for evaluation. As a result, only 64 accessions were evaluated in an 8 x 8 triple lattice design with three replications. Each plot comprised of two 5 m long ridges spaced 1 m apart and were approximately 20 cm in height. Two-thirds of tip-cuttings about 20 to 30 cm in length were inserted into a ridge at 25 cm intra-row spacing. The trial was planted on 5 December 2006 when the rains stabilised. Soil analysis was conducted to determine the nutrient status of the trial site (Appendix 3.1). No fertilizers were applied to the trial. Weeding was done by hand hoes as required.

Morphological characterisation was carried out for all accessions maintained in the collection. Observations were made 80 to 100 days after planting. The shape of mature leaves, the pigmentation of the abaxial leaf, petiole pigmentation and length, vine internode diameter and length, vine pigmentation, plant type, leaf colour, and storage root skin and flesh colour were used as indicators as described by Huaman (1991). The colour chart developed at CIP was used to record storage root skin and flesh colour.

Roots were harvested at 6 months after planting using hand hoes. The number of plants harvested, number of marketable and unmarketable roots and their yields were recorded. Root morphological characterization was done at harvest. Root samples were obtained for dry mass determination. Five hundred gram samples were dried in a forced draught oven for 72 h until they attained constant mass. Scores for root cracking, weevil damage and mole *(Cryptomys amatus)* damage were recorded (Table 3.1).

Table 3.1 Score definitions for sweetpotato root cracking, weevil damage and mole damage

Score	Definition			Reaction
	Cracking	Weevil damage	Mole damage	
1	No symptom	No symptom	No symptom	Highly resistant
2	1-5 roots with cracks in a plot of 20 plants	1-5 roots with weevil damage in a plot of 20 plants	1-5 roots with mole damage in a plot of 20 plants	Resistant
3	More than five roots affected slightly (5-10% of root area)	More than five roots damaged slightly (5-10% of root area)	More than five roots damaged slightly (5-10% of root area)	Moderately resistant
4	All roots affected moderately (11 - 25% of root area)	All roots damaged moderately (11 - 25% of root area)	All roots damaged moderately (11 - 25% of root area)	Susceptible
5	All roots affected severely (>25% of root area)	All roots damaged severely (>25% of root area)	All roots damaged severely (>25% of root area)	Highly susceptible

3.2.3 Data Analysis

The data for yield and yield traits and some biotic stresses were analysed using the REML (residual maximum likelihood) procedure in Genstat version 11.1 (Payne *et al.,* 2007). Raw data for root cracking, weevil damage, mole damage, sprouting, and root fresh colour exhibited skew distribution and were therefore transformed. Log transformation was performed on root cracking and sprouting data, exponential transformation (e^x, where x is the observed value) on weevil damage data, and square root transformation on mole damage and root fresh colour data. All analyses were performed on transformed data. Mean squares (Table 3.3) and means (Appendix 3.3) of the traits are presented.

3.3 Results

3.3.1 Sweetpotato germplasm collection

A total of 70 sweetpotato accessions were collected in four districts of Luapula Province, of which 13 were orange-fleshed genotypes and the rest white-fleshed. There was

considerable variation in the accessions collected. Detailed information about each collected accession and the attributes the farmers considered important for each accession were recorded (Appendix 3.1). High yield and high RDM ranked highly as the most preferred traits (Table 3.2).

Table 3.2 Reasons provided by farmers for using a particular sweetpotato genotype in order of preference

Ranks for preferences		**Ranks for uses**	
Rank	**Reasons for preferring genotypes**	**Rank**	**Uses of the genotypes**
1	High yield	1	Boil for breakfast or snack
2	High root dry mass	2	Leaves for vegetable
3	Big roots	3	Dried snack (Insemwa)
4	Good taste	4	Cooked with groundnuts as a meal
5	Not fibrous	5	Fried snack
6	Good storage	6	Source of income
7	Good for leaves	7	Roasted snack
8	Planting materials readily available	8	Control termites
8	Source of Vitamin A		

3.3.2 Germplasm screening and evaluation

Only 64 of the 70 genotypes collected were ultimately analysed. Several variables were evaluated for each of the 64 accessions, namely cracked roots (CK), weevil damage (WD), mole damage (MD), sprouting (SP), harvest index (HI), number of roots (both marketable and total), yield of roots (both marketable and total), vine yield (above-ground biomass) and colour of both flesh and skin. Morphological characterisation was done as well but the results have not been presented in this document. The REML analyses for the traits revealed significant differences among the accessions except for MD and SP (Table 3.3).

Table 3.3 REML analysis of selected traits of 64 sweetpotato accessions evaluated in an 8 x 8 triple lattice design

Traits	ndf‡	Wald statistic◊	ddf† statistic	F probability
Weevil damage (score)*	63	97.41	1.55	0.020
Vine yield (t ha^{-1})	63	144.46	2.29	<0.001
Total roots (ha^{-1})	63	213.08	3.38	<0.001
Total plant yield (t ha^{-1})	63	337.98	5.36	<0.001
Sprouting (score)*	63	73.08	1.18	0.219
Total root yield (t ha^{-1})	63	365.68	11.03	<0.001
Root flesh colour (score)*	63	695.15	11.03	<0.001
Marketable root yield (t ha^{-1})	63	337.37	5.36	<0.001
Marketable roots (number ha^{-1})	63	134.02	2.13	<0.001
Mole damage (score)*	63	71.87	1.14	0.264
Harvest index	63	205.80	3.27	<0.001
Root dry mass (%)	63	261.13	4.14	<0.001
Cracking (score)	63	110.31	1.75	0.004

*REML analyses performed on transformed data; ‡ndf=numerator degree of freedom; †ddf=denominator degree of freedom; ◊Wald Stastic is equivalent to a Mean Square in ANOVA

Table 3.4 Mean, standard error, and range of measured traits of 64 sweetpotato accessions at harvest

Trait	Statistic				
	Mean	S.E.	Minimum	Maximum	CV (%)
Cracking (score)*	0.10	0.04	0	0.36	37.4
Root dry mass (%)	34.57	0.38	22.50	47.50	8.1
Harvest index	0.73	0.02	0.1071	0.95	13.4
Marketable root yield (t ha^{-1})	8.21	0.54	0.25	20.63	28.5
Marketable root number ha^{-1}	41 924	4527	2 500	103 750	39.1
Root flesh colour (score)*	0.24	0.02	0	2	31.2
Total root yield (t ha^{-1})	8.86	0.55	0.38	21.75	25.1
Sprouting (score)*	0.06	0.01	0	0.3	
Total root number ha^{-1}	65 186	7993	5 000	278 750	36.7
Vine yield (t ha^{-1})	2.99	0.66	0.25	13.75	47.3
Weevil damage (scores)*	15.35	4.90	2.72	43.09	38.5
Mole damage (score)*	1.30	0.05	1.00	1.72	41.4

*Statistics based on transformed data

Thirty two of the accessions had a WD score of less than two. The other 32 had scores between 2 and 4 (Figure 3.2). Root CK were predominant (score 2 to 3) in 8% of the accessions. The other genotypes had scores of less than 2 (Figure 3.3).

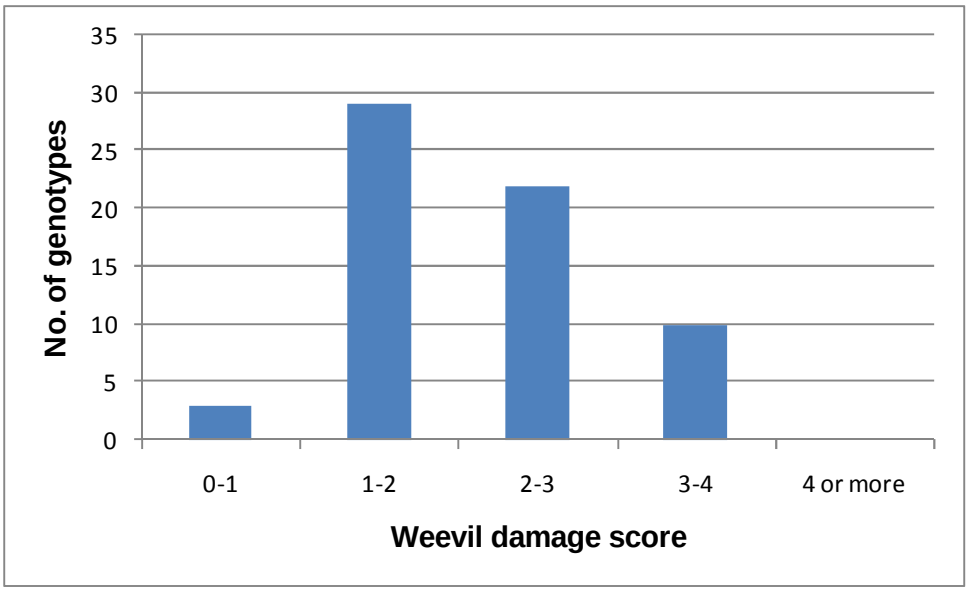

Figure 3.2: Frequency distribution of weevil damage scores for 64 sweetpotato accessions

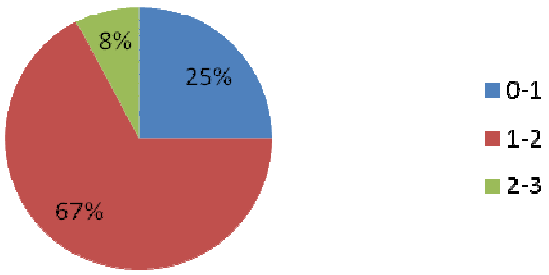

Figure 3.3: Frequency distribution of root cracking scores of 64 sweetpotato accessions

The majority of the accessions (57) were cream or white with very few orange types. There were more white types (37) than cream types (20). In general, some variability was observed in root flesh colour though the data were skewed towards the white flesh colour (Figure 3.4).

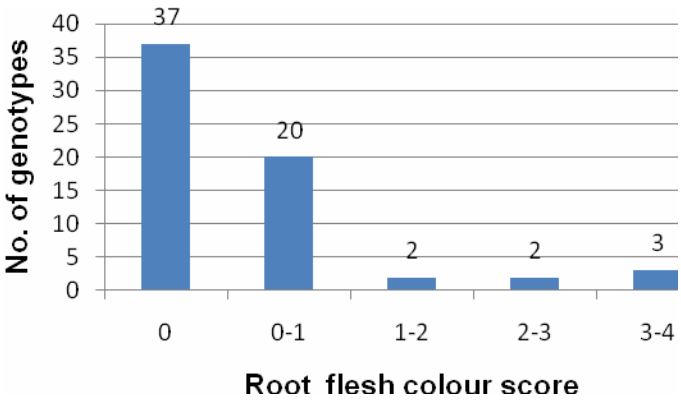

Figure 3.4: Root orange flesh colour scores of 64 sweetpotato accessions

The HI values for most of the accessions were above 0.5. In fact, more than 50% of the accessions had a HI greater than 0.7. The HI of 0.5 and above is desirable as it means more photosynthates were allocated to the economic part of the plant. In this case, only two accessions had unacceptable HI (Figure 3.5).

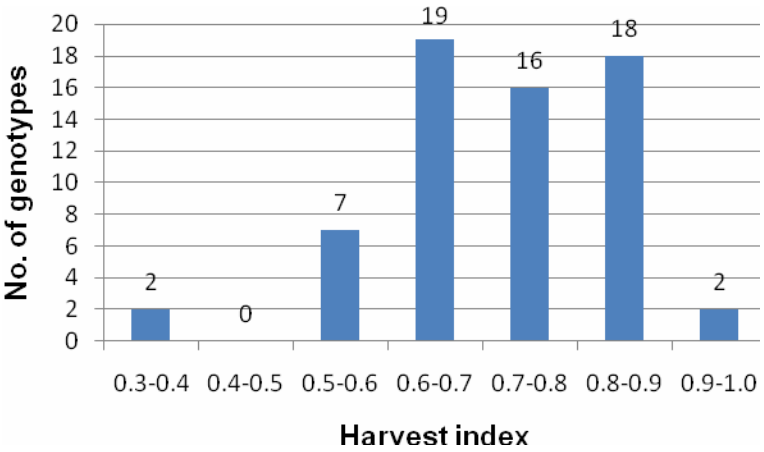

Figure 3.5: Harvest index of 64 sweetpotato accessions

Root dry mass (RDM) was greater than 30% in 58 accessions. About half (31) of the accessions recorded RDM >35%. However, some of the orange fleshed genotypes were among the low RDM (<30%) accessions. In addition, it was observed that six accessions had very high RDM (>40%) (Figure 3.6).

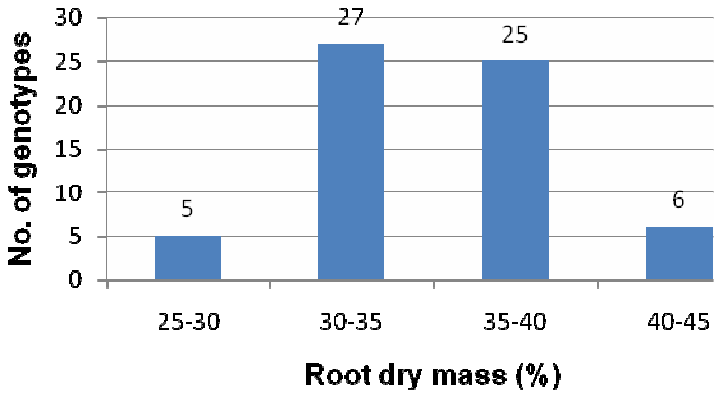

Figure 3.6: Root dry mass of 64 sweetpotato accessions

Thirty four of the accessions had vine yields of less than 3 t ha^{-1} (on a fresh mass basis). Conversely, there were three accessions with more than 6 t ha^{-1} (Figure 3.7). The number of marketable roots for 84% of the accessions was more than 30 000 ha^{-1} (at least one root per plant). Sixteen percent of the accessions had less than 30 000 marketable roots ha^{-1} (Figure 3.8). The mean marketable root yield ranged from 1.2 to 15.6 t ha^{-1} (Appendix 3.2). Thirty eight of the accessions yielded above 8 t ha^{-1} (above average) (Figure 3.9).

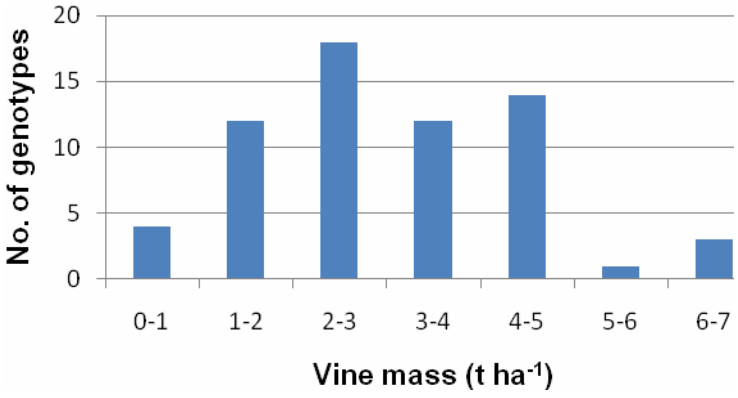

Figure 3.7: Vine yield for 64 sweetpotato accessions

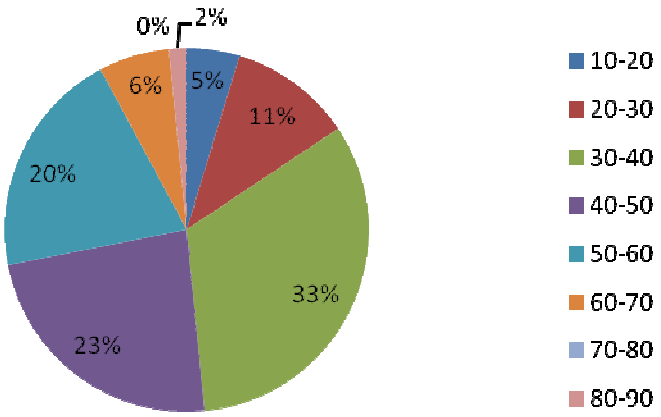

Figure 3.8: Distribution of marketable root numbers per hectare ('000) of 64 sweetpotato accessions

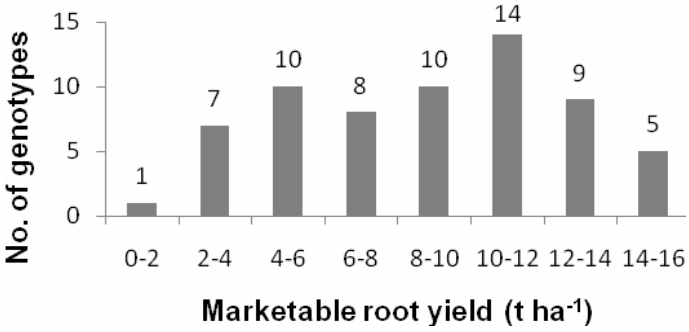

Figure 3.9: Marketable root yield for 64 sweetpotato accessions

3.3.3 Selection of preferred genotypes from the germplasm accessions

The following selection index (SI) based on farmer preferences was applied to the replicate means of the selected traits:

$SI = 5P_1 + 4P_2 + 3P_3 - 2P_4 + P_5$

Where: P_1 = genotype root yield (t ha^{-1})

P_2 = root dry mass %

P_3 = marketable root number

P_4 = Weevil damage (transformed scores)

P_5 = vine yield (t ha^{-1})

The numbers (5, 4, 3, -2, 1) represent the weights in terms of importance accorded to each trait as determined by farmer preferences (Baker, 1986). For example, weevil damage had a negative value because weevil damage is obviously not desirable. The 10 best performing accessions based on the selection index were selected as parents for the β-carotene breeding programme (Table 3.5). Among the 10 best accessions were three orange-fleshed genotypes (No name, Carrots, and Carrots Mwewa). These 10 best accessions were also used as parents in a polycross (Chapter 5).

3.4 Discussions and Conclusions

The aim of this study was to identify superior genotypes that could be used as parents in a breeding programme to produce progeny that are high in β-carotene and dry mass while maintaining preferred consumer attributes. The fact that orange-fleshed sweetpotato are already grown by farmers should mean that orange fleshed, high dry mass genotypes arising from the breeding programme will be readily accepted, depending on combinations with other traits.

Farmers provided their opinion on the preferred attributes for sweetpotato genotypes they utilize. Their responses related to the taste of the genotypes as well as to the survival of the plants in the field. Preferred taste attributes were: sweetness of the roots; high RDM; acceptability of the leaves; and low root fibre. Survival attributes were: ready availability of vines and leaf retention. The implications of these results are that in selecting new sexual recombinants, taste and survival are priority traits for their acceptance by farmers and consumers.

Table 3.5 Ten sweetpotato accessions selected for use as parents in a breeding programme ranked according to a selection index

Accession Genotype Number	ID	Name	Total root yield (t ha^{-1})	Root dry mass (%)	No of marketable roots ha^{-1}	Weevil damage score*	Vine yield (t ha^{-1})	Selection index score
52	13K	No Name	6.29	27.32	80990	1.833	1.02	243069
4	3K	Matembele	11.78	34.70	68177	1.542	2.46	204720
2	12N	Munwe umo	11.93	25.90	68021	3.562	1.27	204150
15	1M	Matembele	12.48	31.67	66979	2.625	2.50	201082
29	15S	Kabalenge	13.61	30.91	65130	1.729	3.62	195574
64	6S	Kasompe	10.50	34.29	59310	3.062	3.70	178077
34	14N	No Name	13.94	30.83	57253	1.750	1.55	171939
19	9S	Carrots	14.99	33.46	56979	2.146	2.26	171108
40	13S	Carrots Mwewa	15.40	35.21	56693	3.188	2.91	170245
56	3S	Katansha	11.29	36.56	55898	3.625	2.54	167821
		Mean	12.22	32.08	63543	2.510	2.38	

*Weevil damage score 1 = No symptom, 2 = 1-5 roots with weevil damage in a plot of 20 plants, 3 = Many roots slightly damaged (5-10% of root area), 4 = All roots moderately damaged (11-25% of root area), and 5 = All roots severely damaged (>25% of root area). Exponential transformed scores.

There was considerable variation in all the measured attributes, except for MD and SP which could be exploited for genetic gain in future breeding programmes. There were 31 accessions that had relatively low levels of weevil damage (Figure 3.2). Ninety two percent of the accessions had relatively low cracking levels (Figure 3.3). Weevil damage and cracking make sweetpotato genotypes undesirable. The results indicate that there are genotypes that may serve as sources of resistance to weevils and cracking. Although moderate levels of resistance to the sweetpotato weevil have been recorded (Jones *et al.*, 1983; Talekar, 1987), two critical problems have prevented meaningful levels of resistance being achieved. Firstly, the expression of several key genes controlling resistance appear to be environmentally modulated, thus the level of resistance can readily change over time and location (Son *et al.,* 1991; Marti *et al.,* 1993a, b). Secondly, the minimal success achieved via years of breeding for weevil resistance suggests that it is doubtful that a single biochemical determines resistance to weevils.

There was wide variation in root flesh colour though more accessions were white-fleshed than the other colours (Table 3.4; Figure 3.4). This finding confirms Kays' (1985) assertion that the genepool of sweetpotato contains a wide range of root flesh colours that can be selected relatively easily. In addition, there are a number of studies related to sweetpotato nutritional traits that indicate a considerable variability in sweetpotato germplasm for food quality traits that include flesh colour (Colllins, 1990; Woolfe, 1992; Ravindran *et al.*, 1995).

The genotypes collected from farmers had very high dry mass composition clearly indicative of farmers' preferences. However, one orange-fleshed accession had a very low dry mass of 18% confirming the negative association between these traits. This inverse relationship between orange flesh and high dry mass poses a considerable challenge to a sweetpotato breeding programme (Ameny and Wilson, 1997 and Hagenimana *et al.*, 1999). However, with adequate genetic variability available, the chances of successfully selecting for an increase in both traits are considerably improved. The likelihood of success is supported by the fact that of the 10 selected accessions to be used as parents, two dark orange-fleshed accessions had high root dry masses of 33 and 35%. However, their relatively low RFY of 10.5 and 15 t ha^{-1} needs to

be improved. The significant, negative association between RDM and RFY has been reported by Tsegaye *et al.* (2006).

Harvest index for the 64 accessions was generally high and was associated with vine yield, number and yield of marketable and total roots. This is expected as the statistic is derived from adding the yield of vines and roots. As the vine yield increases the HI declines as photosynthates that would have gone to develop the roots are utilized to develop aboveground vegetative mass. Hence, the root yield is reduced and consequently the HI.

Nine of the 10 selected accessions had HI over 0.8, with the exception recording 0.7. Two unselected accessions had HI of less than 40%. The average for all the accessions was about 0.7. A balance between root yield and vine yield is required if a genotype is to be used both for roots and leaves. A very high HI may result in reduced availability of vines for planting.

Average RDM percentage for the 10 selected parents was 32%, which was higher than 28% of the popular cultivar Chingovwa. The average RDM percentage for the 64 accessions was about 35% indicating that a number of accessions not selected by the SI had RDM above 35%, but these genotypes had other undesirable traits**.** The high mean RDM percentage for all the accessions relative to cultivar Chingovwa indicates that potentially the RDM of high β-carotene genotypes could be significantly improved. This argument stems from two genotypes that combined high RDM and high β-carotene that were identified in the collection. Therefore, the unselected accessions will also be maintained for use in the breeding programme.

The selection index greatly simplified and speeded up the identification of genotypes that had desirable combinations of the important traits under consideration. It is expected that breeding for any one of these traits will necessitate co-selecting for the other traits. Although the objective of this study is to develop genotypes with high root dry mass combined with orange root flesh, the other important traits will not be compromised in the process as careful application of the selection index will ensure selection pressure is also applied to them.

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Appendices

Appendix 3.1 Soil nutrient analysis of the trial site at Mansa Research Station, Luapula Province, Zambia

Analyte	**pH $CaCl_2$**	**Org. C %**	**N%**	**P mg kg^{-1}**	**K me%**	**Ca me%**	**Mg me%**	**Zn mg kg^{-1}**	**Fe mg kg^{-1}**	**Mn mg kg^{-1}**	**Cu %**
Value	4.6	1.5	0.11	4	0.05	0.25	0.22	Trace	3.91	2.22	0.07

Appendix 3.2: General farmer profile for sweetpotato accessions collected in Luapula Province, Zambia

Date*	District	Name of farmer	Gender	Chief / Village	Genotype	Sample no.	Source of cultivar	Colour of genotype		Use for the genotype	Farmers' remarks on each genotype
								Skin	Flesh		
28/6/06	Mwense	Mubanga L. James	M	Mwenda Fisheries Camp	Matembele	1 M	From local farmer	Cream	White	Mainly as a vegetable Roots are boiled	It is not high yielding; produces more leaves for vegetable; farmer likes small leaves for vegetable
28/6/06	Mwense	Chola Queen Chenga	F	Mwenda Rural Health Centre	Chimpempe	2 M	From friend locally	Cream	Cream & purple	Mainly boiled to eat as snack and also processed into insemwa	Does not rot; sweet; high dry mass and big roots
28/6/06	Mwense	Eliza Mambwe	F	Mwenda Luminu farm centre	Chilamba	3 M	Parent (mother)	Red	White	Boiled, process insemwa, vegetable	Sweet when cooked; stands the cold hence provides vegetable throughout the year and high dry mass
28/6/06	Mwense	Milika Mwila	F	Mwenda Bwalya	No name	4 M	Nearby village	Red	Yellow	Boiled, cooked with peanut	Has big leaves; sweet; no rotting; high yielding; high dry mass
28/6/06	Mwense	Milika Mwila	F	Mwenda Bwalya	Kandolo	5 M	Friend	Red	White	Boiled, cooked with peanut, vegetable	Good for vegetable; high dry mass; flat taste; high yielding; rots fast
28/6/06	Mwense	Mwansa Jeffrey	M	Mwenda Mukanga Resettlement scheme	No name	6 M	Friend within the village	Red	Light orange	Boiled, cooked with peanut, vegetable	Does not shed leaves fast; high yield
3/7/06	Mwense	Chibanda Erica	F	Kanyembo Chibanda	Kolwezi	7 M	Friend in Mulundu	Red	Yellow	Boiled, cooked with peanut	High yielding
28/6/06	Mwense	Johnson Mpashi (CEO)	M	Mwenda Mukonshi camp	No name	8 M	Valley – mulundu area	Cream	Cream	Boiled, cooked with peanut, vegetable	High yielding, high dry mass; flat taste; spreading type

*****Date of acquisition

Appendix 3.2 (Continued)

Date	District	Name of farmer	Gender	Chief / Village	Genotype	Sample no.	Source of cultivar	Colour of genotype		Use for the genotype	Remarks on the genotype by farmer
								Skin	Flesh		
28/6/06	Mwense	Johnson Mpashi (CEO)	M	Mwenda Mukonshi camp	Chilamba	9 M	Friend within the area	Red	White	Mainly for vegetable	Spreading type with small leaves that are good for vegetable
28/6/06	Mwense	Johnson Mpashi (CEO)	M	Mwenda Mukonshi camp	Chilamba	10 M	Friend within the area	Red	White	Boiled, cooked with peanut, vegetable	Prone to weevil damage; good for vegetable; high dry mass; big roots; gets established well and planting material preserves well in the soil
28/6/06	Mwense	Johnson Mpashi (CEO)	M	Mwenda Mukonshi camp	No name	11 M	Found in the field as a weed	Cream	Cream	Roots are boiled	Low yielding
28/6/06	Mwense	Johnson Mpashi (CEO)	M	Mwenda Mukonshi camp	No name	12 M	Valley Mulundu area	Red	Light orange	Roots are boiled	Tastes good – no fibre, high dry mass, high yielding, root is deep rooted- makes harvesting difficult as the roots get injured
28/6/06	Mwense	Johnson Mpashi (CEO)	M	Mwenda Mukonshi camp	No name	13 M	Cannot trace	Red	Light orange	Boiled together with other cultivars, process chips	Low dry mass, small roots and high yielding
29/6/06	Kawambwa	Elizabeth Muleba	F	Mushota ShiLemmy	Kandolo	1 K	Own seed	Red	White	Boiled insemwa	High yielding, good for insemwa – it dries well & does not get mouldy in store, not fibrous and vines do not dry easily

Appendix 3.2: (Continued)

Date	District	Name of farmer	Gender	Chief / Village	Genotype	Sample no.	Source of cultivar	Colour of genotype		Use for the genotype	Remarks on the genotype by farmer
								Skin	Flesh		
29/6/06	Kawambwa	Simon Bwalya	M	Mushota Shilemmy	Kandolo	2 K	Own seed	Purple	White	Boiled Vegetable	Big roots, produces more planting material, high yielding, roots are fibrous, vines are used to control termites in a storage bins – vines are first placed at the base of the bin and the top part is plastered with mud. This makes the base termite proof.
29/6/06	Kawambwa	Simon Bwalya	M	Mushota Shilemmy	Matembele	3 K	Own seed	Cream	Cream	Mainly grown for vegetable	Depending on soil fertility, roots grow big, yield is medium
29/6/06	Kawambwa	Danken Mulenga	M	Mushota Tea Estate-Luena block	Kandolo	4 K	Lengwe Area from friend	Red	White	Insemwa Vegetable Boiling	High yielding; takes long to mature; resistant to diseases; high dry mass; not fibrous & vines do not dry
29/6/06	Kawambwa	Biswell Mpundu	M	Kabila Lengwe area Chiyeye	No name	5 K	Valley area from relative	Cream	White	Boiled plain Boiled with peanut butter, fried	High dry mass, vines do not dry, bid roots, vines break easily when folding
30/6/06	Kawambwa	Yolum Kasongo	M	Munkanta Lupili - town centre	Kandolo	6 K	Friend within the area	Red	White	Leaves for roots Boiled as snack	Low dry mass; a bit fibrous; takes long to mature; produces leaves for vegetable throughout the year, has been planted in the dambo, does not get very stressed in cold season.
30/6/06	Kawambwa	Lillian Ntalasha	F	Munkanta Fruit nursery Compound	No name	7 K	Own seed	Red	White	Boiled snack, Vegetable, chips	Does not rot, high yielding, big roots, high dry mass, not fibrous
30/6/06	Kawambwa	Lillian Ntalasha	F	Munkanta Fruit nursery Compound	No name	8 K	From farm institute in Mansa	Cream	Light orange	Snack- fried & boiled	Sweet high yielding Not fibrous

Appendix 3.2: (Continued)

Date	District	Name of farmer	Gender	Chief / Village	Genotype	Sample no.	Source of cultivar	Colour of genotype		Use for the genotype	Remarks on the genotype by farmer
								Skin	Flesh		
30/6/06	Kawambwa	Lillian Ntalasha	F	Munkanta Fruit nursery Compound	Kandolo	9 K	Own seed	Red	White	Boiled & eaten as snack Vegetable Insemwa	High yielding; Does not rot
30/6/06	Kawambwa	Lillian Ntalasha	F	Munkanta Fruit nursery Compound	Kandolo	10 K	Own seed			Boiled & eaten as snack	High yielding; Produces very big leaves
30/6/06	Kawambwa	Yolum Kasongo	M	Munkanta Lupili - town centre	Kandolo	11 K	Own seed				Will be observed at the research station, has not followed the genotype closely to know it's traits
30/6/06	Kawambwa	Elbilian Chongo	F	Mutondolo Totolo	Kandolo	12 K	Own seed	Red	Cream	Insemwa Boiled	Low yield; high dry mass & not fibrous
30/6/06	Kawambwa	Elbilian Chongo	F	Mutondolo Totolo	No name	13 K	From Agriculture	Copper	Orange	Boiled	Yields high, flat taste
30/6/06	Kawambwa	Margie Lyonze	F	Kala Refugee Camp	Matembele banji	14 K	Congo DR	Cream	Cream	Vegetable	Like small leaves for vegetable
30/6/06	Kawambwa	Kamona Kazi	F	Kala Refugee Camp	Kandolwa	15 K	Congo DR	Cream	White	Boiled, fried & leaves for vegetable	high yielding
30/6/06	Kawambwa	Mutono Kizyala	F	Kala Refugee Camp	Matembele bangi	16 K	Congo DR	Cream	White	Vegetable	Low yielding of roots
30/6/06	Kawambwa	Kibaya	F	Kala Refugee Camp	Don't know	17 K	Nearby village-Chungu			Boiled Insemwa	Big roots, high dry mass

Appendix 3.2: (Continued)

Date	District	Name of farmer	Gender	Chief / Village	Genotype	Sample no.	Source of cultivar	Colour of genotype		Use for the genotype	Remarks on the genotype by farmer
								Skin	Flesh		
1/7/06	Nchelenge	Florence Katebe	F	Kanyembo Chomba	Chintobenge	1 N	Parent, within	Cream	White	Boiled Sold	High yielding, does not rot, not fibrous, dry mass, sweet & big roots
1/7/06	Nchelenge	Stain Chilufya	M	Kanyembo Chabilikila sub-research station	Don't know	2 N	Weed	Cream	Cream	Boil, sell	High dry mass, sweet, not fibrous, rots when harvesting is delayed
1/7/06	Nchelenge	Stain Chilufya	M	Kanyembo Chabilikila sub-research station	Ndola	3 N	Own seed	Red	White	Vegetable, insemwa, boiled	Sweet, stores well in the soil; planting vines available
1/7/06	Nchelenge	Mumpa Chipenya	M	Kanyembo Chabilikila	Chimpempe	4 N	From friend within	Cream	Yellow	Insemwa, boiled, roasted, vegetable	Depending on soil fertility, roots get big, high dry mass, very sweet, not fibrous, long roots – good shape
1/7/06	Nchelenge	Mumpa Chipenya	M	Kanyembo Chabilikila	Kalukuluku	5 N	Own seed	Cream	White & purple	boiled	Sweet; few roots per plant; a bit fibrous, liked by rats & moles
1/7/06	Nchelenge	Mumpa Chipenya	M	Kanyembo Chabilikila	No name	6 N	Own seed	Cream	White	Boiled	High yielding, spreading type
1/7/06	Nchelenge	Kayanda	M	Kanyembo Chabilikila	Chintobenge	7 N	Own seed	Cream	White	boiled	Sweet, big, high yield, high dry mass, does not rot easily
1/7/06	Nchelenge	Rose Chansa	F	Kanyembo Chipulumushi	Mutoba - mputa	8 N	Congo DR	Red	White	vegetable boiled roots	High yielding, high dry mass, big roots, not fibrous. Tender leaves are used for vegetable

Appendix 3.2: (Continued)

Date	District	Name of farmer	Gender	Chief / Village	Genotype	Sample no.	Source of cultivar	Colour of genotype		Use for the genotype	Remarks on the genotype by farmer
								Skin	Flesh		
1/7/06	Nchelenge	Rose Chansa	F	Kanyembo Chipulumushi	No name	9 N	Friend within village	Cream	White	Vegetable	Has big leaves, high yielding, not fibrous, high dry mass
1/7/06	Nchelenge	Eliza Mulenga	F	Kanyembo Chipulumushi	Matembele	10 N	Friend within village	Red	White & purple	Boiled	High yielding, vegetable, small/mediun size, high dry mass, not fibrous
1/7/06	Nchelenge	Getrude Musonda	F	Kanyembo Chipulumushi	Mwimbwan amakuku	11 N	Chisenga Island	Cream	White	Boiled	Leaves not palatable for vegetable, high yielding, high dry mass
2/7/06	Nchelenge	Emmy Mulenga	F	Kambwali Shishibeti	Munwe umo	12 N	Bought within village	Red	Cream	Boiled Vegetable	High dry mass, high yielding, still gives high yields when planted towards end of rainy seasons, does not rot in the soil, big and gives about five roots per station, not fibrous
2/7/06	Nchelenge	Emmy Mulenga	F	Kambwali Shishibeti	No name	13 N	Bought within village	Red	Cream	Boiled	Not good for vegetable, not fibrous, high yielding
2/7/06	Nchelenge	Eners Katele	F	Kambwali Shishibeti	Don't know	14 N	Kabuta area Nchelenge	Cream	White	Boiled,	High yielding, tastes well- not fibrous, high dry mass, bigger roots than Chingovwa, stores well, sweet after curing
2/7/06	Nchelenge	Eners Katele	F	Kambwali Shishibeti	No name	15 N	Kenani area in Nchelenge	Red	White and purple	Boiled, dried chips	Good for making dried chips, high yielding, very big roots, becomes fibrous when very big
2/7/06	Nchelenge	Eners Katele	F	Kambwali Shishibeti	No name	16 N	Lwenge area from farmers	Red		Boiled	Early maturing, planted twice in one rainy season, yields high, more roots per station
2/7/06	Nchelenge	Mambwe Agness	F	Kambwali Mubamba	Pakamana	17 N	Within village from farmer	Red	White	Boiled, dried chips, Vegetable	Very big leaves, good for vegetable – big leaves, sweet, high dry mass, big roots

Appendix 3.2: (Continued)

Date	District	Name of farmer	Gender	Chief / Village	Genotype	Sample no.	Source of cultivar	Colour of genotype		Use for the genotype	Remarks on the genotype by farmer
2/7/06	Nchelenge	Patrick Kaluba	M	Kambwali Rubber plantation area Mutepuka	Chisenga	20 N	Chisenga island	Red	White	Boiled, insemwa	Sweet, smells well, big roots in fertile soils, high dry mass, high yielding, not fibrous but leaves not good for vegetable- it easily over cooks
3/7/06	Nchelenge	Ronia Chibesa	F	Kambwali Rubber plantation area Mutepuka	Spoon	21 N	Friend within	Red	white	Vegetable, roots boiled	High yielding, yields twice a year , planted in Dec & Feb, not fibrous, high dry mass
3/7/06	Nchelenge	Florence Mumpa	F	Chabilikila Rural Health Centre	Carrot	22 N	Friend	Cream	Orange	Boiled, fried, cooked with peanut butter	Tastes nice, source of Vitamin A, high yielding, high dry mass, does not rot
3/7/06	Nchelenge	Monica Nkandu	F	Kanyembo Chabilikila	Chilubi	23 N	Chilubi Island in Northern province	Cream	White	Boiled, fried, cooked with peanut butter	Big roots, very high yielding
3/7/06	Nchelenge	Monica Nkandu	F	Kanyembo Chabilikila	Chilubi	24 N	From friend within	Red	White	Boiled, fried, cooked with peanut butter	High dry mass, sweet
3/7/06	Nchelenge	Monica Nkandu	F	Kanyembo Chabilikila	Chilubi (2)	25 N	Chilubi Island in Northern province			Boiled, fried, cooked with peanut butter	Very high yielding, high dry mass, big roots, does not rot

Appendix 3.2: (Continued)

Date	District	Name of farmer	Gender	Chief / Village	Genotype	Sample no.	Source of cultivar	Colour of genotype		Use for the genotype	Remarks on the genotype by farmer
								Skin	Flesh		
28/6/06	Samfya	Christine Kunda	F	Katanshya area Ponga	Unknown	1 S	Chipepa village in Mansa	White	Red	Home consumption	Very good
28/6/06	Samfya	Christine Kunda	F	Katanshya area Ponga	Unknown	2 S	Chipepa village in Mansa	Red	White	Home consumption	Very good
28/6/06	Samfya	Sepeti Chitalanda	M	Katanshya area Sepeti	Katanshya	3 S	Own seed	White	Cream	Home consumption	Liked
29/6/06	Samfya	Mary C. Kafuta	F	Katanshya area Kasompe	Kalukuluk u	4 S	Rural reconstructio n centre in Samfya	Pink	White & pink	Home consumption	Low yield but tasty
29/6/06	Samfya	Lewis	M	Lubwe area Wakubula	Zimbabwe	5 S	Musaila area from parents	Cream	Orange	Home consumption	Good
29/6/06	Samfya	Lewis	M	Lubwe area Wakubula	Kasompe	6 S	Musaila area from parents	Yellow	White	Home consumption	Good
29/6/06	Samfya	Lewis	M	Lubwe area Wakubula	Chansa	7 S	Musaila area from parents	Pink	White	Home consumption	Fair
29/6/06	Samfya	Lewis	M	Lubwe area Wakubula	Unknown (2)	8 S	Musaila area from parents	White	White	Home consumption	Fair
29/6/06	Samfya	Chishimba Kachula	F	Lubwe area Mashitolo	Carrot	9 S	Within the village	White	Orange	Vegetable and home consumption	Good

Appendix 3.2: (Continued)

Date	District	Name of farmer	Gender	Chief / Village	Genotype	Sample no.	Source of cultivar	Colour of genotype		Use for the genotype	Remarks on the genotype by farmer
29/6/06	Samfya	Chishimba Kachula	F	Lubwe area Mashitolo	Mitanda-nsoka	10 S	Within the village			Home consumption	Good
29/6/06	Samfya	Chishimba Kachula	F	Lubwe area Mashitolo	Matuwa	11 S	Within the village	White	white	Home consumption	Good
29/6/06	Samfya	Chishimba Kachula	F	Lubwe area	Unknown (3)	12 S	Within the village	White	white	Home consumption	Good
29/6/06	Samfya	Edwin Bwalya	F	Along Tuta road Mushiku – mutanda	Carrot	13 S	Chitembo-mbilima-mwenge 's area	Red	Orange	Home consumption	Very good, very much liked by children, older people do not like the smell (aroma)
30/7/06	Samfya	Beaty Mwape	F	Along Tuta rd Foloko	Unknown (4)	14 S	Within the village	Red	Light orange	Home consumption & for sale	Very good
30/7/06	Samfya	Chushi Mulenga	F	Along Tuta rd Foloko	Kabelenge	15 S	Within the village	Crea m	white	Home consumption & for sale	Good for vegetable

Appendix 3.3 Replicate means of agronomic data of 64 sweetpotato accessions collected in Luapula Province, Zambia and evaluated in an 8 x 8 triple lattice experimental design

Accession Genotype Number	ID	Name	Mole damage (score)*	Weevil damage (score)*	Cracking (score)*	Flesh colour (score)*	Harvest index	RDM (%)	Vine yield (t ha^{-1})	No of marketable roots ha^{-1}	Yield of marketable roots (t ha^{-1})	Total number of roots ha^{-1}	Total root mass (t ha^{-1})
1	7M	Kolwezi	1.138	5.83	0.00	0.67	0.78	35.99	2.98	48307	8.94	70885	9.62
2	12N	Munwe umo	1.276	38.86	0.20	0.33	0.93	25.9	1.27	68021	10.95	98698	11.93
3	8N	Mutobamputa	1.382	7.39	0.20	0.33	0.54	36.84	4.94	34427	4.70	48932	5.19
4	3K	Matembele	1.276	5.83	0.30	0.00	0.85	34.70	2.46	68177	10.67	100234	11.78
5	S12	Unknown 3	1.471	21.57	0.10	0.00	0.86	30.86	1.14	20208	7.96	28359	8.34
6	7K	No Name	1.138	10.06	0.00	0.00	0.64	35.62	0.47	20990	0.39	33281	1.23
7	9M	Nankomesha	1.276	27.36	0.00	0.00	0.88	33.69	1.52	46484	10.96	57474	11.09
8	S1	Katansha 1	1.520	11.62	0.10	0.00	0.56	36.44	2.79	30612	4.31	54674	4.99
9	12M	Kolwezi	1.382	4.28	0.10	0.33	0.90	37.12	1.73	44375	11.44	62891	12.08
10	25N	Chilubi 2	1.276	27.36	0.26	0.00	0.66	34.63	4.08	52943	7.57	70078	8.41
11	18N	Chisenga	1.276	10.06	0.00	0.00	0.92	32.08	1.40	55156	13.03	70495	13.60
12	6K	Kandolo	1.276	5.83	0.20	0.00	0.75	35.66	4.48	42604	12.43	62057	13.01
13	10N	Matembele	1.138	43.09	0.10	0.00	0.79	36.25	3.04	41302	10.56	54557	11.11
14	11K	Kandolo	1.138	21.57	0.00	0.00	0.73	40.10	1.66	34219	3.92	67135	5.15
15	1M	Matembele	1.520	23.13	0.00	0.00	0.84	31.67	2.50	66979	11.55	102318	12.48
16	S11	Matuwa	1.138	21.57	0.10	0.00	0.39	36.78	3.36	11523	2.43	18633	2.35
17	14M	No Name	1.138	5.83	0.00	0.33	0.64	36.85	4.46	32682	6.48	59115	7.72
18	6M	No Name	1.244	5.83	0.00	0.91	0.62	34.20	3.04	32057	4.48	55651	5.17
19	S9	Carrots	1.138	20.01	0.10	1.82	0.88	33.46	2.26	56979	13.68	100443	14.99
20	5K	Kabila	1.276	5.83	0.20	0.00	0.70	35.54	4.41	40234	8.71	56354	9.41
21	5N	Kalukuluku 1	1.609	27.36	0.10	0.00	0.60	32.9	6.12	28724	7.28	46172	7.68

*Scores for mole damage, weevil damage, and cracking were as follows (Data shown was transformed) : 1 = No symptom, 2 = 1-5 roots affected in a plot of 20 plants, 3 = any roots affected slightly (5-10% of root area), 4 = All roots affected moderately (11 - 25% of root area), and 5 = All roots affected severely (>25% of root area). Flesh colour was scored as follows: 0 = white, 1 = cream, 2 = light orange, 3 = medium orange, 4 = orange, and 5 = dark orange.

Appendix 3.3 (Continued)

Accession Genotype Number	ID	Name	Mole damage (score)*	Weevil damage (score)*	Cracking (score)*	Flesh colour (score)*	Harvest index	RDM (%)	Vine yield (t ha^{-1})	No of marketable roots ha^{-1}	Yield of marketable roots (t ha^{-1})	Total number of roots ha^{-1}	Total root mass (t ha^{-1})
22	12K	Kandolo	1.276	15.85	0.10	0.00	0.69	39.76	6.82	51823	11.32	90156	12.65
23	4M	Unknown	1.382	4.28	0.00	0.00	0.71	30.62	4.34	29896	12.25	32734	12.45
24	S8	Unknown 2	1.414	20.01	0.10	0.00	0.65	39.95	4.07	36706	7.24	62539	7.67
25	16M	Matembele	1.138	4.28	0.00	0.33	0.54	32.10	3.43	36823	3.16	50182	3.56
26	24N	No Name	1.414	38.86	0.00	0.33	0.70	40.51	4.28	49479	10.06	96562	11.06
27	17N	Pakamana	1.276	4.28	0.16	0.00	0.63	32.44	6.19	41042	8.83	45703	8.82
28	2K	Kandolo	1.138	10.06	0.16	0.00	0.78	35.96	4.23	51068	15.19	72656	15.65
29	S15	Kabalenge	1.138	5.83	0.10	0.00	0.80	30.91	3.62	65130	12.38	93021	13.61
30	10K	Kandolo	1.276	5.83	0.20	0.00	0.60	33.49	5.28	38646	9.63	59453	6.56
31	3M	Chilamba	1.276	11.62	0.10	0.00	0.69	32.7	4.17	47318	8.75	66771	9.14
32	S2	Unknown Katansha	1.414	5.83	0.26	0.33	0.68	35.94	4.37	47096	8.20	71315	8.42
33	8M	No Name	1.276	2.72	0.36	0.00	0.87	36.33	2.06	54596	13.65	80195	14.74
34	14N	No Name	1.520	7.39	0.20	0.00	0.90	30.83	1.55	57253	13.08	86367	13.94
35	11N	Mwimbwanamakuku	1.276	27.36	0.00	0.00	0.80	39.36	0.82	36107	3.31	54076	3.48
36	9K	Kandolo	1.244	11.62	0.26	0.00	0.80	33.30	3.99	41289	14.62	60326	15.12
37	2N	No Name	1.138	5.83	0.00	0.00	0.82	41.56	2.39	42487	9.89	80169	10.67
38	13M	No Name	1.138	25.80	0.26	1.14	0.82	33.90	0.23	48659	1.97	67565	3.18
39	10M	Chilamba	1.138	38.86	0.00	0.00	0.68	42.04	4.02	24206	5.45	43867	6.28
40	S13	Carrots Mwewa	1.715	27.36	0.00	1.63	0.82	35.21	2.91	56693	14.43	87161	15.40
41	15N	No Name	1.626	5.83	0.26	0.00	0.78	35.22	3.49	39714	12.02	54115	12.48
42	19N	No Name	1.520	38.86	0.00	0.33	0.81	33.64	2.11	37422	9.42	68776	10.24

*Scores for mole damage, weevil damage, and cracking were as follows (Data shown was transformed): 1 = No symptom, 2 = 1-5 roots affected in a plot of 20 plants, 3 = Many roots affected slightly (5-10% of root area), 4 = All roots affected moderately (11 - 25% of root area), and 5 = All roots affected severely (>25% of root area). Flesh colour was scored as follows: 0 = white, 1 = cream, 2 = light orange, 3 = medium orange, 4 = orange, and 5 = dark orange; [a]RDM = Root dry mass

Appendix 3.3 (Continued)

Accession Genotype Number	ID	Name	Mole damage (score)*	Weevil damage (score)*	Cracking (score)*	Flesh colour (score)*	Harvest index	RDM (%)	Vine yield (t ha^{-1})	No of marketable roots ha^{-1}	Yield of marketable roots (t ha^{-1})	Total number of roots ha^{-1}	Total root mass (t ha^{-1})
43	4N	Chimpempe	1.276	11.62	0.10	0.00	0.80	37.51	1.83	42708	6.79	66224	7.62
44	1K	Kandolo	1.138	4.28	0.00	0.00	0.81	31.34	0.55	22474	2.56	47005	2.87
45	1N	Chitobenge	1.000	27.36	0.00	0.00	0.79	40.19	2.21	31745	8.29	42396	8.84
46	15K	Kandindolwa	1.138	25.8	0.00	0.00	0.67	36.96	1.40	28854	2.83	48750	4.18
47	7N	Chitobenge	1.276	20.01	0.10	0.00	0.71	32.44	4.75	36875	11.09	53151	11.81
48	S4	Kalukuluku	1.471	5.83	0.16	0.67	0.69	32.00	3.93	53685	9.31	97747	10.32
49	11M	No Name	1.276	2.72	0.32	0.00	0.73	27.55	1.21	17135	3.40	26432	3.64
50	23N	Chilubi 1	1.626	10.06	0.10	0.00	0.82	36.15	2.36	55443	9.36	82917	10.38
51	S5	Zimbabwe	1.382	14.3	0.10	1.82	0.89	27.15	1.51	46875	10.99	80260	11.99
52	13K	No Name	1.000	21.57	0.00	2.00	0.85	27.32	1.02	80990	4.91	189948	6.29
53	S10	Mutandansoka	1.382	5.83	0.10	0.00	0.82	35.44	2.33	51302	9.61	70156	10.31
54	17K	No Name	1.414	7.39	0.20	0.00	0.61	31.71	2.79	34219	3.90	51276	5.03
55	13N	No Name	1.138	5.83	0.10	0.33	0.60	34.67	2.50	34115	4.24	49635	4.93
56	S3	Katansha	1.382	38.86	0.20	0.00	0.80	36.56	2.54	55898	10.46	76914	11.29
57	22N	Carrots	1.276	4.28	0.00	1.73	0.82	32.03	2.16	34453	7.57	79505	8.72
58	6N	No Name	1.138	21.57	0.00	0.00	0.60	29.85	3.07	36094	5.58	48021	5.61
59	3N	Ndola	1.471	20.01	0.00	0.00	0.65	36.36	2.93	32292	5.27	54688	5.67
60	4K	No Name	1.520	5.83	0.00	0.00	0.68	43.62	2.61	35625	4.94	62865	5.79

*Scores for mole damage, weevil damage, and cracking were as follows (Data shown was transformed): 1 = No symptom, 2 = 1-5 roots affected in a plot of 20 plants, 3 = Many roots affected slightly (5-10% of root area), 4 = All roots affected moderately (11 - 25% of root area), and 5 = All roots affected severely (>25% of root area). Flesh colour was scored as follows: 0 = white, 1 = cream, 2 = light orange, 3 = medium orange, 4 = orange, and 5 = dark orange.

Appendix 3.3 (Continued)

Accession Genotype Number	ID	Name	Mole damage (score)*	Weevil damage (score)*	Cracking (score)*	Flesh colour (score)*	Harvest index	RDM (%)	Vine yield (t ha^{-1})	No of marketable roots ha^{-1}	Yield of marketable roots (t ha^{-1})	Total number of roots ha^{-1}	Total root mass (t ha^{-1})
61	5N	Kalukuluku 2	1.138	21.57	0.00	0.00	0.68	36.33	4.59	34 688	8.45	44115	8.74
62	14K	Matembele Banji 1	1.276	10.06	0.00	0.00	0.39	31.17	3.99	16 302	1.83	36328	2.88
63	5M	Kandolo	1.138	5.83	0.00	0.00	0.69	38.13	3.22	31 589	6.88	42370	7.19
64	S6	Kasompe	1.244	23.13	0.00	0.00	0.71	34.29	3.70	59 310	9.93	79023	10.50
		Grand Mean	1.295	15.35	0.09	0.24	0.73	34.72	2.99	41 924	8.21	65 186	8.86
		s.e.d.	0.210	12.78	0.11	0.22	0.09	2.51	1.26	14 600	2.08	21 257	1.98
		s.e.	0.050	4.90	0.04	0.16	0.10	2.82	1.42	16 409	2.34	23 891	2.22
		l.s.d.	NS	25.28	0.22	0.43	0.17	4.98	2.50	28949	4.14	42 148	3.92

*Scores for mole damage, weevil damage, and cracking were as follows (Data shown was transformed): 1 = No symptom, 2 = 1-5 roots affected in a plot of 20 plants, 3 = Many roots affected slightly (5-10% of root area), 4 = All roots affected moderately (11 - 25% of root area), and 5 = All roots affected severely (>25% of root area). Flesh colour was scored as follows: 0 = white, 1 = cream, 2 = light orange, 3 = medium orange, 4 = orange, and 5 = dark orange.

Chapter 4: Diallel analysis of sweetpotato for beta-carotene content and yield components

Abstract

Five sweetpotato genotypes were crossed in a 5 x 5 full diallel mating design excluding selfs. Observations were recorded on four root traits viz., β-carotene content, root dry mass (RDM) composition, harvest index (HI) and root fresh yield (RFY). The 20 crosses with 20 F_1 progeny per family and their five parents were evaluated in a 5 x 5 triple lattice design. The cross mean squares of the four traits were highly significant ($p<0.001$). The general combining ability (GCA) and specific combining ability (SCA) mean squares were significant for β-carotene content ($p<0.001$), RDM ($p<0.001$), HI ($p<0.001$), and RFY ($p<0.001$). The ratios of GCA to SCA variances were 0.76 for both β-carotene content and HI, 0.68 for RFY and 0.92 for RDM indicating that additive gene action was predominant in the inheritance of the traits. The two high β-carotene parents used in this study exhibited high, positive GCA effects, indicating that additive gene action was predominant in the inheritance of β-carotene. However, high β-carotene parents (1 and 3) with positive high GCA effects did not necessarily result in desirable progeny in every cross as some of their progeny were low in β-carotene. Therefore, parents must also be selected on the basis of their SCA effects and the actual performance of the cross. Additionally, high RDM parents that exhibited positive and highly significant ($p<0.001$) GCA effects produced only one cross with positive and significant ($p = 0.01$) SCA effects. The best performing progeny for RDM were obtained from a reciprocal cross (5 x 1; SCA effect = 0.6). Again, selection of parents for a hybrid programme needs to take into account the GCA and SCA effects in combination with the performance of progeny within a cross. The estimates of narrow sense heritability were low at 20.9% for β-carotene content, 29.1% for HI, 34.9% for RFY and high at 76.3% for RDM suggesting that rapid genetic gains should be possible with mass selection breeding techniques based on the phenotype of the parent for RDM but progress will be slow for β-carotene content HI, and RFY.

4.1 Introduction

One of the major nutritional problems worldwide is vitamin A deficiency (VAD), which is a leading cause of early childhood death and a major risk factor for pregnant women in Africa, Micronesia, and other parts of the world. Vitamin A is essential for the normal development of children, and deficiency can lead to night-blindness (estimated to afflict 3 million sub-Saharan children under the age of five), as well as resulting in an increased susceptibility to a variety of other diseases due to a weakened immune system (Fraser and Bramley, 2004). In low-income, impoverished populations, it has been estimated that up to 82% of the dietary vitamin A is derived primarily from plant sources as so-called provitamin A carotenoids (van den Berg *et al.*, 2000). According to WHO (1995), VAD is a problem of public health significance in Zambia. Subclinical VAD is significant, with a prevalence rate of 13-17% among children ranging from 6 months to 12 years of age. Therefore, improved vitamin A intake through increased consumption of OFSP will make a significant contribution to improved health. The enrichment of β-carotene, a precursor to vitamin A, in the local sweetpotato genotypes, is an attractive alternative to improving vitamin A intake. There is wide, natural genetic variability in provitamin A content in sweetpotato (Woolfe, 1992). This means that conventional breeding techniques can be employed to incorporate β-carotene into sweetpotato by crossing local genotypes with genotypes that have high β-carotene content.

Diallel mating designs have been widely used in genetic research to investigate the inheritance of important traits in a set of genotypes (Collins, 1977; Mwanga *et al.*, 2002). Diallel mating designs were devised, specifically, to investigate the combining ability of the parental lines for the purpose of identification of superior parents for use in hybrid development programmes. A diallel cross is a set of p^2 possible single crosses and selfs between p homozygous (Hayman, 1954a, b, '58, '60) or heterozygous (Dickinson and Jinks, 1956) parents; it provides a powerful method for investigating the relative genetic properties of these parents. It is possible to partition treatment variation into components due to general combining ability (GCA) and specific combining ability (SCA) (Griffing 1956; Collins 1977; Bradshaw *et al.,* 2000; Mihovilovich *et al.,* 2000; Yan and Hunt, 2002). The estimates of the relative magnitude of the variances of GCA and SCA indicate the type of gene action determining the traits. Variance due to GCA indicates the predominance of additive gene action while that of SCA indicates the predominance

of non-additive gene action arising largely from dominance and epistatic deviations (Rojas and Sprague, 1952).

The present research examined the quantitative inheritance of important traits in sweetpotato by means of a diallel analysis with a view to estimating the GCA and SCA components of genetic variance, and to determine the associated type of gene action controlling β-carotene content, root dry mass (RDM), harvest index (HI) and root fresh yield (RFY).

4.2 Materials and Methods

Diallel crosses

Hand crosses were carried out in a 5 x 5 full diallel, excluding selfs from 2006 to 2008 at Mansa Research Station (11° 14.396' S and 028° 57.226' E) , Mansa, Zambia. The parents consisted of two introductions from CIP and three advanced breeding lines developed in the local sweetpotato breeding programme at Mansa Research Station (Table 4.1). The advanced breeding lines were selected on the basis of being cross compatible with the CIP lines.

Table 4.1 Parental genotypes and their traits used in a 5x5 full diallel excluding selfs

No.	Genotype	Root flesh colour	Root dry mass (%)	Source
1	Excel	deep orange	29	CIP
2	L4-138/3	White	30	Zambia (bred clone)
3	W-119	Orange	25	CIP
4	Unknown 2/1	Cream	32	Zambia (bred clone)
5	L3-199084/1	Orange	21	Zambia (bred clone)

Botanical seed (Figure 4.1) obtained from the crosses were germinated in a sand and vermiculite mix contained in 20 x 12 cell polystyrene seedling trays which were placed in a screenhouse (Figure 4.2).

Figure 4.1: Sweetpotato botanical seeds

Figure 4.2: Sweetpotato seedlings growing in a sand and vermiculite mix in 20 x 12 polystyrene trays placed in a screenhouse

Seedlings were transplanted to 1 L plastic pots (Figure 4.3). Once the plants were about 50 mm tall, they were transplanted to raised ridges in the wetland (wetlands are called dambos in Zambia) to allow for further growth in a non-competitive environment (Figure 4.4).

Figure 4.3: Sweetpotato seedlings growing in 1 L plastic pots

Figure 4.4: Sweetpotato plants growing in the dambo

The F_1 progeny in each cross were randomly selected from the wetland site on the basis of producing adequate good quality vegetative cuttings for the field trial. This was the only pre-trial selection criterion that was imposed on the progeny to be evaluated. On that basis for a given cross, 20 F_1 progeny were chosen to represent each cross. The selected F_1 progeny along with their parental lines were planted in the same field trial. The trial was laid out as a 5 x 5 triple lattice (Appendix 4.2). The experimental plot was a

single 6 m long row with an inter-row spacing of 1 m and an intra-row spacing of 30 cm. Each single row plot comprised the selected 20 progeny of a cross. Hills were planted for a final plant density of about 40 000 plants ha^{-1}. The trial was planted in the rainy season in November and cultural practices and weed control were performed according to standard field practices. No external inputs such as fertilizers were applied. Soil analysis results for the site are presented in Appendix 4.1.

All data were recorded on individual plant basis and then averaged across the 20 progeny of each F_1 cross. The quantitative traits were evaluated as follows: (a) β-carotene content – expressed as mg 100 g^{-1}; (b) RDM - root dry mass (g) expressed as a percentage of root fresh mass (g); c) HI – expressed as a ratio of RFY to total biomass (mass of roots and vines); and d) RFY – expressed as harvested fresh roots in tonnes per hectare (t ha^{-1}).

Statistical analysis of triple lattice

General analyses of variance were conducted for all four traits using Genstat version 11.1 (Payne *et al.*, 2007). Pseudofactors for analysing the triple lattice design were generated in the Genstat procedure. The block corrected means across the three replications for each full-sib family were used in the diallel analysis.

Diallel analysis

To test the null hypothesis of no genotypic differences among parents and crosses (collectively referred to as treatments) a one way analysis of variance was performed. Treatment sum of squares were partitioned into three components, parents (P), crosses (C), and P vs. C. The GCA and SCA variance components of the C mean square were computed according to Griffing's (1956) fixed-effects model I, method 1 (parents, and F_1s including reciprocals) using the DIALLEL-SAS05 program developed by Zhang *et al.* (2005). Reciprocals were defined as being below the diagonal. Adopting Griffing's (1956) notation the following genetic statistical model for an analysis within one environment was considered:

$$y_{ij} = u + g_i + g_j + s_{ij} + r_{ij} + \frac{1}{bc}\sum_k \sum_l e_{ijkl} \begin{cases} i, j = 1,..., p, \\ k = 1,..., b, \\ l = 1,..., c, \end{cases}$$

where u is the overall mean of the cross involving the i^{th} and j^{th} parents in block k and replication l; $g_i\left(g_j\right)$ is the general combining ability (GCA) effect for the $i^{th}\left(j^{th}\right)$ parents; s_{ij} is the specific combining ability (SCA) effect for the cross between the i^{th} and j^{th} parents such that $s_{ij} = s_{ji}$; r_{ij} is the reciprocal effect involving the reciprocal crosses between the i^{th} and j^{th} parents such that $r_{ij} = -r_{ji}$, and e_{ijkl} is the environmental effect associated with the $ijkl^{th}$ individual observation; p, b and c are the numbers of parents, blocks and replications, respectively. The mean squares and the F-tests for overall statistical differences among the various classes are provided (Table 4.2). In the analysis, $M_e^{'} = M_e / bc$, where M_e is the error mean square for the randomised block design and its expectation, $M_e^{'}$ is denoted as $E\left(M_e^{'}\right) = M_e / bc = \sigma^2$.

Table 4.2 Analysis of variance for Griffing's (1956b) Model I, Method I and the expected mean squares for a full diallel, excluding selfs

Source	df	Sum of Squares *	Mean Squares	Expected Mean Squares	F-ratios
GCA	$p-1$	S_g	M_g	$\sigma^2 + 2p\left(\frac{1}{p-1}\right)\sum g_i^2$	M_g / M_e'
SCA	$p(p-1)/2$	S_s	M_s	$\sigma^2 + \frac{1}{p(p-1)}\sum_i\sum_j s_{ij}^2$	M_s / M_e'
Reciprocal effects	$p(p-1)/2$	S_r	M_r	$\sigma^2 + 2\left(\frac{2}{p(p-1)}\right)\sum_i \langle \sum_j r_{ij}^2$	M_r / M_e'
Error	m	S_e	M_e'	σ^2	

*Where:

$$S_g = \frac{1}{2p}\sum_i \left(X_{i.} + X_{.j}\right)^2 - \frac{2}{p^2} X_{..}^2;$$

$$S_s = \frac{1}{2}\sum_i\sum_j \left(x_{ij} + x_{ji}\right)^2 - \frac{1}{2p}\sum_i \left(X_{i.} + X_{.j}\right)^2 + \frac{1}{p^2} X_{..}^2;$$

$$S_r = \frac{1}{2}\sum_i \langle \sum_j \left(x_{ij} - x_{ji}\right)^2;$$

and

$X_{i.}$ is the marginal mean for the i^{th} parent;

$X_{.j}$ is the marginal mean for the j^{th} parent;

$X_{..}$ is the grand mean;

x_{ij} is the mean for an above diagonal cross of the i^{th} and j^{th} parents; and

x_{ji} is the mean for a below diagonal reciprocal cross of the j^{th} and i^{th} parents.

The relative importance of GCA and SCA for selected traits was assessed by expressing their variances in the ratio, $2\sigma^2_g/(2\sigma^2_g + \sigma^2_s)$, according to Baker (1978).

The narrow sense heritability estimates were obtained from the DIALLEL-SAS05 program based on the cross heritability formula of van Buijtenen (1976):

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

where:

h^2_c = cross narrow sense heritability estimate;

σ^2_{GCA} = genetic variance component for general combining ability obtained as: $(p\text{-}1)/2p[M_g - M_e']$; notation as in Table 4.1;

σ^2_{SCA} = genetic variance component for specific combining ability obtained as: $p(p\text{-}1)/2p[M_s - M_e']$; notation as in Table 4.1; and

σ^2_e/r = error variance divided by the number of replications = M_e' .

4.3 Results

4.3.1 Analysis of variance for β-carotene content, root dry mass, harvest index and root fresh yield

The ANOVA of the 5x5 triple lattice provides the variances (mean squares) and block corrected means of the parents and their crosses (collectively referred to as treatments in Table 4.3) for the traits: β-carotene content, RDM, HI, and RFY. There was highly significant ($p<0.001$) variation among the parents and crosses for all four traits.

Table 4.3 ANOVA for four traits of five sweetpotato parents and their 20 F_1 families evaluated in a triple lattice design

Source	*df*	Mean Squares			
		β-carotene content (mg 100 g^{-1})	**Root dry mass (%)**	**Harvest index**	**Root fresh yield (t ha^{-1})**
Rep	2	0.57^{NS}	6.99^{NS}	0.004^{NS}	0.28^{NS}
Treatments	24	42.34***	38.28***	0.065***	198.16***
Blocks within reps	12	11.20	22.64	0.032	79.68
Intra-block error	36	0.12	4.60	0.003	1.22
Total	74				

*** Significant at *P*<0.001 (*F*-probability); NS=not significant

The mean performance of some of the crosses exceeded that of both their parents for the four traits (Table 4.4). Cross 1 x 2 and the cross 3 x 2 were the best performers for β-carotene content with means of 13.69 and 13.72 mg 100 g^{-1}, respectively. Cross 2 x 5 and 2 x 1 were the lowest performers with means of 0.04 and 0.03 mg 100 g^{-1}, respectively. The best performing individual progeny for β-carotene content overall came from the cross 3 x 2 with 17.57 mg 100 g^{-1} followed by a progeny from cross 1 x 2 with 17.34 mg 100 g^{-1}. The majority of the progeny with high β-carotene content came from the two crosses, 3 x 2 and 1 x 2 (Appendix 4.3.1).

The cross 5 x 1 was the best performer for RDM with a mean of 37.9%, followed by crosses 2 x 5 and 4 x 3 with means of 34.0 and 33.7%, respectively. Both crosses 1 x 3 and 5 x 3 had the lowest means of 24.7% (Table 4.4). The best performing progeny came from the reciprocal cross (5 x 1) with RDM of 44.3% followed by a progeny from a cross (1 x 4) with RDM of 43.8%. The lowest performing progeny overall was from cross (3 x 5) with a RDM of 15.5% (Appendix 4.3.2).

Two crosses (1 x 3 and 1 x 4) with their reciprocals (3 x 1 and 4 x 1), together with crosses 5 x 1, 4 x 2, and 4 x 3 had higher HI than the 0.81 recorded for the best parent, namely parent 3. The HI means for crosses 1 x 3 and 1 x 4 were 0.84 and 0.92, respectively. The means for their reciprocals 3 x 1 and 4 x 1 were 0.87 and 0.86, respectively. The means for crosses 5 x 1, 4 x 2, and 4 x 3 were 0.88, 0.91 and 0.83,

respectively. The cross 2 x 5 had the lowest HI mean value of 0.25 (Table 4.4). The best four performing progeny were from the cross 1 x 4 with two recording HI of 0.97 and the other two, 0.96. The progeny with the lowest HI was from the cross 2 x 5 (Appendix 4.3.4).

The highest performers for RFY were crosses 4 x 5 and 4 x 3 with mean values of 26.5 and 32.8 t ha^{-1}, respectively. The lowest performers for RFY were crosses 1 x 5 and 5 x 2, yielding a mean of 0.5 and 0.6 t ha^{-1}, respectively (Table 4.4). The 13 best performing progeny came from the cross (4 x 3) with yields ranging from 35 to 38 t ha^{-1}. The lowest yielding progeny was from the cross (1 x 5) with 0.12 t ha^{-1} (Appendix 4.3.3).

Table 4.4 Block corrected means for four traits of five sweetpotato parents and their 5 x 5 diallel crosses (excluding selfs) evaluated in a 5 x 5 triple lattice experimental design

Parents/Crosses[a]	β-carotene content (mg 100 g^{-1})	Root dry mass (%)	Harvest index	Root fresh yield (t ha^{-1})
1 x 2	13.69	28.27	0.55	1.12
1 x 3	0.18	24.74	0.84	8.21
1 x 4	0.06	31.49	0.92	14.95
1 x 5	1.66	27.36	0.50	0.50
2 x 3	5.75	31.85	0.56	2.77
2 x 4	0.17	29.76	0.68	15.95
2 x 5	0.04	34.03	0.25	2.31
3 x 4	4.59	29.42	0.60	2.81
3 x 5	4.70	24.27	0.59	0.99
4 x 5	0.13	30.83	0.73	26.49
Reciprocals (below the diagonal)				
2 x 1	0.03	28.77	0.79	13.65
3 x 1	0.06	27.18	0.87	16.67
4 x 1	0.07	28.75	0.86	15.53
5 x 1	0.16	37.89	0.88	11.76
3 x 2	13.72	29.41	0.74	7.59
4 x 2	0.08	31.44	0.91	8.84
5 x 2	1.79	26.20	0.50	0.58
4 x 3	0.24	33.66	0.83	32.79
5 x 3	0.26	24.07	0.55	0.90
5 x 4	0.09	33.99	0.81	17.34
Parent 4	0.07	32.51	0.78	10.92
Parent 2	0.19	35.54	0.63	11.35
Parent 3	4.89	24.43	0.81	25.44
Parent 5	3.51	36.12	0.69	18.93
Parent 1	6.65	25.78	0.76	4.84
Mean	2.51	29.91	0.71	10.93
s.e	0.34	2.14	0.05	1.11
CV (%)	13.7	7.2	7.6	10.1
$LSD_{(0.05)}$	0.65	4.05	0.10	2.09

[a]1 = Excel, 2 = L4-138/3; 3 = W-119, 4 = Unknown 2/1, 5 = L4-199084/1

4.3.2 General and specific combining ability analysis for β-carotene content, root dry mass, harvest index and root fresh yield

4.3.2.1 Combining ability mean squares

The GCA and SCA mean squares for β-carotene content, RDM, HI and RFY were highly significant (p<0.001) (Table 4.5). The mean squares for reciprocals were also highly significant (p<0.001) except for RDM which was not significant (Table 4.4). The GCA to SCA variance ratios were 0.76 for β-carotene content, 0.92 for RDM, 0.76 for HI, and 0.68 for RFY.

Table 4.5 Combining ability ANOVA for four traits of five sweetpotato parents and their 5 x 5 diallel crosses (excluding selfs)

Source	***df***	**Mean Squares**			
		β-carotene content (mg 100 g^{-1})	**Root dry mass (%)**	**Harvest index**	**Root fresh yield (t ha^{-1})**
Rep	2	0.57***	7.00^{NS}	0.01^{NS}	0.11^{NS}
Parent	4	25.62***	101.24***	0.25***	269.38***
Parent x Cross	1	9.48***	19.74^{NS}	0.01^{NS}	251.33***
Crosses	9	56.41***	22.96***	0.21***	225.03***
GCA	4	71.36***	42.32***	0.27***	235.77***
SCA	5	44.45***	7.47^{NS}	0.17***	217.87***
Reciprocal	10	43.20***	8.17^{NS}	0.23***	225.03***
Error	48	0.104	5.46	0.003	1.50
Total	74				

*** Significant at *p*<0.001 (by *F*-probability); NS=not significant; GCA=variation due to general combining ability, SCA=variation due to specific combining ability, reciprocal=variation between reciprocals

4.3.2.2 Combining ability effects

Beta-carotene content

The GCA effects for parent 1 and 3 were positive and highly significant ($p<0.01$) (Table 4.6). The GCA effects for parent 4 and 5 were significant ($p<0.01$) but negative (Table 4.6). The GCA effect for parent 2 was not significant (Table 4.6). The SCA effects of crosses 1 x 2, 2 x 5, and 3 x 4 were positive and highly significant ($p<0.01$) (Table 4.7). The rest of the crosses, apart from 4 x 5 which was not significant, had highly significant ($p<0.01$), negative SCA effects. Two reciprocals (2 x 1 and 5 x 2) were also positive and highly significant ($p<0.01$). Crosses 3 x 1 and 4 x 3 were negative though highly significant ($p<0.01$) (Table 4.7).

Table 4.6 Estimates of GCA effects for four traits of five sweetpotato parents

Parent[a]	**β-carotene content (mg 100g^{-1})**	**Root dry mass (%)**	**Harvest index**	**Root fresh yield (t ha^{-1})**
1	1.650**	-2.612**	0.0623**	-5.082**
2	-0.023^{NS}	2.981**	0.0129^{NS}	1.301**
3	0.354**	-2.807**	-0.0848**	2.533**
4	-1.044**	1.837**	0.0126^{NS}	-0.152^{NS}
5	-0.937**	0.602^{NS}	-0.0031^{NS}	1.400**

* and ** Significant at $p<0.01$ and 0.05, respectively (by *F*-probability); NS=not significant; [a]1=Excel, 2=L4-138/3; 3=W-119, 4=Unknown 2/1, 5=L4-199084/1

Table 4.7 Estimates of SCA effects for the 5 x 5 diallel analysis of four traits

Crosses[a]	β-carotene content (mg 100 g^{-1})	Root dry mass (%)	Harvest index	Root fresh yield (t ha^{-1})
1 x 2	5.655**	-0.745^{NS}	-0.141**	-4.754**
1 x 3	-2.105**	1.144^{NS}	0.114**	-3.320**
1 x 4	-3.018**	1.257^{NS}	0.194**	9.939**
1 x 5	-2.416**	-0.378^{NS}	-0.193**	-10.399**
2 x 3	-2.722**	0.563^{NS}	0.153**	6.797**
2 x 4	-1.373**	1.849*	-0.070**	-4.517**
2 x 5	3.184**	-1.343^{NS}	0.097*	6.414**
3 x 4	5.088**	-0.690^{NS}	-0.084**	-7.629**
3 x 5	-3.364**	-2.904^{NS}	0.547**	-14.979**
4 x 5	-0.113^{NS}	0.571^{NS}	-0.292**	-4.111**
Reciprocals (Below the diagonal)				
2 x 1	3.917**	-1.437^{NS}	-0.0002^{NS}	-0.722^{NS}
3 x 1	-2.303**	-0.112^{NS}	0.127**	3.611**
4 x 1	0.005^{NS}	1.465^{NS}	0.027^{NS}	-0.370^{NS}
5 x 1	0.003^{NS}	0.653^{NS}	0.000^{NS}	0.000^{NS}
3 x 2	0.000^{NS}	0.000^{NS}	-0.025^{NS}	-5.111**
4 x 2	-0.040^{NS}	-1.763^{NS}	-0.316**	-4.889**
5 x 2	2.257**	-1.972*	-0.117**	-15.042**
4 x 3	-6.802**	-0.317^{NS}	0.332**	-2.434**
5 x 3	-0.005^{NS}	0.728^{NS}	0.160**	7.889**
5 x 4	0.005^{NS}	-1.160^{NS}	-0.344**	0.780^{NS}

* and ** Significant at *p*<0.01 and 0.05, respectively (*F*-probability); NS=not significant; [a]1=Excel, 2=L4-138/3; 3=W-119, 4=Unknown 2/1, 5=L4-199084/1

Root dry mass composition

The GCA effects for parent 2 and 4 were positive and highly significant (p<0.01). The GCA effects for parent 1 and 3 were also highly significant (p<0.01) but negative. The GCA effect for parent 5 was not significant (Table 4.6). Only cross 2 x 4 had a positive

and highly significant ($p<0.01$) SCA effect whereas the rest of the crosses were not significant. Only one cross 5 x 2 had a highly significant ($p<0.01$) SCA effect though negative while the rest were not significant (Table 4.7).

Harvest index

The GCA effect was highly significant ($p<0.01$) and positive for parent 1. It was also highly significant ($p<0.01$) for parent 3 but negative. The GCA effects for the other parents were not significant (Table 4.6). The SCA effects were significant ($p<0.05$) for all the crosses except for four, namely: 2 x 1, 4 x 1, 5 x 1, and 3 x 2. However, half of the crosses with significant ($p<0.05$) SCA effects had negative effects, namely: 1 x 2, 1 x 5, 2 x 4, 3 x 4, 4 x 5, 4 x 2, 5 x 2, and 5 x 4 (Table 4.7).

Roor fresh yield

The GCA effect for parent 1 was negative and significant ($p<0.01$). Parents 2, 3, and 5 had GCA effects that were positive and significant ($p<0.01$). The GCA effect for parent 4 was not significant (Table 4.6). Three crosses had positive and significant ($p<0.01$) SCA effects, namely: 1 x 4, 2 x 3, and 2 x 5. The other crosses were significant ($p<0.01$) but had negative SCA effects. Two reciprocals (3 x 1 and 5 x 3) had positive and significant ($p<0.01$) SCA effects. Some reciprocals had significant ($p<0.01$) negative effects (3 x 2, 4 x 2, and 5 x 2). The SCAs of the other reciprocal crosses were not significant (Table 4.7).

4.3.2.3 Narrow and broad sense heritability estimates

The narrow sense heritability estimates for RDM calculated from variance components was high at 76.3%. The estimates for the other three traits were, however, relatively low at 20.9% for β-carotene content, 29.1% for HI, and 34.9% for RFY. Broad sense heritability estimates were 89.6% for RDM, 99.4% for β-carotene content, 84.4% for HI, and 96.9% for RFY.

4.3.2.4 Estimates of heterosis

Percent heterosis was calculated for 30 progeny selected on the basis of the selection index presented in Chapter 3. The most positive % heterosis for β-carotene content relative to both mid-parent and best parent mean value was observed in progeny 10 (592% and 2595, respectively) and 18 (461% and 191, respectively) both from cross 3 x 2. The most negative percentage hybrid vigour relative to mid parent and best parent mean value for β-carotene content were observed in progeny 7 (-98% and -99%, respectively) from cross 1 x 4 and progeny 9 (-98% and 99, respectively) from cross 4 x 3 (Table 4.8). Progeny 15 and 10 from cross 4 x 3 had the highest positive mid-parent heterosis of 42 and 29%, respectively for RDM. Again, progeny 15 from cross 4 x 3 had the highest best parent heterosis of 24% followed by progeny 11 from cross 1 x 3 with 21% (Table 4.8). The most positive mid-parent heterosis% for RFY was observed in progeny 7 (111%) from cross 1 x 4 and progeny 9 (111%) from cross 4 x 3, while the highest positive best parent heterosis % was observed in progeny 7 (52%) from cross 1 x 4 and progeny 1 (51%) from cross 2 x 4 among the top 30 genotypes (Table 4.8).

Table 4.8 Hybrid vigour of 30 progeny selected using a selection index for β-carotene, root dry mass and root fresh yield

		Hybrid vigour (Heterosis) percentage						
		β-carotene content (mg 100 g^{-1})		Root dry mass (%)		Root fresh yield (t ha^{-1})		Selection
Cross[a]	Progeny ID	Mid parent†	Best parent‡	Mid parent	Best parent	Mid parent	Best parent	Index
4 x 3	9	-98.0	-99.0	10.0	-3.6	110.8	50.6	171.71
4 x 3	10	-91.9	-95.9	29.3	13.3	103.6	45.5	186.17
4 x 3	15	-79.4	-89.6	41.9	24.2	100.6	43.4	197.03
4 x 5	20	-97.2	-98.6	6.5	1.2	70.8	34.6	161.75
2 x 4	1	200.0	105.3	-18.9	-22.4	54.0	51.2	119.50
1 x 4	7	-98.2	-99.1	16.4	4.3	111.1	52.3	136.24
2 x 1	12	-83.9	-91.7	-9.3	-21.7	104.3	45.8	119.68
3 x 1	8	-98.4	-98.6	15.8	12.8	5.7	-37.1	120.49
3 x 1	4	-97.4	-97.7	13.9	10.9	3.6	-38.3	118.69
1 x 3	11	-97.4	-97.7	24.4	21.1	-1.0	-41.1	124.87
2 x 1	7	-76.3	-87.8	-4.6	-17.7	71.0	22.0	119.61
5 x 4	7	-86.6	-93.2	2.3	-2.8	-15.1	-33.1	132.30
5 x 4	6	-83.8	-91.7	-3.5	-8.3	-21.4	-38.0	124.89
3 x 2	18	460.6	191.2	-11.2	-25.1	-47.7	-62.1	156.93
3 x 2	10	591.7	259.3	-6.9	-21.5	-50.4	-64.1	173.14
1 x 3	16	-97.4	-97.7	12.2	9.2	-46.4	-68.1	101.91
3 x 4	19	329.4	117.8	-10.7	-21.8	-66.3	-75.9	131.80
3 x 4	18	281.9	93.7	-1.3	-13.6	-69.7	-78.3	133.91
2 x 3	20	226.4	69.5	-8.8	-23.1	-75.4	-82.2	124.86
3 x 4	4	330.2	118.2	-12.1	-23.0	-76.8	-83.4	126.94
2 x 3	8	178.3	44.6	5.1	-11.3	-78.5	-84.5	131.49
1 x 2	19	331.9	122.1	-1.4	-14.9	-56.8	-69.2	157.36
5 x 2	2	73.0	-8.8	-21.0	-21.7	-80.1	-84.0	104.21
1 x 2	16	146.8	26.9	5.8	-8.7	-77.0	-83.6	135.47
3 x 5	4	88.1	61.6	-0.3	-16.4	-91.5	-92.6	126.55
1 x 5	17	-77.2	-82.6	2.2	-12.4	-84.8	-90.5	103.78
1 x 2	1	310.5	111.1	-6.4	-19.2	-82.3	-87.4	145.92
5 x 2	6	30.8	-31.1	-19.1	-19.7	-92.6	-94.1	99.42
1 x 5	20	-66.9	-74.7	-4.8	-18.4	-91.4	-94.6	97.87
1 x 5	14	-65.7	-73.8	-3.1	-17.0	-95.8	-97.4	98.61

[a]1=Excel, 2=L4-138/3; 3=W-119, 4=Unknown 2/1, 5=L4-199084/1; † (Hybrid vigour relative to the mid parent value); ‡ (Hybrid vigour relative to the best parent value)

4.4 Discussion and conclusion

4.4.1 Analysis of variance for β-carotene content, root dry mass, harvest index and root fresh yield evaluated in a triple lattice experimental design

The significant ($p<0.001$) mean square for treatments for β-carotene content, RDM, HI, and RFY is indicative of the genetic variation among the parents and their crosses. Crosses outperforming their parents can be attributed to transgressive segregation which is desirable for improving β-carotene content and RDM. Selection imposed on all of the progeny using a selection index and 30 progeny were selected across the 20 crosses. Progeny 15 from cross 4 x 3 was the best overall. Several of the selected progeny had high percentage hybrid vigour for the traits measured. For example, progeny 10 from cross 3 x 2 had high mid-parent heterosis of 592% for β-carotene content; progeny 15 from cross 4 x 3 had mid-parent heterosis of 42% for RDM; and progeny 7 from cross 1 x 4 had high mid-parent heterosis of 111% for RFY.

4.4.2 General and specific combining ability for β-carotene content, root dry mass, harvest index and root fresh yield

The magnitudes of the GCA and SCA variances (Table 4.5) imply that both additive and non-additive gene action are important in controlling the expression of the four traits. The GCA and SCA mean squares for the four traits were significant ($p<0.001$). This implies that both additive and non-additive gene action were involved in the expression of β-carotene content, RDM, HI, and RFY. The GCA to SCA variance ratios were 0.76 for β-carotene content, 0.92 for RDM, 0.76 for HI, and 0.68 for RFY indicating that additive gene action was relatively more predominant than non-additive gene action in controlling the expression of the traits. Hence, predicting progeny performance based on GCA for the four traits will be largely successful. The highly significant ($p<0.001$) reciprocal mean squares for β-carotene content, HI, and RFY is an indication that maternal effects play a role in the inheritance of these traits and consequently the performance of a parent in a cross is dependant on whether it is used as a female or a male.

β-carotene content

The GCA effects for parent 1 (1.65) and 3 (0.35) were significant ($p<0.01$) indicating that additive gene action contributed positively to the expression of the trait. However, their cross 1 x 3 had a negative (-2.1) and highly significant ($p<0.01$) SCA effect. This means that the non-additive gene action arising from the interaction between the parents resulted in the cross performing below the expectation based on additive effects. The crosses that had positive and significant ($p<0.01$) SCA effects were 1 x 2, 2 x 5, and 3 x 4 indicating that the non-additive gene action arising from the interaction of the parents contributed positively to the expression of the trait. Parent 1 and 3 were only able to produce a desirable (positive and significant SCA effect) cross with parents 2 and 4, respectively. Parents 2 and 5 that had negative GCA effects (-0.023 and -0.937, respectively) produced a cross with a positive (3.184) and highly significant ($p<0.01$) SCA effect (Table 4.6). Therefore, parents cannot be disqualified solely on the basis of negative GCA effects. Conversely, parents with high positive GCA effects did not necessarily produce crosses with the desired performance. In this study desirable crosses were obtained from crossing parents with high GCA effects with parents with low GCA effects viz. 1 x 2 and 3 x 4 and a parent with low GCA effect with a parent with a low GCA effect 2 x 5. The GCA to SCA ratio was 0.76 for β-carotene content indicating that additive gene action was relatively more important than non-additive gene action in conditioning this trait. Similar results have been reported in cucumber (*Cucumis sativus* L.) where additive gene effects conditioned carotenoid accumulation in mature fruits (Navazio and Simon, 2001).

The crosses, 2 x 1 and 5 x 2, had highly significant ($p<0.01$), positive SCA effects (3.9 and 2.2, respectively) for β-carotene content (Table 4.7). This implies that parent 2 interacted positively as either the female or male parent when crossed with either parent 1 or 5, respectively. Parents 2 and 5 had negative GCA effects whereas parent 1 had a high, positive GCA effect (Table 4.6). However, reciprocal cross 2 x 1 had the lowest mean β-carotene content (0.03 mg 100 g^{-1}) of all the crosses. In contrast, cross 1 x 2 had the highest mean β-carotene content (13.69 mg 100 g^{-1}) suggesting that maternal effects influenced the performance of the crosses. Among the reciprocal crosses, the mean for reciprocal cross 5 x 2 was 1.79 mg 100 g^{-1} which was second after reciprocal cross 3 x 2, 13.72 mg 100 g^{-1}.

The best cross overall with a mean β-carotene content of 13.69 mg 100 g^{-1} resulted from crossing a parent with a high positive GCA effect (1.6) with a parent with a low GCA effect (-0.023) viz. 1 x 2 (SCA effect = 5.6). The second best cross was between a parent with a high positive GCA effect and a parent with a high negative GCA effect viz. 3 x 4 (SCA effect = 5.1). The best reciprocal cross with a mean β-carotene content of 13.72 mg 100 g^{-1} resulted from a parent with a positive and significant GCA effect combining with a parent with a negative and non-significant GCA effect, namely: 3 x 2 (SCA effect = 0). The implication of the performances of these crosses in relation to their respective GCA (and SCA) effects is that predicting the performance of crosses cannot be based simply on the magnitude of the GCA effects of the parents. It is worth noting that all the parents were involved in a cross that produced at least one progeny worthy of further evaluation (Table 4.8 and Appendix 4.3.1) in terms of β-carotene content.

Root dry mass composition

The GCA and SCA mean squares for RDM were significant ($p<0.01$), but the reciprocal mean square was not significant. The ratio of GCA to SCA mean squares was 0.92. Accordingly, gene action controlling this trait was predominantly additive. The result concurs with that of Grüneberg *et al.* (2005). Similar results were obtained in cassava (Jaramillo *et al.*, 2005). Parents 2 and 4 had positive and large GCA effects (3.0 and 1.8) that were significant ($p<0.01$). Their cross 2 x 4 exhibited the highest significant ($p<0.01$) and positive SCA effects (1.85) (Table 4.7). Nevertheless, their cross mean (29.8%) was only fifth highest among crosses (Table 4.4). The reciprocal cross 5 x 1 with a mean RDM of 38% was the best overall performer and the best performing progeny overall came from this reciprocal cross with a RDM of 44% (Appendix 4.3.2). This result emphasises the value of conducting reciprocal crosses in order to increase the likelihood of generating progeny with high RDM even though in this study the reciprocal mean square was not significant.

Harvest index

The GCA and SCA mean squares were significant ($p<0.001$). The GCA and SCA mean square ratio was 0.76 which indicated that additive gene action was dominant over non-additive. A number of crosses had positive and significant ($p<0.05$) SCA effects, namely: 1 x 3, 1 x 4, 2 x 3, 3 x 5, and 2 x 5 (Table 4.7). This implies that the non-additive gene action arising from the interaction between these parents contributed positively to the expression of the trait. Cross 1 x 4 involving parents with negative GCA effects had the best cross mean of 0.92 and the highest performing individual progeny with a HI of 0.97 (Appendix 4.3.4).

The best performing progeny within a cross came from cross 4 x 2 (0.96). This was followed by progeny from four other crosses (2 x 1, 5 x 1, 4 x 3, and 5 x 4) each with a HI of 0.95 (Appendix 4.3.4). The within cross progeny performance is obviously important in selecting the best progeny as the mean of a cross does not provide an indication of how the individual progeny performed. This is exemplified by cross 3 x 1 which had a high cross mean (0.87) but its best performing progeny (HI = 0.94) was outperformed by progeny from crosses with lower cross means e.g. cross 2 x 1 which had a mean HI = 0.79 but its best performing progeny had a HI = 0.95.

Root fresh yield

The ratio of GCA to SCA mean squares was 0.68 indicating that additive gene action contributed more to the expression of RFY than non-additive gene action. The GCA effects for RFY for parents 2, 3, and 5 were positive (1.3, 2.5 and 1.4, respectively) and significant ($p<0.01$) indicating the involvement of additive gene action in the expression of the trait (Table 4.6). The SCA effects were significant ($p<0.01$) and positive (9.9, 6.8, and 6.4, respectively) for crosses 1 x 4, 2 x 3, and 2 x 5, indicating that non-additive gene action contributed positively to the expression of RFY. Parents 2, 3, and 5 with high GCA effects (1.3, 2.5, and 1.4, respectively) resulted in crosses (2 x 3 and 2 x 5) with high positive SCA effects (6.8 and 6.4, respectively) (Table 4.7). Again, non-additive gene action contributed positively to the expression of the trait in the two crosses. Cross 4 x 3 with a significant ($p<0.01$), negative (-2.43) SCA effect produced the majority of the outstanding progeny most of which had RFYs above 30 t ha^{-1}. The mean for the cross

was 32.7 t ha^{-1} while the best performing individual progeny, coming from the same cross, yielded 38.3 t ha^{-1}. Conversely, the cross 3 x 4 had a very low mean RFY of 0.26 t ha^{-1} with the best performing progeny within the cross yielding only 0.61 t ha^{-1} (Appendix 4.3.3). This was an indication that maternal effects were involved in determining RFY in some of the crosses.

Two reciprocal crosses, 3 x 1 and 5 x 3, had positive (3.6 and 7.9, respectively) and highly significant ($p<0.01$) SCA effects for RFY (Table 4.7). Thus, parent 3 combined well as a female with parent 1 and combined well as a male with parent 5. Parents 3 and 5 were significant, positive GCA effect parents whereas parent 1 was a significant, negative GCA effect parent (Table 4.5). It was noted that the cross between the positive, high GCA effect parent 3 and the negative, high GCA effect parent 1, had an "unexpected" positive, high SCA effect while the cross 5 x 3 between two positive, high GCA effect parents had an "expected" positive, high SCA effect. Again this confirms that the positive contribution of non-additive gene action to the expression of RFY does not necessarily depend on the signage of the GCA effects of the parents involved.

4.2.3 Heritability estimates

The h^2 for β-carotene, HI, and RFY were low suggesting that progress in selection will be slow. Hernandez *et al.* (1967) indicated that the character of orange root flesh colour was controlled by several genes, most likely six, that are probably additive in effect. They concluded that inheritance of flesh colour was a quantitative character. In addition, they found that certain parents transmitted high carotenoid content to a greater degree than others and crosses between certain parents produced transgressive segregants. Their findings concur with results of this study where hybrid vigour was recorded for a number of progeny.

The h^2 for RDM was high indicating that the environment had less influence on the trait. A negative association between of orange root flesh colour and RDM has been noted by others (Hernandez *et al.,* 1967; Jones *et al.,* 1969). To simultaneously improve both these traits their negative linkages will have to be broken.

The broad sense heritability estimates were much higher (>80%) for all the four traits, as expected. Rapid genetic gains should be expected, as H is high, through use of mass selection based on the phenotype of the parent.

4.2.4 General conclusion

The analysis of variance revealed significant ($p<0.01$) differences among the treatments for all the traits indicating the probability of selecting high performing progeny from the crosses (Table 4.4). The GCA and SCA mean squares were highly significant ($p<0.001$) for the four traits. The ratios of GCA to SCA variances were generally large (0.68 to 0.92). Reciprocal effects were significant ($p<0.01$) for all traits studied except RDM. It is concluded that additive gene action was dominant over non-additive for the determination of β-carotene, HI, RDM, and RFY.

The two high β-carotene parents (1 and 3) used in this study exhibited high GCA effects, indicating that additive gene effects were predominant in the inheritance of β-carotene. However, β-carotene parents with high GCA effects did not result in crosses with the highest SCA effects. The highest β-carotene progeny were obtained from crosses between a parent with positive, high GCA effects and a parent with negative, low GCA effects, namely: reciprocal cross 3 x 2 (SCA effect = 0) and cross 1 x 2 (SCA effect = 5.6).

Progeny with the highest RDM were obtained from a cross between a parent with a significantly ($p<0.01$) positive, high (2.9) GCA effect and a parent with a non-significant GCA effect (0.6), namely 2 x 5 (SCA effect = -1.3), and a cross between a parent with non-significant, positive GCA effect (0.6) and a parent with significant ($p<0.01$) negative, high (-2.6) GCA effect, namely 5 x 1 (SCA effect = 0.6). This implies that selection of parents for the hybrid programme needs to take into account the GCA and SCA effects in combination with the actual performance of progeny within a cross. As sweetpotato clones are released as highly heterozygous F_1 progeny, the breeding programme will take advantage of the occurrence of heterosis concomitant with the utilisation of additive genes by mass recurrent selection.

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Appendices

Appendix 4.1 Soil analysis for field trial site at Mansa Research Station (11° 14.396' S and 028° 57.226' E) , Mansa, Zambia

Analyte	Result	Critical value
pH $CaCl_2$	4.6	4.5
Org. C%	0.86	1.58
N%	0.06	0.1
P ppm	8	15
K me%*	0.14	0.15
Ca me%	0.54	2.5
Mg me%	0.21	1.56
Na me%	-	>2.0
Zn ppm	Trace	0.2
Fe ppm	5.82	-
Mn ppm	1.63	-
Cu %	0.06	0.2

*me% = meq 100 g^{-1} soil

Appendix 4.2 Field trial layout of a 5 x 5 triple lattice experimental design conducted at Mansa Research Station (11°14.396' S and 028°57.2 26' E), Mansa, Zambia

Replication 1

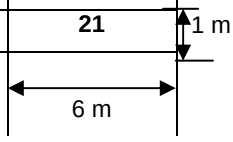
	Plots				
Blocks	1	2	3	4	5
1	**1**	**2**	**3**	**4**	**5**
2	**6**	**7**	**8**	**9**	**10**
3	**11**	**12**	**13**	**14**	**15**
4	**16**	**17**	**18**	**19**	**20**
5	**21**	**22**	**23**	**24**	**25**

Replication 2

	Plots				
Blocks	1	2	3	4	5
1	**1**	**6**	**11**	**16**	**21**
2	**2**	**7**	**12**	**17**	**22**
3	**3**	**8**	**13**	**18**	**23**
4	**4**	**9**	**14**	**19**	**24**
5	**5**	**10**	**15**	**20**	**25**

Replication 3

	Plots				
Blocks	1	2	3	4	5
1	**1**	**10**	**14**	**18**	**22**
2	**2**	**6**	**15**	**19**	**23**
3	**3**	**7**	**11**	**20**	**24**
4	**4**	**8**	**12**	**16**	**25**
5	**5**	**9**	**13**	**17**	**21**



Gross plot size: 6.6 m x 1 m
Net plot size: 6 m x 1 m
Horizontal and vertical lines indicate 1 m wide paths
The crosses corresponding to the treatments were as follows: 1 = 1 x 2, 2 = 1 x 3, 3 = 1 x 4, 4 = 1 x 5, 6 = 2 x 3, 7 = 2 x 4, 8 = 2 x 5, 9 = 3 x 4, 10 = 4 x 5, 11 = 2 x 1, 12 = 3 x 1, 13 = 4 x 1, 14 = 5 x 1, 15 = 3 x 2, 16 = 4 x 2, 17 = 5 x 2, 18 = 4 x 3, 19 = 5 x 3, 20 = 5 x 4, 21 = parent 4, 22 = parent 2, 23 = parent 3, 24 = parent 5, and 25 = parent 1.

Appendix 4.3.1 Within cross ranking of β-carotene content (mg 100 g^{-1}) of sweetpotato progeny evaluated in a 5 x 5 triple lattice experiment conducted at Mansa Research Station, Zambia

Progeny No	Crosses* (above diagonal)																			
	1 x 2		1 x 3		1 x 4		1 x 5		2 x 3		2 x 4		2 x 5		3 x 4		3 x 5		4 x 5	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
1	14.04	11	0.02	13	0.00	9	1.54	10	8.39	6	0.39	3	0.33	1	0	17	0.83	20	0	11
2	16.63	2	0.13	5	0.04	7	0.00	20	10.19	3	0.00	10	0	9	7.82	6	1.09	19	2.03	1
3	13.76	12	0	20	0.00	9	4.44	2	6.74	11	0.07	4	0	9	1.28	15	1.43	16	0	11
4	13.57	13	0.01	16	0.64	1	1.73	6	10.54	2	0	10	0	9	10.67	3	7.90	3	0	11
5	15.30	7	0.05	9	0.05	6	1.29	14	7.37	9	0.03	6	0.02	5	8.96	5	1.19	18	0.04	6
6	14.62	10	0.08	7	0.05	5	1.30	13	1.74	16	0.04	5	0.04	3	3.66	12	4.59	9	0.03	8
7	11.94	15	0.11	6	0.06	4	1.72	7	6.42	12	0	10	0.01	7	7.02	7	3.82	12	0.07	2
8	11.32	17	0.05	10	0.00	9	1.04	18	7.07	10	0	10	0	9	3.39	13	12.66	1	0.05	4
9	10.59	18	0.04	11	0.00	9	2.03	4	7.90	8	0	10	0	9	5.41	8	7.13	4	0	11
10	12.33	14	0.07	8	0.03	8	1.17	16	11.35	1	0.02	7	0	9	0.58	16	5.32	7	0	11
11	15.05	8	0.15	3	0.00	9	3.02	3	0.00	19	1.17	1	0	9	0	19	5.76	6	0.02	9
12	17.34	1	0.04	12	0.00	9	4.91	1	9.20	5	0.01	8	0	9	4.54	9	5.15	8	0.06	3
13	10.23	19	0.01	17	0.06	3	1.32	12	0.00	20	0	10	0	9	11.20	1	10.23	2	0	11
14	16.01	3	0.02	14	0.00	9	1.74	5	4.63	13	0	10	0.04	4	3.95	10	2.92	15	0	11
15	15.42	6	0.61	1	0.47	2	1.67	9	0.62	18	0	10	0	9	0	20	3.51	14	0.02	10
16	8.44	20	0.15	4	0.00	9	0.69	19	3.64	14	0.66	2	0	9	3.75	11	4.45	10	0	11
17	15.73	4	0.61	2	0.00	9	1.16	17	9.57	4	0	10	0.17	2	0	18	6.87	5	0.03	7
18	11.69	16	0.02	15	0.00	9	1.20	15	2.75	15	0	10	0	9	9.47	4	3.63	13	0	11
19	14.77	9	0.01	18	0.00	9	1.45	11	1.14	17	0	10	0.01	8	10.65	2	1.40	17	0	11
20	15.43	5	0.01	19	0.00	9	1.68	8	8.29	7	0.01	9	0.02	6	3.39	14	4.41	11	0.05	5
Mean	13.71		0.11		0.07		1.75		5.88		0.12		0.03		4.77		4.71		0.12	

*1 = Excel, 2 = L4-138/3; 3 = W-119, 4 = Unknown 2/1, 5 = L4-199084/1; S.E. = 0.27; CV% = 10.5; LSD = 0.43; Grand mean = 2.53

Appendix 4.3.1 (Continued)

Progeny No	Reciprocal crosses (below the diagonal)*																			
	2 x 1		3 x 1		4 x 1		5 x 1		3 x 2		4 x 2		5 x 2		4 x 3		5 x 3		5 x 4	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
1	0.00	10	0.00	9	0.00	7	0.00	8	15.57	5	0	9	0.03	15	0.56	1	0	7	0	12
2	0.00	10	0.00	9	0.00	7	0.30	3	13.25	17	0.0567	8	3.20	5	0.31	2	0.69	2	0	12
3	0.14	6	0.03	8	0.00	7	0.00	8	15.48	6	0.0633	7	0.76	11	0	10	1.25	1	0.12	6
4	0.17	5	0.15	2	0.00	7	0.00	8	16.01	3	0	9	0.34	14	0	10	0	7	0.06	10
5	0.03	9	0.04	7	0.03	4	0.05	6	4.34	19	0	9	0	16	0	10	0	7	0	12
6	0.00	10	0.00	9	0.00	7	0.00	8	16.82	2	0	9	2.42	8	0	10	0	7	0.29	3
7	0.81	1	0.00	9	0.03	6	0.00	8	15.59	4	0	9	0	16	0	10	0	7	0.24	4
8	0.00	10	0.09	4	0.00	7	0.00	8	14.38	9	0.4	3	0	16	0.03	7	0	7	0.01	11
9	0.04	7	0.00	9	0.00	7	0.00	8	3.67	20	0.28	4	3.03	6	0.05	6	0.18	3	0.09	8
10	0.00	10	0.00	9	0.00	7	1.08	1	17.57	1	0.47	2	0	16	0.20	5	0	7	0	12
11	0.00	10	0.00	9	0.00	7	0.00	8	14.78	7	0	9	0.42	13	0.46	3	0.05	6	0	12
12	0.55	2	0.00	9	0.88	1	0.19	4	14.67	8	0	9	0.76	12	0.02	8	0	7	0.11	7
13	0.00	10	0.07	5	0.00	7	0.03	7	14.32	11	0	9	4.60	2	0	10	0	7	0.17	5
14	0.00	10	1.64	1	0.00	7	0.00	8	13.78	16	0	9	0	16	0	10	0.14	4	0	12
15	0.35	3	0.00	9	0.00	7	0.00	8	14.12	14	1.0133	1	3.42	3	0.51	2	0	7	0.42	1
16	0.04	8	0.00	9	0.03	5	0.00	8	13.05	18	0	9	6.48	1	0	9	0	7	0	12
17	0.00	10	0.06	6	0.05	3	0.07	5	14.23	13	0	9	2.64	7	0	10	0	7	0.09	9
18	0.00	10	0.13	3	0.00	7	0.48	2	14.24	12	0.1633	5	3.4	4	0	10	0.09	5	0	12
19	0.00	10	0.00	9	0.00	7	0.00	8	14.05	15	0.1533	6	2.32	9	0	10	0	7	0	12
20	0.00	10	0.00	9	0.85	2	0.00	8	14.38	10	0	9	1.10	10	0	10	0	7	0.41	2
Mean	0.11		0.11		0.09		0.11		13.72		0.13		1.75		0.11		0.12		0.10	

*1 = Excel, 2 = L4-138/3; 3 = W-119, 4 = Unknown 2/1, 5 = L4-199084/1; S.E. = 0.27; CV% = 10.5; LSD = 0.43; Grand mean = 2.53

Appendix 4.3.2 Within cross ranking of root dry mass (%) of sweetpotato progeny evaluated in a 5 x 5 triple lattice experiment conducted at Mansa Research Station, Zambia

Progeny No	Crosses* (above diagonal)																			
	1 x 2		1 x 3		1 x 4		1 x 5		2 x 3		2 x 4		2 x 5		3 x 4		3 x 5		4 x 5	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
1	28.71	10	20.79	19	30.42	12	25.87	12	26.38	15	27.58	16	33.3	13	36.68	2	29.43	6	27.53	16
2	22.45	20	17.51	20	27.06	18	27.15	9	20.96	19	33.58	6	37.48	6	32.73	11	16.58	18	28.43	14
3	31.34	4	28.62	4	28.53	15	24.63	18	25.98	16	27.88	14	38.56	4	35.02	7	30.03	4	34.85	6
4	29.78	7	24.51	11	28.73	14	26.04	11	19.83	20	39.6	1	35.4	9	25.02	19	30.2	3	27.69	15
5	30.25	5	21.83	16	27.13	17	23.82	19	30.56	11	30.59	11	34.53	10	25.06	18	26.4	11	25.12	19
6	27.44	12	28.62	5	39.4	2	31	4	38.9	1	34.65	3	32.37	16	30.75	14	28.53	7	30.37	10
7	31.44	3	27.64	8	33.92	6	31.54	3	30.4	12	32.87	7	32.74	15	28.33	15	25.18	13	19.47	20
8	22.79	19	24.47	12	43.75	1	22.56	20	31.52	10	31.88	9	36.94	7	32.24	12	23.16	15	36.65	1
9	29.6	8	22.61	14	32.93	8	24.83	17	33.73	9	32.46	8	34.23	11	30.98	13	25.33	12	35.38	4
10	26.86	15	23.38	13	23.95	20	25.54	14	25.42	17	27.76	15	36.38	8	33.02	10	21.92	16	27.24	17
11	28.1	11	31.23	2	33.32	7	25.21	16	37.81	4	29.05	12	37.95	5	35.35	4	23.98	14	29.37	13
12	27.25	13	27.27	9	35.66	4	25.39	15	22.99	18	34.5	4	38.78	3	40.02	1	28.08	8	33.15	7
13	32.19	2	26.18	10	28.32	16	31	5	38.45	2	24.45	20	31.47	17	21.54	20	15.64	19	34.98	5
14	27	14	29.26	3	26.75	19	29.98	6	35.08	8	25.28	18	30.84	18	33.67	8	20.71	17	29.9	12
15	24.05	18	22.18	15	31.21	11	26.86	10	37.94	3	25.8	17	40.36	2	35.05	6	29.59	5	30.05	11
16	32.44	1	28.15	6	31.76	10	34.78	1	35.82	6	30.78	10	26.97	20	36.27	3	26.93	10	26.07	18
17	26.32	16	20.8	18	29.9	13	31.64	2	26.75	14	28.11	13	32.86	14	35.22	5	15.53	20	32.74	8
18	24.72	17	31.44	1	35.36	5	27.83	8	35.81	7	37.71	2	42.11	1	28.1	16	34.87	2	35.72	3
19	30.23	6	21.65	17	32.33	9	25.66	13	37.8	5	24.63	19	33.71	12	25.41	17	27.86	9	31.7	9
20	28.98	9	27.66	7	38.2	3	29.47	7	27.33	13	33.78	5	29.68	19	33.2	9	34.88	1	36.55	2
Mean	28.10		25.29		31.93		27.54		30.97		30.65		34.83		31.68		25.74		30.65	

*1 = Excel, 2 = L4-138/3; 3 = W-119, 4 = Unknown 2/1, 5 = L4-199084/1; S.E. = 1.72; CV% = 5.7; LSD = 4.74; Grand mean = 29.97

Appendix 4.3.2 (Continued)

Progeny No	Reciprocal crosses* (below diagonal)																			
	2 x 1		3 x 1		4 x 1		5 x 1		3 x 2		4 x 2		5 x 2		4 x 3		5 x 3		5 x 4	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
1	25.61	15	29.68	2	31.28	5	37.89	14	30.62	6	33.92	4	24.06	15	27.08	19	27.95	4	31.47	15
2	25.29	18	28.88	5	31.07	6	32.76	19	32.27	5	29.3	13	28.3	6	31.27	16	21.18	19	33.2	7
3	19.3	20	22.88	19	32.6	2	38.07	12	27.75	9	24.72	17	26.77	11	39.01	5	18.16	20	33.22	6
4	27.27	12	28.6	6	27.32	16	37.49	15	24.12	19	31.95	11	29.7	2	34.76	10	25.08	10	32.73	10
5	24.48	19	24.6	16	24.21	20	34.39	17	36.61	2	31.13	12	27.9	8	31.66	12	23.65	13	36.53	3
6	25.47	16	28.37	7	28.09	13	39.18	10	32.38	4	32.93	7	29	5	35.97	7	27.44	8	33.11	8
7	29.25	7	27.02	8	29.35	8	40.83	5	34.77	3	35.29	2	33.42	1	40.25	2	28.51	2	35.11	4
8	26.65	13	29.07	4	29.93	7	39.55	7	25.73	14	22.2	20	26.76	12	34.42	11	28.74	1	29.34	18
9	28.78	8	31.3	1	28.61	11	40.93	4	39.71	1	25.56	16	17.17	20	31.33	13	22.78	16	30.72	16
10	31	5	26.78	9	27.83	14	33.06	18	27.91	7	23.76	18	28.12	7	36.82	6	24.39	12	30.47	17
11	32.05	3	29.23	3	28.25	12	42.72	3	23.78	20	32.46	10	29.07	4	31.32	14	21.41	18	32.87	9
12	27.82	11	24.68	15	24.35	19	42.8	2	25.18	17	36.47	1	23.48	17	27.97	18	23.47	14	28.85	19
13	28.33	9	20.08	20	32.42	3	38.6	11	24.23	18	34.92	3	23.67	16	39.97	3	25.29	9	27.44	20
14	27.86	10	25.03	13	32.3	4	44.27	1	25.92	13	33.67	5	27.67	9	26.13	20	22.72	17	32.33	11
15	25.37	17	26.57	11	34.4	1	40.4	6	27.75	8	22.41	19	19.72	19	40.39	1	24.9	11	36.74	2
16	26.07	14	24.52	17	26.22	17	39.4	8	25.7	15	32.89	8	25.18	13	35.53	9	27.73	6	31.63	14
17	32.02	4	23.9	18	27.48	15	29.9	20	25.4	16	32.8	9	27.15	10	37.02	5	27.7	7	33.52	5
18	32.1	2	26.47	12	29.15	10	37.33	16	26.62	12	27.55	15	24.33	14	31.1	17	22.98	15	32.05	12
19	30.7	6	26.73	10	29.24	9	38.02	13	27.69	10	28.19	14	23.4	18	31.32	15	28.43	3	38.33	1
20	33.23	1	24.98	14	24.38	18	39.22	9	27.26	11	33.25	6	29.34	3	35.88	8	27.89	5	32.01	13
Mean	27.93		26.47		28.92		38.34		28.57		30.27		26.21		33.96		25.02		32.58	

*1 = Excel, 2 = L4-138/3; 3 = W-119, 4 = Unknown 2/1, 5 = L4-199084/1; S.E. = 1.72; CV% = 5.7; LSD = 4.74; Grand mean = 29.97

Appendix 4.3.3 Within cross ranking of root fresh yield (t ha^{-1}) of sweetpotato progeny evaluated in a 5 x 5 triple lattice experiment conducted at Mansa Research Station, Zambia

	Crosses* (above diagonal)																			
Progeny No	**1 x 2**		**1 x 3**		**1 x 4**		**1 x 5**		**2 x 3**		**2 x 4**		**2 x 5**		**3 x 4**		**3 x 5**		**4 x 5**	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
1	1.43	3	5.83	20	20.44	4	0.12	20	1.05	18	17.16	6	0.85	18	1.72	14	2.35	1	21.88	19
2	0.40	17	7.82	9	8.41	17	0.76	7	1.78	15	16.71	8	0.65	20	3.61	5	0.33	20	25.45	12
3	1.25	4	6.80	16	16.44	11	0.25	15	2.90	9	17.36	5	2.67	6	2.07	10	1.20	7	27.78	6
4	0.40	18	8.32	7	8.06	18	0.35	14	0.72	19	18.56	2	1.72	11	4.22	4	1.88	3	33.72	1
5	1.16	7	6.37	19	5.66	19	0.20	18	0.62	20	14.21	19	0.87	17	3.35	6	0.55	15	28.08	5
6	0.91	12	7.02	13	4.65	20	0.74	8	2.48	11	14.16	20	4.19	3	1.22	19	0.72	13	22.25	18
7	0.62	16	6.83	15	16.63	10	0.22	16	2.08	13	15.06	13	6.19	1	1.36	16	0.76	12	28.27	4
8	0.85	14	9.99	3	14.68	13	0.38	13	3.95	3	18.19	3	2.90	5	1.76	12	0.89	10	25.91	9
9	1.05	10	6.94	14	12.71	15	0.55	9	1.49	17	14.30	15	2.39	8	2.19	9	0.42	19	27.38	7
10	1.23	6	6.58	18	18.86	5	0.50	10	3.58	5	14.21	17	4.70	2	1.37	15	0.56	14	25.26	14
11	0.40	18	14.98	1	15.16	12	1.00	5	2.73	10	14.27	16	1.47	13	1.93	11	1.35	5	21.23	20
12	0.86	13	9.98	4	13.61	14	0.15	19	1.53	16	19.56	1	1.16	16	1.25	18	1.03	8	23.96	17
13	0.75	15	9.01	6	17.76	7	0.80	6	6.62	1	15.96	11	0.85	19	4.62	3	1.89	2	29.71	3
14	0.40	19	7.17	11	8.60	16	0.50	11	2.98	8	16.71	7	2.46	7	0.80	20	0.45	17	25.27	13
15	1.02	11	12.01	2	21.08	1	0.45	12	3.43	6	16.26	9	2.27	9	2.50	8	1.22	6	24.71	16
16	1.87	2	8.12	8	18.04	6	0.20	17	2.18	12	15.17	12	1.38	14	3.10	7	0.93	9	25.16	15
17	1.07	8	7.15	12	16.86	9	1.80	2	1.97	14	16.00	10	1.48	12	1.28	17	1.85	4	30.19	2
18	1.25	5	6.63	17	20.56	3	2.21	1	3.75	4	14.21	18	1.82	10	5.52	2	0.78	11	25.83	10
19	3.50	1	7.35	10	17.31	8	1.20	3	3.01	7	14.41	14	1.17	15	6.13	1	0.42	18	26.92	8
20	0.32	20	9.55	5	20.86	2	1.03	4	4.52	2	17.51	4	3.28	4	1.75	13	0.47	16	25.48	11
Mean	1.04		8.22		18.82		0.67		2.67		16.00		2.22		2.59		1.00		26.22	

*1 = Excel, 2 = L4-138/3; 3 = W-119, 4 = Unknown 2/1, 5 = L4-199084/1; s.e. = 80.67; CV% = 7.6; LSD = 129.26; Grand Mean = 1065

Appendix 4.3.3 (Continued)

Progeny No	Reciprocal crosses* (below diagonal)																			
	2 x 1		3 x 1		4 x 1		5 x 1		3 x 2		4 x 2		5 x 2		4 x 3		5 x 3		5 x 4	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
1	8.31	19	12.06	17	14.87	11	16.18	4	5.63	18	15.25	1	0.25	18	34.37	13	1.08	9	13.63	1
2	7.88	20	15.66	12	14.78	12	8.93	13	5.93	16	7.97	14	3.02	1	35.92	9	0.67	18	11.20	15
3	10.87	16	15.36	14	16.77	4	11.98	10	6.38	13	8.28	12	0.94	4	32.64	14	1.00	11	11.17	16
4	14.80	10	15.69	11	15.97	6	14.90	6	5.98	15	12.38	2	0.90	5	38.22	2	0.95	13	12.03	4
5	15.27	9	18.91	4	13.28	18	8.65	14	6.38	14	10.18	4	0.40	14	35.69	11	1.07	10	10.92	18
6	16.20	6	17.93	6	15.84	7	12.93	8	5.48	19	10.32	3	1.12	2	35.77	10	0.78	17	11.73	7
7	13.85	11	17.81	7	12.71	20	15.72	5	5.33	20	7.45	18	0.44	13	23.20	18	1.61	4	12.67	3
8	15.60	8	16.01	8	13.10	19	6.68	16	7.78	11	8.21	13	0.18	20	36.70	7	1.73	2	11.74	6
9	12.05	15	11.66	19	23.44	1	22.42	2	5.88	17	7.87	16	0.45	11	38.32	1	1.31	6	11.29	13
10	9.62	17	15.71	10	13.36	17	10.85	12	9.13	5	9.68	7	0.53	7	37.02	4	1.08	8	11.42	11
11	17.55	3	15.91	9	18.56	2	5.50	17	7.93	10	8.37	11	0.34	17	22.17	19	1.58	5	11.21	14
12	16.55	5	18.26	5	18.07	3	4.95	19	8.93	8	9.70	6	0.50	8	36.84	5	0.85	15	10.68	20
13	15.70	7	19.61	3	14.47	14	11.60	11	9.13	4	7.17	20	0.25	19	37.55	3	1.62	3	11.05	17
14	13.81	12	11.66	18	15.84	8	23.30	1	9.03	6	9.91	5	0.40	15	23.95	17	0.95	12	11.70	8
15	8.36	18	20.89	1	15.51	10	4.85	20	7.68	12	7.68	17	0.85	6	36.47	8	0.58	19	11.63	9
16	22.60	1	14.66	15	15.99	5	7.25	15	8.78	9	7.31	19	0.45	12	14.15	20	0.82	16	10.90	19
17	13.28	13	12.31	16	14.06	16	14.22	7	9.18	3	8.77	9	0.48	10	30.70	16	0.88	14	11.42	12
18	12.72	14	9.74	20	14.24	15	12.37	9	9.63	2	9.10	8	0.40	16	32.01	15	1.15	7	11.45	10
19	16.86	4	15.41	13	14.66	13	5.30	18	10.03	1	7.92	15	0.50	9	34.99	12	0.47	20	11.76	5
20	18.11	2	20.36	2	15.61	9	21.42	3	8.98	7	8.74	10	1.00	3	36.71	6	2.02	1	13.06	2
Mean	14.00		15.78		15.56		12.60		7.66		9.11		0.67		32.67		1.11		11.63	

*1 = Excel, 2 = L4-138/3; 3 = W-119, 4 = Unknown 2/1, 5 = L4-199084/1; s.e. = 80.67; CV% = 7.6; LSD = 129.26; Grand Mean = 1065

Appendix 4.3.4 Within cross ranking of harvest index of sweetpotato progeny evaluated in a 5 x 5 triple lattice experiment conducted at Mansa Research Station, Zambia

Progeny No	Crosses* (above diagonal)																			
	1 x 2		1 x 3		1 x 4		1 x 5		2 x 3		2 x 4		2 x 5		3 x 4		3 x 5		4 x 5	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
1	0.76	1	0.63	9	0.87	17	0.46	12	0.60	8	0.89	1	0.21	14	0.61	9	0.65	3	0.80	11
2	0.59	10	0.69	4	0.93	11	0.69	3	0.51	14	0.32	20	0.24	8	0.51	17	0.54	18	0.88	7
3	0.59	11	0.71	2	0.92	13	0.54	8	0.43	17	0.63	13	0.31	4	0.59	12	0.63	4	0.90	5
4	0.54	12	0.70	3	0.77	20	0.48	11	0.63	7	0.61	15	0.29	7	0.76	2	0.59	8	0.82	10
5	0.41	18	0.62	12	0.95	5	0.43	14	0.56	11	0.87	2	0.20	15	0.60	11	0.58	11	0.75	13
6	0.66	3	0.62	13	0.93	12	0.27	19	0.68	3	0.42	19	0.24	9	0.18	20	0.61	7	0.31	19
7	0.63	6	0.60	16	0.97	2	0.53	9	0.41	18	0.73	8	0.16	19	0.54	15	0.62	5	0.88	8
8	0.63	7	0.62	14	0.95	7	0.43	15	0.75	1	0.68	10	0.23	11	0.68	7	0.58	9	0.42	17
9	0.50	14	0.60	17	0.97	1	0.43	13	0.31	20	0.66	11	0.30	5	0.84	1	0.58	12	0.91	4
10	0.37	19	0.67	5	0.91	15	0.23	20	0.46	16	0.65	12	0.19	16	0.69	6	0.57	13	0.92	2
11	0.44	17	0.61	15	0.93	10	0.41	17	0.64	5	0.85	3	0.23	10	0.53	16	0.56	16	0.74	14
12	0.33	20	0.66	7	0.96	3	0.38	18	0.64	6	0.73	7	0.17	18	0.40	19	0.54	19	0.38	18
13	0.65	5	0.66	8	0.83	19	0.55	7	0.55	12	0.76	6	0.22	13	0.58	13	0.61	6	0.88	9
14	0.47	16	0.59	19	0.92	14	0.71	1	0.72	2	0.61	16	0.16	20	0.49	18	0.56	15	0.47	16
15	0.54	13	0.60	18	0.88	16	0.62	5	0.57	10	0.82	5	0.29	6	0.56	14	0.57	14	0.67	15
16	0.66	4	0.63	10	0.95	8	0.43	16	0.52	13	0.72	9	0.33	3	0.60	10	0.38	20	0.77	12
17	0.73	2	0.66	6	0.86	18	0.62	4	0.39	19	0.85	4	0.51	1	0.63	8	0.74	1	0.89	6
18	0.53	13	0.62	11	0.94	9	0.50	10	0.48	15	0.55	18	0.17	17	0.70	5	0.58	10	0.29	20
19	0.59	9	0.71	1	0.96	4	0.60	6	0.60	9	0.62	14	0.22	12	0.72	4	0.69	2	0.91	3
20	0.48	15	0.57	20	0.95	6	0.69	2	0.67	4	0.58	17	0.35	2	0.74	3	0.54	17	0.94	1
Mean	0.55		0.64		0.92		0.50		0.56		0.68		0.25		0.60		0.59		0.73	

*1 = Excel, 2 = L4-138/3; 3 = W-119, 4 = Unknown 2/1, 5 = L4-199084/1; S.E. = 0.04; CV% = 6.4; LSD = 0.07; Grand mean = 0.699

Appendix 4.3.4 (Continued)

Progeny No	Reciprocal crosses* (below diagonal)																			
	2 x 1		3 x 1		4 x 1		5 x 1		3 x 2		4 x 2		5 x 2		4 x 3		5 x 3		5 x 4	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
1	0.69	18	0.91	8	0.88	9	0.80	19	0.82	6	0.92	10	0.64	1	0.88	6	0.61	7	0.87	11
2	0.66	19	0.90	12	0.80	17	0.87	14	0.78	11	0.94	5	0.47	15	0.85	12	0.68	3	0.89	7
3	0.79	11	0.86	19	0.78	18	0.87	15	0.75	12	0.88	17	0.53	6	0.64	20	0.34	20	0.92	3
4	0.94	2	0.91	9	0.88	12	0.91	8	0.83	3	0.91	14	0.38	19	0.73	17	0.51	14	0.95	1
5	0.79	10	0.91	10	0.91	4	0.92	7	0.79	9	0.86	19	0.52	8	0.87	10	0.53	13	0.88	8
6	0.81	9	0.86	18	0.92	3	0.94	2	0.61	17	0.80	20	0.50	12	0.87	9	0.61	6	0.94	2
7	0.92	4	0.88	15	0.76	19	0.94	4	0.64	16	0.91	12	0.52	9	0.77	16	0.50	16	0.67	17
8	0.75	15	0.90	11	0.89	8	0.90	9	0.60	18	0.95	3	0.49	13	0.84	15	0.69	2	0.43	20
9	0.74	17	0.89	14	0.85	15	0.81	18	0.82	4	0.95	2	0.40	18	0.88	5	0.41	19	0.91	5
10	0.88	5	0.94	1	0.90	6	0.83	17	0.87	1	0.93	6	0.58	3	0.87	7	0.49	17	0.82	14
11	0.95	1	0.93	2	0.85	16	0.89	12	0.79	8	0.92	11	0.48	14	0.86	11	0.65	4	0.83	13
12	0.92	3	0.93	3	0.87	14	0.92	6	0.82	5	0.95	4	0.64	2	0.87	8	0.51	15	0.91	4
13	0.87	6	0.92	7	0.88	11	0.88	13	0.71	15	0.91	13	0.51	10	0.68	19	0.54	12	0.90	6
14	0.77	12	0.93	4	0.89	7	0.90	11	0.81	7	0.87	18	0.50	11	0.89	3	0.65	5	0.87	12
15	0.55	20	0.87	16	0.92	2	0.71	20	0.78	10	0.89	15	0.44	17	0.88	4	0.55	9	0.60	19
16	0.75	14	0.85	20	0.88	13	0.90	10	0.49	20	0.93	7	0.53	5	0.69	18	0.54	11	0.87	10
17	0.76	13	0.92	6	0.88	10	0.85	16	0.73	14	0.93	9	0.53	7	0.90	2	0.75	1	0.60	18
18	0.85	7	0.87	17	0.90	5	0.94	3	0.85	2	0.89	16	0.32	20	0.95	1	0.54	10	0.77	15
19	0.81	8	0.93	5	0.74	20	0.95	1	0.57	19	0.93	8	0.57	4	0.84	14	0.44	18	0.88	9
20	0.74	16	0.89	13	0.92	1	0.93	5	0.75	13	0.96	1	0.47	16	0.85	13	0.56	8	0.76	16
Mean	0.80		0.90		0.86		0.88		0.74		0.91		0.50		0.83		0.56		0.81	

*1 = Excel, 2 = L4-138/3; 3 = W-119, 4 = Unknown 2/1, 5 = L4-199084/1; S.E. = 0.04; CV% = 6.4; LSD = 0.07; Grand mean = 0.699

Appendix 4.4.1 Combining ability estimates for β-carotene content of parents and crosses for the 5 x 5 diallel (excluding self) of sweetpotato output from the DIALLEL-SAS05 program of Zhang *et al.*, 2005.

Observation	Parameter*	Estimate	Standard error	tValue	Probability
1	Intercept	2.790800000	0.09929849	28.11	<.0001
2	REP	-0.140000000	0.04596627	-3.05	0.0037
3	G1	1.650200000	0.05307728	31.09	<.0001
4	G2	-0.022800000	0.05307728	-0.43	0.6694
5	G3	0.353866667	0.05307728	6.67	<.0001
6	G4	-1.044466667	0.05307728	-19.68	<.0001
7	G5	-0.936800000	0.05307728	-17.65	<.0001
8	S11	0.942133333	0.15012521	6.28	<.0001
9	S12	5.655133333	0.10942161	51.68	<.0001
10	S13	-2.104866667	0.10942161	-19.24	<.0001
11	S14	-3.018200000	0.10942161	-27.58	<.0001
12	S15	-2.416333333	0.21396134	-11.29	<.0001
13	S22	-2.371866667	0.15012521	-15.80	<.0001
14	S23	-2.721866667	0.10942161	-24.88	<.0001
15	S24	-1.373533333	0.10942161	-12.55	<.0001
16	S25	3.184000000	0.21396134	14.88	<.0001
17	S33	1.551466667	0.15012521	10.33	<.0001
18	S34	5.088133333	0.10942161	46.50	<.0001
19	S35	-3.36433333 3	0.21396134	-15.72	<.0001
20	S44	-0.291866667	0.15012521	-1.94	0.0576
21	S45	-0.112666667	0.21396134	-0.53	0.6009
22	S55	2.709333333	0.37531302	7.22	<.0001
23	R12	3.916666667	0.13269319	29.52	<.0001
24	R13	-2.303333333	0.13269319	-17.36	<.0001
25	R14	0.005000000	0.13269319	0.04	0.9701
26	R15	0.003333333	0.13269319	0.03	0.9801
27	R23	0.000000000	0.13269319	0.00	1.0000
28	R24	-0.040000000	0.13269319	-0.30	0.7643
29	R25	2.256666667	0.13269319	17.01	<.0001
30	R34	-6.801666667	0.13269319	-51.26	<.0001
31	R35	-0.005000000	0.13269319	-0.04	0.9701
32	R45	0.005000000	0.13269319	0.04	0.9701

*G refers to general combining ability for parents, S refers to specific combining ability for crosses, R refers to specific combining ability for reciprocals; Numbers 1 – 5 after each letter (G, S, and R) represent the parent (one digit) or parents (two digits) of a cross in the following order: 1 = Excel, 2 = L4-138/3; 3 = W-119, 4 = Unknown 2/1, 5 = L4-199084/1.

Appendix 4.4.2 Within cross ranking of root dry mass (%) of sweetpotato progeny evaluated in a 5 x 5 triple lattice experiment conducted at Mansa Research Station, Zambia

Observation	Parameter*	Estimate	Standard error	tValue	Probability
1	Intercept	30.96800000	0.70674635	43.82	<.0001
2	REP	-0.52880000	0.32715999	-1.62	0.1124
3	G1	-2.61240000	0.37777181	-6.92	<.0001
4	G2	2.98060000	0.37777181	7.89	<.0001
5	G3	-2.80706667	0.37777181	-7.43	<.0001
6	G4	1.83660000	0.37777181	4.86	<.0001
7	G5	0.60226667	0.37777181	1.59	0.1173
8	S11	-0.63893333	1.06850005	-0.60	0.5526
9	S12	-0.74526667	0.77879655	-0.96	0.3433
10	S13	1.14406667	0.77879655	1.47	0.1482
11	S14	1.25706667	0.77879655	1.61	0.1129
12	S15	-0.37800000	1.52284687	-0.25	0.8050
13	S22	-0.16160000	1.06850005	-0.15	0.8804
14	S23	0.56273333	0.77879655	0.72	0.4734
15	S24	1.84906667	0.77879655	2.37	0.0215
16	S25	-1.34333333	1.52284687	-0.88	0.3820
17	S33	0.94373333	1.06850005	0.88	0.3814
18	S34	-0.68993333	0.77879655	-0.89	0.3800
19	S35	-2.90433333	1.52284687	-1.91	0.0624
20	S44	-1.49360000	1.06850005	-1.40	0.1685
21	S45	0.57100000	1.52284687	0.37	0.7093
22	S55	4.05466667	2.67125012	1.52	0.1355
23	R12	-1.43666667	0.94442954	-1.52	0.1346
24	R13	-0.11166667	0.94442954	-0.12	0.9064
25	R14	1.46500000	0.94442954	1.55	0.1273
26	R15	0.65333333	0.94442954	0.69	0.4923
27	R23	0.00000000	0.94442954	0.00	1.0000
28	R24	-1.76333333	0.94442954	-1.87	0.0679
29	R25	-1.97166667	0.94442954	-2.09	0.0420
30	R34	-0.31666667	0.94442954	-0.34	0.7388
31	R35	0.72833333	0.94442954	0.77	0.4443
32	R45	-1.16000000	0.94442954	-1.23	0.2252

*G refers to general combining ability for parents, S refers to specific combining ability for crosses, R refers to specific combining ability for reciprocals; Numbers 1 – 5 after each letter (G, S, and R) represent the parent (one digit) or parents (two digits) of a cross in the following order: 1 = Excel, 2 = L4-138/3; 3 = W-119, 4 = Unknown 2/1, 5 = L4-199084/1.

Appendix 4.4.3 Within cross ranking of harvest index of sweetpotato progeny evaluated in a 5 x 5 triple lattice experiment conducted at Mansa Research Station, Zambia

Observation	Parameter*	Estimate	Standard error	tValue	Probability
1	Intercept	0.597000000	0.59700000	34.10	<.0001
2	REP	0.012180000	0.00810379	1.50	0.1393
3	G1	0.062340000	0.00935745	6.66	<.0001
4	G2	0.012906666	0.00935745	1.38	0.1741
5	G3	-0.084760000	0.00935745	-9.06	<.0001
6	G4	0.012640000	0.00935745	1.35	0.1830
7	G5	-0.003126667	0.00935745	-0.33	0.7397
8	S11	0.012960000	0.02646687	0.49	0.6266
9	S12	-0.141106667	0.01929088	-7.31	<.0001
10	S13	0.114393333	0.01929088	5.93	<.0001
11	S14	0.194326667	0.01929088	10.07	<.0001
12	S15	-0.193533333	0.03772110	-5.13	<.0001
13	S22	-0.014173333	0.02646687	-0.54	0.5947
14	S23	0.152660000	0.01929088	7.91	<.0001
15	S24	-0.079906667	0.01929088	-4.14	0.0001
16	S25	0.096700000	0.03772110	2.56	0.0135
17	S33	-0.365173333	0.02646687	-13.80	<.0001
18	S34	-0.083906667	0.01929088	-4.35	<.0001
19	S35	0.547200000	0.03772110	14.51	<.0001
20	S44	0.131026667	0.02646687	4.95	<.0001
21	S45	-0.292566667	0.03772110	-7.76	<.0001
22	S55	-0.157800000	0.06616719	-2.38	0.0210
23	R12	0.030766667	0.00935745	3.29	0.0019
24	R13	-0.091600000	0.00935745	-9.79	<.0001
25	R14	0.078000000	0.00935745	8.34	<.0001
26	R15	-0.077333333	0.00935745	-8.26	<.0001
27	R23	-0.122533333	0.01812063	-6.76	<.0001
28	R24	0.174233333	0.01812063	9.62	<.0001
29	R25	-0.081100000	0.01812063	-4.48	<.0001
30	R34	0.144433333	0.01812063	7.97	<.0001
31	R35	-0.302066667	0.01812063	-16.67	<.0001
32	R45	0.176666667	0.01812063	9.75	<.0001

*G refers to general combining ability for parents, S refers to specific combining ability for crosses, R refers to specific combining ability for reciprocals; Numbers 1 – 5 after each letter (G, S, and R) represent the parent (one digit) or parents (two digits) of a cross in the following order: 1 = Excel, 2 = L4-138/3; 3 = W-119, 4 = Unknown 2/1, 5 = L4-199084/1.

Appendix 4.4.4 Within cross ranking of root fresh yield (t ha^{-1}) of sweetpotato progeny evaluated in a 5 x 5 triple lattice experiment conducted at Mansa Research Station, Zambia

Observation	Parameter*	Estimate	Standard error	tValue	Probability
1	Intercept	10.60838667	0.37114840	28.58	<.0001
2	REP	-0.06408000	0.17180833	-0.37	0.7108
3	G1	-5.08182667	0.19838717	-25.62	<.0001
4	G2	1.30070667	0.19838717	6.56	<.0001
5	G3	2.53287333	0.19838717	12.77	<.0001
6	G4	-0.15226000	0.19838717	-0.77	0.4465
7	G5	1.40050667	0.19838717	7.06	<.0001
8	S11	4.26676000	0.56112365	7.60	<.0001
9	S12	-4.75410667	0.40898562	-11.62	<.0001
10	S13	-3.31994000	0.40898562	-8.12	<.0001
11	S14	9.93919333	0.40898562	24.30	<.0001
12	S15	-10.3986667	0.79972424	-13.00	<.0001
13	S22	-1.97030667	0.56112365	-3.51	0.0010
14	S23	6.79736000	0.40898562	16.62	<.0001
15	S24	-4.51717333	0.40898562	-11.04	<.0001
16	S25	6.41453333	0.79972424	8.02	<.0001
17	S33	9.56536000	0.56112365	17.05	<.0001
18	S34	-7.62900667	0.40898562	-18.65	<.0001
19	S35	-14.97913333	0.79972424	-18.73	<.0001
20	S44	0.71329333	0.56112365	1.27	0.2097
21	S45	0.78040000	0.79972424	0.98	0.3339
22	S55	18.18286667	1.40280911	12.96	<.0001
23	R12	-0.72200000	0.49596792	-1.46	0.1518
24	R13	3.61100000	0.49596792	7.28	<.0001
25	R14	-0.37033333	0.49596792	-0.75	0.4588
26	R15	0.00000000	0.49596792	0.00	1.0000
27	R23	-5.11116667	0.49596792	-10.31	<.0001
28	R24	-4.88883333	0.49596792	-9.86	<.0001
29	R25	-15.04200000	0.49596792	-30.33	<.0001
30	R34	-2.43450000	0.49596792	-4.91	<.0001
31	R35	7.88883333	0.49596792	15.91	<.0001
32	R45	-4.11116667	0.49596792	-8.29	<.0001

*G refers to general combining ability for parents, S refers to specific combining ability for crosses, R refers to specific combining ability for reciprocals; `Numbers 1 – 5` after each letter (G, S, and R) represent the parent (one digit) or parents (two digits) of a cross in the following order: 1 = Excel, 2 = L4-138/3; 3 = W-119, 4 = Unknown 2/1, 5 = L4-199084/1.

Chapter 5: Evaluation of G x E interaction of sweetpotato for beta-carotene content, root dry mass, harvest index, vine fresh yield, and root fresh yield

Abstract

The effect of genotype (G) by environment (E) interaction (G x E) on β-carotene content, root dry mass (RDM), harvest index (HI), vine fresh yield (VFY), and root fresh yield (RFY) of 15 selected progeny from a polycross were investigated at five diverse locations in Zambia. The locations represented the major sweetpotato growing agroecologies in the country. The objective was to identify stable and high performing genotypes. The G x E analysis was conducted with the additive main effects and multiplicative interaction model (AMMI). The performance of genotypes was dependant on location for all the traits considered.

The magnitude of the G x E for β-carotene content, RDM, and HI was small and selection for these traits may be conducted in a few, well selected environments. Conversely, RFY and VFY yield may require early testing in varied environments to select genotypes with either wide or specific adaptation.

The AMMI analysis identified progeny G2, G6, and G8 as stable with above average performance across environments for β-carotene content (5.0, 4.7, and 4.7 mg 100 g^{-1}, respectively), RDM (37, 37, and 35%, respectively), HI (0.7, 0.6, and 0.7, respectively), and RFY (14.2, 13.0, 14.4 t ha^{-1}, respectively). Genotype G3 was specifically adapted to environment E3, E4, and E5 for β-carotene content, RDM, and RFY. It had the highest mean β-carotene content (9.4 mg 100 g^{-1}), high mean RDM (35%), and high RFY (14.7 t ha^{-1}) across the environments. It was concluded that it is possible to breed for high β-carotene, high RDM and high yield sweetpotato genotypes with wide or specific adaptation in Zambia as the AMMI analysis identified genotypes G2, G6, and G8 as stable across environments for both β-carotene content and RDM. They performed above average for both traits.

5.1 Introduction

Genetic adaptation entails the shaping of a population or a species gene pool in response to environmental challenges (Perez-de-la-Vega and Tigerstedt, 1996). A crop's ability to exploit its environment depends on many adaptive features that are controlled by multiple genes, interacting among themselves and with the environment in intricate ways (Hawtin *et al.*, 1997). The genotype by environment interaction (G x E) observed by plant breeders signifies differential responses of the cultivars being tested to different environmental conditions and is a major challenge in plant breeding (Ceccarelli and Hammer, 1996). In essence, G x E reduces the correlation between the phenotype and the genotype.

Ceccarelli *et al.* (1994) suggested that if the G x E is of the crossover type, genotypes developed in favorable environments do not perform well under harsh environments and vice versa. This suggests that the genes for yield expressed in low and high input conditions are different. As a result, breeding procedures conducted under high input and uniform agronomic conditions might favour selection of cultivars adapted to intensive management and might eliminate genotypes adapted to low input conditions (Ceccarelli, 1997). Crossover interaction causes problems in crop breeding because it hinders selection progress due to changing composition of genotypes selected in different environments (Cooper and Delacy, 1994; Crossa *et al.*, 1995). Other workers (Braun *et al.*, 1997; Eberhart and Russell, 1966; Troyer, 1996), however, have suggested that it is possible to breed for wide adaptation provided that the genetic base is broad enough.

It was against this background that this study was designed to determine the adaptability of sweetpotato genotypes across locations for β-carotene content, root dry mass (RDM) composition, harvest index (HI), vine fresh yield (VFY), and root fresh yield (RFY) to determine the magnitude of the effect of G x E on these traits, and to identify stable and high performing genotypes.

5.2 Materials and Methods

5.2.1 Polycross mating design

Sweetpotato genotypes with high β-carotene content and high RDM were open-pollinated in two field grown polycrosses (Figure 5.1) established at Mansa Research Station (11° 14.4' S and 028° 57.2' E), Zambia in D ecember 2005. The high β-carotene germplasm was introduced from the Vegetable and Ornamental Plant Institute, Roodeplaat, South Africa and from the International Potato Centre (CIP) in Kenya. The high dry mass germplasm was obtained from the sweetpotato breeding programme in Zambia which included parents selected from chapter 3 (Appendix 5.1). The first of the two polycrosses had 12 parents planted in a randomised complete block design with 12 replications (Appendix 5.2). The second polycross had 30 parents planted in a randomised complete block design with eight replications (Appendix 5.3). Both polycrosses were planted in areas sufficiently isolated from other sweetpotato plants. Data on plant establishment, vigour, flowering, seed set, and number of seeds produced per parent was collected.

From May to July 2006, seed was collected from the parents. The seed was cleaned by hand and stored for two months in paper bags under room condition in readiness for germination. Prior to planting, the seed was first scarified by immersing in concentrated H_2SO_4 (98%) for 20 minutes (Rossel *et al.*, 2008). The scarified seed was sown in wooden boxes filled with black top soil which were placed in a screen house. Once the seedlings had reached 50 mm in height, they were removed from the screen house and transplanted to the nearby wetland on 10 m long by 1 m wide ridges. The available water in the wetland enabled good seedling establishment. Macro nutrients (10N-20P_5O_2-10K_2O) at a rate of 100 kg ha^{-1} were added to the soil in the wetland to boost vegetative growth of the transplanted seedlings.

5.2.2 Progeny screening

In November 2006, the cuttings from the wetland were planted in the field for evaluation. Cuttings provided a source of potential cultivars and were screened in an observational single plant trial. Cuttings were planted in groups according to family. The plants were screened for pests and diseases and other defects. At maturity the surviving plants were evaluated for good root traits, namely: shape and size, root neck length and root flesh

colour. Flesh colour determinations were made using the 1995 edition of the Royal Horticultural Society (RHS) Colour Chart (Royal Horticultural Society, 1995).

Progeny with desirable characters (orange-fleshed, high RDM, field resistance to major pests and diseases) were selected. The threshold values for selection were predetermined as follows:

1. medium to dark orange root flesh colour (RHS:9 137 U or better)
2. High RDM (above 30%)
3. Marketable root yield (above 120 g root^{-1})

Progeny that did not exceed the threshold in any one trait were discarded. In total, 1470 progeny were evaluated and 35 progeny (Appendix 5.4) met the selection criteria. The selected progeny were maintained in the wetland (Figure 5.2), and at the same time multiplied to increase the vines for planting.

Figure 5.1: Polycross conducted at Mansa Research Station, Zambia

Figure 5.2: Genotypes from seedlings growing in the wetland area

5.2.3 Field trial evaluation of selected progeny for G x E

In November 2007, replicated trials were established in two different locations, namely: Mansa-Mufulira (11° 06'S and 28° 51'E) and Mutanda West (12° 24'S and 26° 15'E) (Appendix 5.5), using 15 of the 35 selected progeny from the previous season (Table 5.1). The criterion on which the 15 progeny were selected was based on genotypes being able to provide at least 500 tip cuttings to ensure enough planting material for the two locations. The remaining progeny were multiplied and evaluated separately. The trial was repeated in 2008 at three locations, namely: Mansa-Main (11° 14.4' S and 028°

57.2' E), Mutanda East (12° 11'S and 26° 24'E), and at Golden Valley Research Trust (GART) (10° 07'S and 30° 55'E) (Appendix 5.5). A ra ndomised complete block design with three replications was used for all the trials. The experimental plot comprised four 6 m long ridges spaced at 1 m. Plants were spaced at 30 cm within each ridge. The two middle ridges were used for data collection and plants on outer ridges were not used. During plant growth, observations were made for any pests and diseases and other biotic stresses. At harvest number of roots, and RFY and RDM composition were determined. Five plants from the central two rows of every experimental plot were randomly selected at harvest time to generate subsamples for root dry mass and β-carotene content determinations. The β-carotene content was determined by the South Africa Bureau of Standards, in Pretoria, South Africa in 2008 and by the Tanzania Food Nutrition Center, Dar-es-Salam, Tanzania in 2009 using the High Performance Liquid chromatography (HPLC) procedure described by Rodriguez-Amaya and Kimura (2004). The β-carotene content was recorded as mg 100 g^{-1} on a fresh mass basis.

5.2.4 Data analysis

Each location in a given season was considered as an individual environment and assigned a code as follows:

Environmental code	Location	Season
E1	Mansa-Mufulira	2007/2008
E2	Mutanda West	2007/2008
E3	Mansa-Main	2008/2009
E4	Mutanda East	2008/2009
E5	GART	2008/2009

Data were initially analyzed by conducting a separate ANOVA for each of the five environments using Genstat version 11.1 (Payne *et al.*, 2007). Bartlett's (1937) and Levene's (1960) tests indicated homogeneity of error variances across environments and therefore data were pooled for the combined ANOVA across environments. Data was not transformed since there were no extreme values to warrant transformation.

Table 5.1 Major traits of the sweetpotato progeny evaluated at five locations in Zambia, 2007/8 season.

		Traits*							
Genotype¤	**ID[a]**	**Root shape**	**Colour Chart**	**Predominant skin Colour**	**Flowering Habit**	**Root dry mass (%)**	**Cracked roots (score)***	**Sprouting (score)***	**Weevil damage (score)***
L7- Chingovwa/36	G1	obvate	RHS:9/2 1355U	brownish orange	none	35.18	1	1	2
L7-W-119/107	G2	elliptic	RHS:9 137U	purple	none	36.98	1	1	2
L7-W-119/13	G3	elliptic	RHS 9/2 1355U	copper	moderate	39.34	1	1	2
L7- Chingovwa/84	G3	long elliptic	RHS:9/3 7507U	cream	sparse	36.73	1	1	2
L7- Chingovwa/62	G5	elliptic	RHS:9/2 1355U	brownish orange	profuse	34.98	1	1	1
L7- Excel/118	G6	long elliptic	RHS:9 137U	orange	none	37.66	1	1	2
L7- W119-c/22	G7	obvate	RHS:9/1 1233U	pink	profuse	36.10	1	1	2
L7-199062.1/95	G8	elliptic	RHS:9/2 1355U	copper	moderate	35.65	1	1	3
L7-15/1/17	G9	obvate	RHS:9 137U	orange	none	35.15	1	1	3
L7- Chingovwa/55	G10	obvate	RHS:9 137U	copper	profuse	41.46	1	1	2
L7- Chingovwa-c/24	G11	elliptic	RHS:9/3 750U	cream	moderate	36.25	1	1	2
L7- Chingovwa/83	G12	obvate	RHS:9/3 7507U	brownish orange	sparse	36.55	1	1	1
L7-W-119/89	G13	round	RHS 9/2 1355U	copper	profuse	35.95	1	1	2
L7- Chingovwa-c/56	G14	round	RHS:9/2 1355U	copper	moderate	37.95	2	1	3
L7- W119-c/65	G15	elliptic	RHS:9 137U	copper	moderate	35.60	1	1	2

[a]ID = identification code for each genotype; **Scores for mole damage, weevil damage, and cracking were as follows: 1 = No symptom, 2 = 1-5 roots affected in a plot of 20 plants, 3 = any roots affected slightly (5-10% of root area), 4 = All roots affected moderately (11 - 25% of root area), and 5 = All roots affected severely (>25% of root area). ¤L7 = Luapula 2007 - meaning a selection done in Luapula Province in 2007

Combined ANOVA across environments, basic rank and Spearman's rank correlation analyses on non-standardized data were conducted using Genstat version 11.1 (Payne *et al.*, 2007). Stability analysis was performed on standardized data using the Additive main effect and Multiplicative Interaction (AMMI) model as described by Gauch and Furnas (1991). This model is more efficient than other methods in determining the most stable and high yielding genotypes in multi-environment trials (Manrique and Hermann, 2002). The model uses ANOVA to partition the Treatment sum of squares (SS) into the main effect SS for genotypes and environments, and the interaction SS for genotype x environment. The model then applies an Interaction Principal Component Analysis (IPCA) to determine pattern in the genotype x environment interaction means (Egesi and Asiedu, 2002). By plotting the main effects on the abscissa and the scores of the IPCA axes on the ordinate of a graph, the AMMI analysis provides a graphical representation (biplot) of the patterns represented by the specific interaction between genotypes and environments while simultaneously accounting for mean performance. The AMMI procedure in Genstat version 11.1 also ranks the top four genotypes in each environment.

5.3 Results

5.3.1 Genotype by Environment analyses of five traits

5.3.1.1 β-carotene content

The mean β-carotene content of the 15 polycross progeny was >4 mg 100 g^{-1} across environments (Table 5.2). Genotype G3 had the highest mean β-carotene content of 9.4 mg 100 g^{-1} across environments whereas G13 was the lowest. The highest mean β-carotene content across genotypes in an environment was recorded at E2 (6.2 mg 100 g^{-1}), followed by E3 (4.6 mg 100 g^{-1}). The E5 environment had the lowest mean β-carotene content (4.3 mg 100 g^{-1}) (Table 5.2). The highest β-carotene content was recorded at environment E2 for genotype G5 (11.3 mg 100 g^{-1}).

The main effect for G, and the G x E interaction were highly significant ($p<0.001$ and $p<0.01$, respectively) for β-carotene content (Table 5.3). The first interaction principal

component (IPCA1) and the second (IPCA2) axes accounted for 86.8 and 9.6%, respectively, of the G x E sum of squares (SS) (Table 5.3).

Genotypes G1, G2, G4, G6, G8, G10, G11, and G12 exhibited IPCA1 values close to zero and above mean performance (>4.8 mg 100 g^{-1}) (Figure 5.1). Genotypes G5, G11, G10, G4, G12, and G1 performed best in environments E3 , G4, G10, G1, G2, G5, and G12 in E4, and G4, G5, G10, G1, G11, and G10 in E5 (Table 5.4). Genotype G14 was stable across all five environments but had low β-carotene content. Genotype G3 had the highest β-carotene content and since it was specifically adapted to three environments (E3, E4, and E5) and had an IPCA1 score of -2.63 it could be classified as unstable. Genotype G5 was the second highest performer across environments and was the highest in environment E1 and E2 (Table 5.2 and 5.4; Figure 5.1). Genotype G13 (0.08 mg 100 g^{-1}) and G7 (0.16 mg 100 g^{-1}) recorded the lowest β-carotene content across environments (Table 5.2) and ranked among the lowest performing genotypes in each environment (Table 5.4). Environments E2 and E1 were unstable with IPCA1 scores of -4.61 and 1.78, respectively (Figure 5.1).

Table 5.2 Mean β-carotene content (mg 100 g^{-1}), root dry mass (%), harvest index, vine yield (t ha^{-1}) and root fresh yield (t ha^{-1}) of 15 genotypes of sweetpotato evaluated at five environments in Zambia

Genotypes	Mean across five environments				
	β-carotene content (mg 100 g^{-1})	**Root dry mass (%)**	**Harvest index**	**Vine yield (t ha^{-1})**	**Root fresh yield (t ha^{-1})**
G1	6.508	33.94	0.744	3.097	8.62
G2	4.957	36.63	0.714	6.418	14.24
G3	9.421	35.47	0.781	5.428	14.72
G4	6.429	28.31	0.802	2.968	10.99
G5	8.428	25.15	0.800	3.032	10.79
G6	4.721	37.04	0.658	7.554	12.96
G7	0.165	33.45	0.725	4.764	11.27
G8	4.707	34.97	0.698	6.867	14.37
G9	1.116	42.07	0.785	4.240	13.97
G10	6.461	25.96	0.865	2.589	15.02
G11	6.537	33.41	0.812	4.081	14.05
G12	5.189	33.35	0.707	4.111	7.94
G13	0.086	37.90	0.787	5.472	17.47
G14	2.819	39.01	0.642	5.782	9.66
G15	4.701	30.50	0.819	3.084	11.29
Mean	4.816	33.81	0.756	4.632	12.49
SE(±)	0.722	1.95	0.041	1.382	2.39
Environment* means					
E1	4.592	34.99	0.803	2.639	11.27
E2	6.196	34.18	0.811	1.722	7.50
E3	4.597	33.10	0.724	4.706	12.86
E4	4.399	33.68	0.794	2.609	10.42
E5	4.299	33.10	0.647	11.486	20.41
Mean	4.816	33.81	0.756	4.632	12.49
SE(±)	0.153	0.42	0.010	0.748	0.72

*E1 = Mansa-Mufulira, E2 = Mutanda West, E3 = Mansa-Main, E4 = Mutanda East, E5 = GART

Table 5.3 AMMI mean squares for β-carotene content (mg 100 g^{-1}) of 15 genotypes of sweetpotato evaluated at five environments in Zambia

Source	df	SS[a]	Mean squares	F value	Probability	% SS of:	
						Treatment	G x E
Treatments	74	7579	102.42	102.33	0.00000	100.00	
Genotypes (G)	14	4932	352.27	351.97	0.00000	65.07	
Environment (E)	4	0	0.00	0.00	1.00000	0.00	
G x E	56	2647	47.27	47.23	0.00000	34.92	
IPCA 1	17	2298	135.20	135.08	0.00000		86.82
IPCA 2	15	253	16.90	16.88	0.00000		9.56
Residual	24	95	3.97	3.96	0.00008		3.59
Error	138	138	1.00				
Total	224	7731	34.51				

[a]SS = Sum of squares.

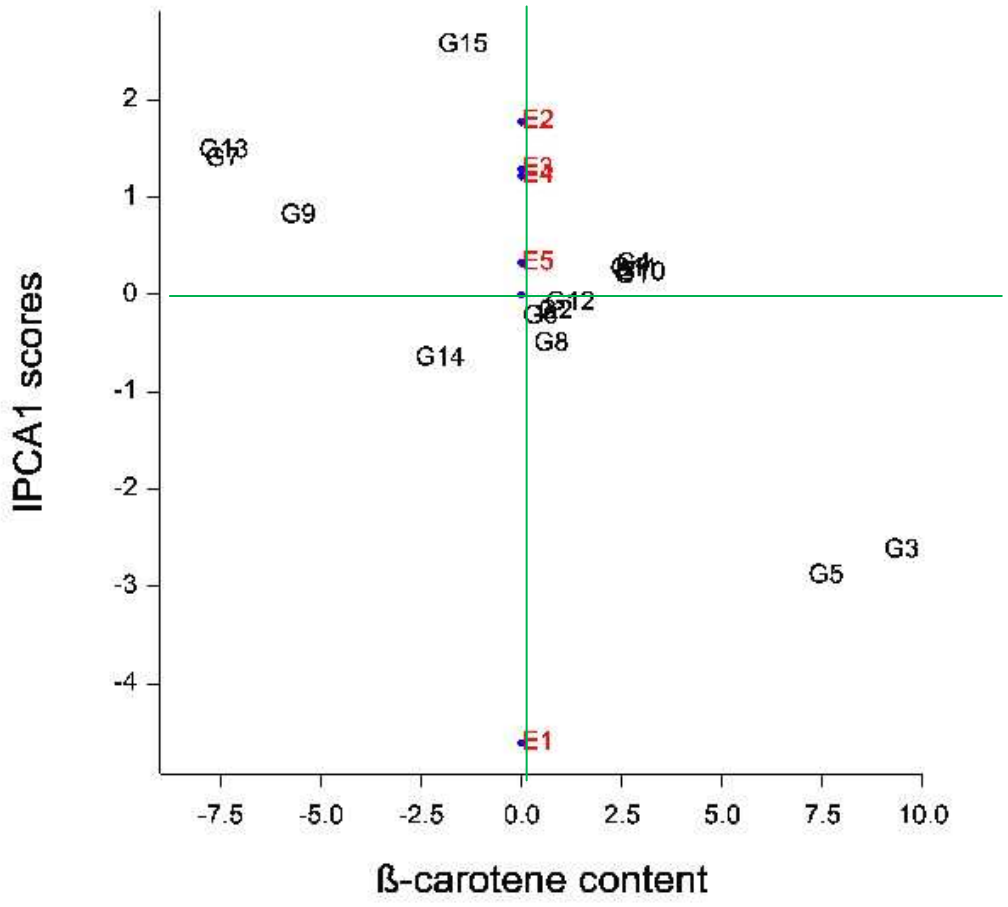


Figure 5.1: Biplot of mean β-carotene content (mg 100 g^{-1}) versus IPCA1 scores for 15 genotypes evaluated in five environments in Zambia. Grand mean = 4.82 mg 100 g^{-1}. Data standardized.

Table 5.4 Genotypes ranked per environment on the basis of mean β-carotene content. Environments ranked by IPCA1 score for β-carotene content (mg 100 g^{-1})

Genotype rank	Environments*				
	E1	**E2**	**E3**	**E4**	**E5**
1	G5	G5	G3	G3	G3
2	G3	G11	G5	G4	G4
3	G8	G15	G11	G10	G5
4	G10	G1	G1	G1	G10
5	G11	G10	G10	G2	G1
6	G6	G3	G4	G5	G11
7	G4	G4	G12	G12	G2
8	G2	G12	G15	G8	G12
9	G12	G6	G2	G11	G8
10	G1	G2	G6	G6	G6
11	G14	G8	G8	G15	G15
12	G9	G14	G14	G9	G14
13	G7	G9	G9	G14	G9
14	G15	G7	G7	G13	G13
15	G13	G13	G13	G7	G7
Mean[a]	0.005	-0.004	-0.003	-0.001	-0.001
Environment rank and (IPCA 1 score)	5 (-4.61)	1 (1.78)	2 (1.29)	3 (1.22)	4 (0.32)

* E1 = Mansa-Mufulira, E2 = Mutanda West, E3 = Mansa-Main, E4 = Mutanda East, E5 = GART; [a]Means generated from standardized data

5.3.1.2 Root dry mass

The genotypes had a mean RDM of 33.1%. Genotype G14 had the highest RDM of 42.1% across environments. The highest mean RDM for all genotypes was recorded at E1 (35.0%), followed by E2 (34.2%). The E5 and E3 environments had the lowest mean RDM for all genotypes (33.1%) (Table 5.2).

The main effect for G, and the G x E interaction were highly significant ($p<0.001$) for RDM. The IPCA1 and IPCA2 axes explained 57.4% and 20.4%, respectively of the total G x E SS. Both IPCA1 and IPCA2 mean squares were highly significant ($p<0.001$ and $p<0.01$, respectively) (Table 5.5). The most stable genotypes for RDM with IPCA1 scores close to zero were G2, G3, G6, G8, G13, G14, and G9 (Figure 5.2; Table 5.6). Genotype G9 had the highest mean RDM (42.1%) across environments. The genotypes

that performed below average across environments were also unstable (G15, G4, and G10). Genotype G5 recorded the lowest RDM (25.2%) across environments (Table 5.6) and was stable (IPCA = 0.11). All the environments performed similarly (range of 1.89%) but E2 (IPCA1 = -1.82) was the most unstable environment. Environments E4 (IPCA1 = -0.25) and E5 (IPCA1 = 0.27) were stable for RDM (Figure 5.2).

Table 5.5 AMMI mean squares for root dry mass (%) of 15 genotypes of sweetpotato evaluated at five environments in Zambia, 2008/2009.

Source	**df**	**SS**	**Mean squares**	**F value**	**Probability**	**% SS of:**	
						Treatment	**G x E**
Treatments	74	1462.3	19.76	19.77	0.00000	100.00	
Genotypes (G)	14	1301.3	92.95	93.00	0.00000	88.99	
Environments (E)	4	0.0	0.00	0.00	1.00000	0.00	
G x E	56	161.0	2.88	2.88	0.00005	11.01	
IPCA 1	17	92.5	5.44	5.45	0.00000		57.45
IPCA 2	15	32.8	2.19	2.19	0.00938		20.37
Residual	24	35.7	1.49	1.49	0.08151		22.17
Error	138	137.9	1.00				
Total	224	1608.1	7.18				

[a]SS = Sum of squares

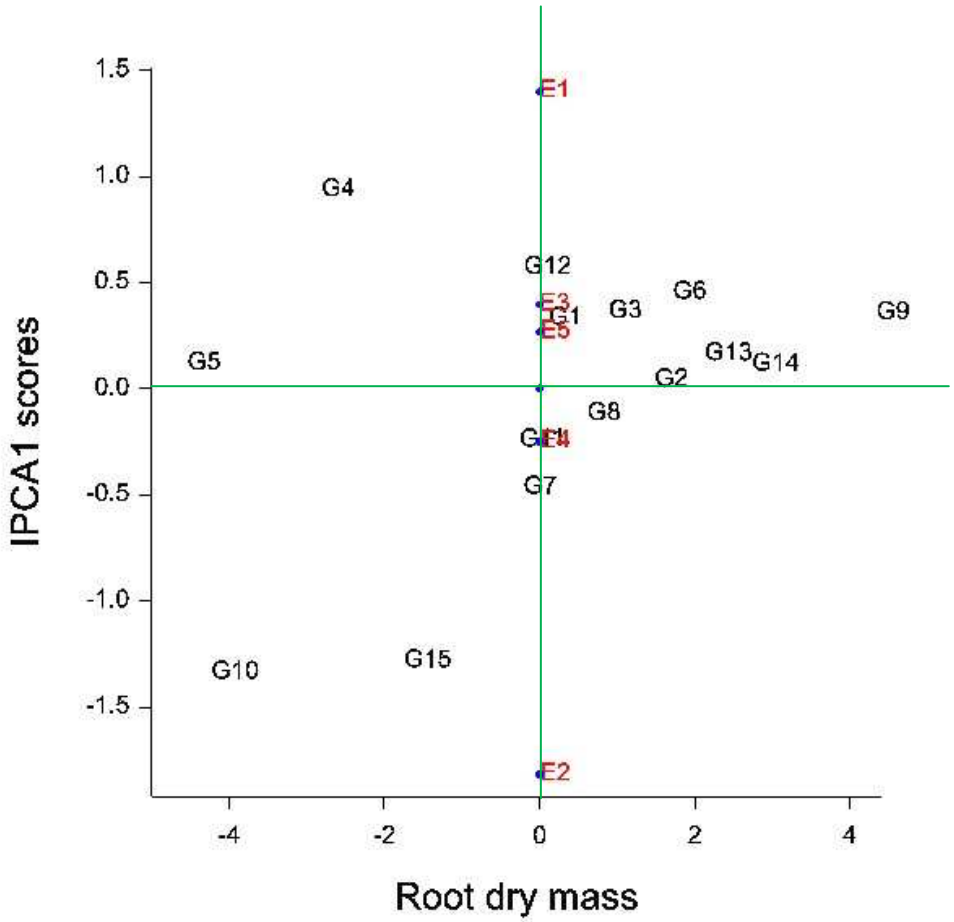


Figure 5.2: Biplot of mean root dry mass (%) and IPCA1 scores of 15 genotypes planted at five locations in Zambia. Grand mean = 33.8%. Data standardized.

Table 5.6 Genotypes ranked per environment on the basis of mean root dry mass. Environments ranked by IPCA1 score for root dry mass (%)

Genotype rank	Environments*				
	E1	**E2**	**E3**	**E4**	**E5**
1	G9	G9	G9	G9	G9
2	G14	G14	G14	G14	G14
3	G6	G13	G13	G13	G13
4	G13	G15	G6	G2	G2
5	G2	G2	G2	G6	G6
6	G3	G6	G3	G3	G3
7	G8	G7	G8	G11	G11
8	G1	G8	G1	G8	G8
9	G12	G3	G12	G1	G1
10	G7	G1	G11	G12	G12
11	G4	G11	G7	G7	G7
12	G11	G12	G4	G15	G15
13	G15	G10	G15	G4	G4
14	G5	G4	G5	G10	G10
15	G10	G5	G10	G5	G5
Mean[a]	-0.0007	0.0006	-0.0012	0.0019	0.0027
Environment rank and (IPCA 1 score)	1 (1.40)	5 (-1.82)	2 (0.40)	3 (-0.25)	4 (0.27)

*E1 = Mansa-Mufulira, E2 = Mutanda West, E3 = Mansa-Main, E4 = Mutanda East, E5 = GART; [a]Means generated from standardized data

5.3.1.3 Harvest index

The genotypes had a mean HI of 0.756. Genotype G10 had the highest HI of 0.865 across environments. The lowest mean HI was recorded for G14 (0.642) across environments. The highest mean HI was calculated at environment E2 (0.811), followed by E1 in the same year (0.803). The E5 environment had the lowest mean HI (0.647) (Table 5.2).

The G and the G x E were highly significant ($p<0.001$). The IPCA1 and the IPCA2 mean squares were both highly significant ($p<0.001$) and their SSs accounted for 75.6% and 15.1%, respectively, of the G x E SS (Table 5.7). The most stable (IPCA1 scores close to zero) genotypes for HI with above average performance (>0.75) were G10, G15, G11, G4, G5, G13, and G9 and ranked highly across environments. Another set of genotypes,

G2, G12, G7, G8, and G6 with IPCA1 scores close to zero, had below average HI and their ranks were low across the environments (Figure 5.3; Table 5.8). Genotype G10 was stable across the five environments and had the highest mean HI (0.86) across environments. Genotype G14 and G6 had the lowest mean HI (0.66 and 0.64, respectively) across environments but G6 was stable (IPCA1 = 0.07) whereas G14 was unstable (IPCA1 = -2.4). Environment E1 was the most stable (IPCA1 = -0.52) for all the genotypes followed by E4 (IPCA1 = 0.9) (Table 5.8).

Table 5.7 AMMI mean squares for harvest index of 15 genotypes of sweetpotato evaluated at five environments in Zambia, 2008/2009.

Source	**df**	**SS[a]**	**Mean squares**	**F value**	**Probability**	**% SS of:**	
						Treatment	**G x E**
Treatments	74	662.8	8.956	10.84	0.00000	100.00	
Genotypes (G)	14	380.1	27.153	32.85	0.00000	57.35	
Environments (E)	4	0.0	0.003	0.00	0.99997	0.00	
G x E	56	282.6	5.047	6.11	0.00000	42.64	
IPCA 1	17	213.6	12.567	15.21	0.00000		75.58
IPCA 2	15	42.7	2.847	3.44	0.00003		15.11
Residual	24	26.3	1.095	1.32	0.15903		9.31
Error	138	114.1	0.826				
Total	224	783.3	3.497				

[a]SS = Sum of squares

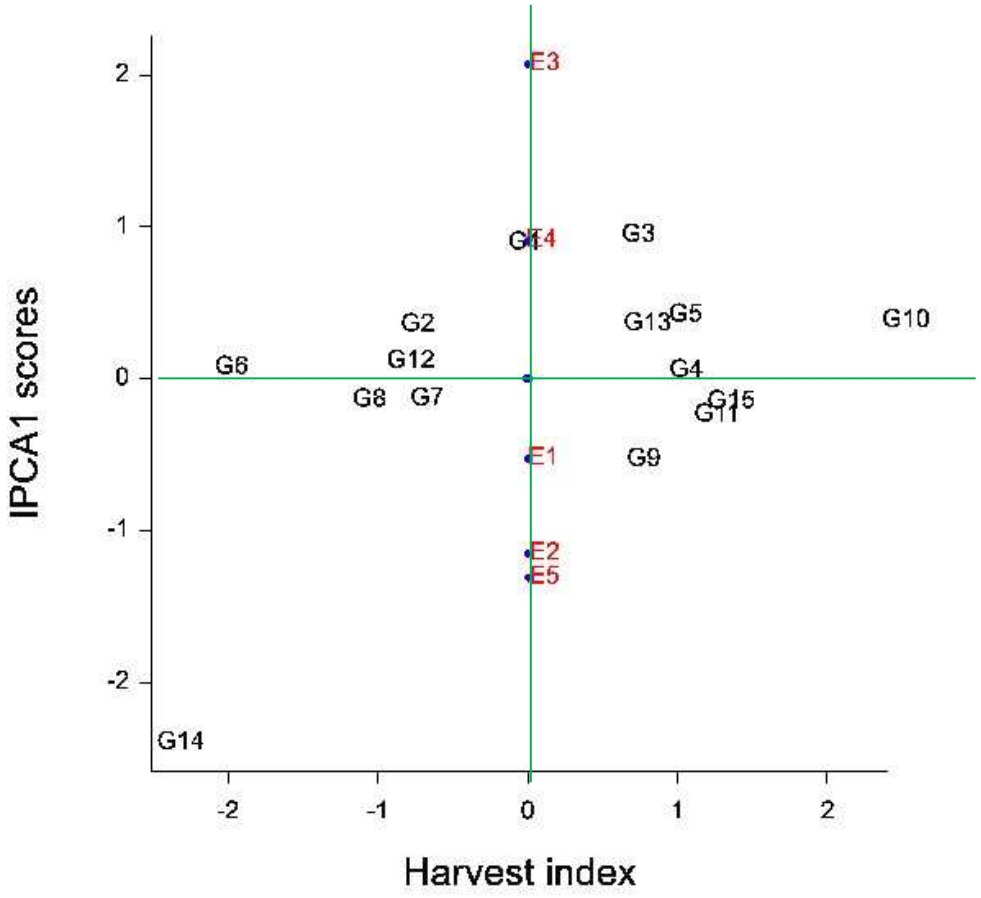


Figure 5.3: Biplot of mean harvest index and IPCA1 scores of 15 genotypes evaluated in five environments in Zambia. Grand mean = 0.76. Data standardized.

Table 5.8 Genotypes ranked per environment on the basis of mean harvest index. Environments ranked by IPCA1 score for harvest index

Genotype rank	Environments*				
	E1	**E2**	**E3**	**E4**	**E5**
1	G15	G15	G10	G10	G10
2	G10	G10	G3	G15	G4
3	G11	G11	G5	G5	G11
4	G13	G9	G1	G11	G9
5	G9	G4	G4	G13	G14
6	G5	G13	G13	G3	G5
7	G4	G5	G11	G4	G15
8	G7	G7	G2	G9	G13
9	G3	G14	G15	G1	G3
10	G1	G3	G12	G7	G8
11	G12	G8	G9	G2	G12
12	G2	G12	G8	G12	G2
13	G8	G1	G7	G8	G1
14	G6	G2	G6	G6	G7
15	G14	G6	G14	G14	G6
Mean[a]	0.001	0.008	0.008	-0.010	0.006
Environment rank and (IPCA 1 score)	3 (-0.52)	4 (-1.15)	1 (2.07)	2 (0.91)	5 (-1.31)

*E1 = Mansa-Mufulira, E2 = Mutanda West, E3 = Mansa-Main, E4 = Mutanda East, E5 = GART; [a]Means generated from standardized data

5.3.1.4 Vine fresh yield

The genotypes had a mean VFY of 4.6 t ha^{-1}. Genotype G6 had the highest mean VFY of 7.5 t ha^{-1} across environments. The highest mean (11.49 t ha^{-1}) vine fresh yield across genotypes, however, was recorded at environment E5, followed by environment E3 (4.71 t ha^{-1}). The mean (11.5 t ha^{-1}) VFY for Environment E5 was more than double the mean (4.7 t ha^{-1}) VFY of E3 and five times more than the other environments (Table 5.2).

The G x E was highly significant ($p<0.001$). The IPCA1 and the IPCA2 accounted for 55% and 22.5%, respectively, of the G x E SS (Table 5.9). Genotype G7 was the most stable (IPCA1 = 0.13) combined with above average mean performance (4.76 t ha^{-1}). Other stable genotypes with high mean VFY were G13 and G8 (5.47 and 6.87 t ha^{-1}, respectively). Genotype G2 and G6 performed above average but were less stable. There were more stable genotypes combined with below average mean performance

(<4.6 t ha^{-1}); for example: G7, G9, G4, G11, and G14 (Table 5.10). In terms of environments, E1 was most stable (IPCA1 = -0.16). Environment E2 was a high yielding environment but was most unstable (Figure 5.4; Table 5.10). Genotype G6 was the best performing in all environments except in E3 where it ranked third (Table 5.10).

Table 5.9 AMMI mean squares for vine fresh yield (t ha^{-1}) of 15 genotypes of sweetpotato evaluated in five environments in Zambia, 2008/2009.

Source	**df**	**SS[a]**	**Mean squares**	**F value**	**Probability**	**% SS of:**	
						Treatment	**G x E**
Treatments	74	849.1	11.47	14.33	0.00000	100.00	
Genotypes (G)	14	254.8	18.20	22.73	0.00000	30.01	
Environments (E)	4	403.3	100.82	38.17	0.00000	47.50	
G x E	56	191.1	3.41	4.26	0.00000	22.50	
IPCA 1	17	105.1	6.18	7.72	0.00000		55.00
IPCA 2	15	43.0	2.86	3.58	0.00003		22.50
Residual	24	43.0	1.79	2.24	0.00198		22.50
Error	138	110.5	0.80				
Total	224	968.0	4.40	19.00			

[a]SS = Sum of squares

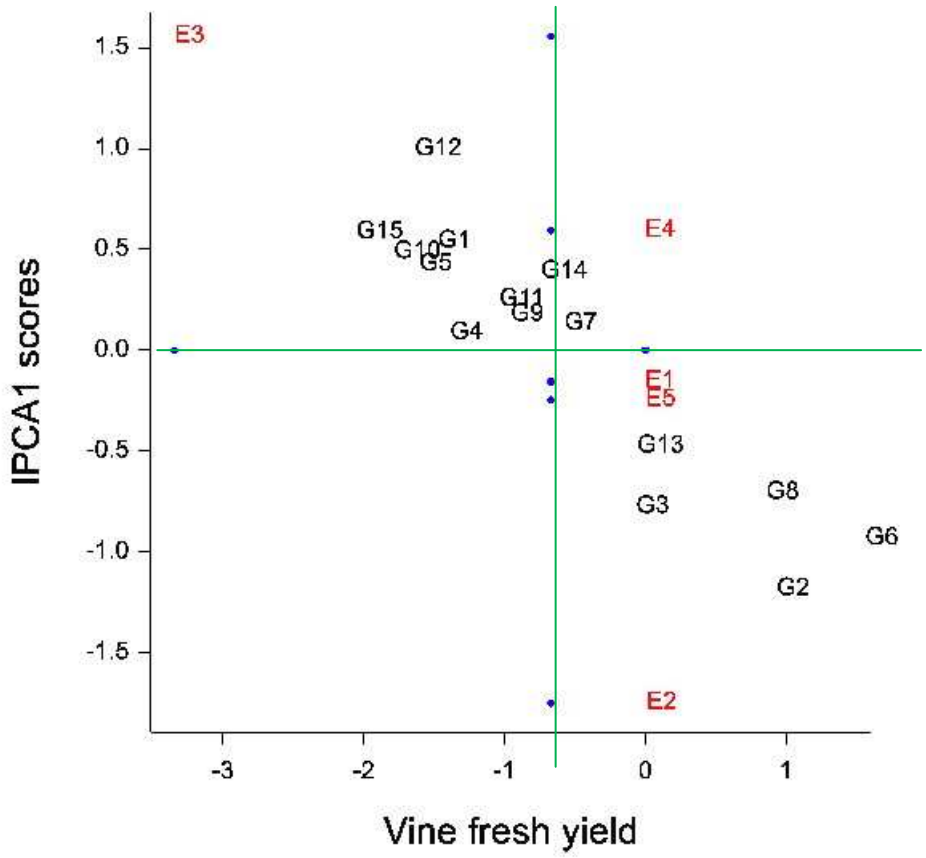


Figure 5.4: Biplot of mean vine fresh yield (t ha^{-1}) and IPCA1 scores of 15 genotypes planted at five locations in Zambia. Grand mean = 4.6 t ha^{-1}. Data standardized.

Table 5.10 Genotypes ranked per environment on the basis of mean vine fresh yield (t ha^{-1}). Environments ranked by IPCA1 score for vine fresh mass (t ha^{-1})

Genotype rank	Environments*				
	E1	**E2**	**E3**	**E4**	**E5**
1	G6	G6	G8	G6	G6
2	G8	G2	G14	G8	G3
3	G2	G8	G6	G2	G2
4	G13	G3	G13	G7	G8
5	G7	G13	G7	G13	G14
6	G14	G7	G2	G14	G13
7	G9	G11	G9	G9	G11
8	G3	G9	G12	G4	G12
9	G4	G1	G4	G1	G7
10	G1	G4	G1	G3	G9
11	G11	G10	G15	G5	G15
12	G12	G5	G3	G11	G1
13	G5	G14	G5	G10	G5
14	G10	G12	G11	G12	G10
15	G15	G15	G10	G15	G4
Mean[a]	-0.001	0.007	-3.346	-0.002	0.0001
Environment rank and (IPCA 1 score)	3 (-0.16)	5 (-1.75)	1 (1.56)	2 (0.59)	4 (-0.24)

* E1 = Mansa-Mufulira, E2 = Mutanda West, E3 = Mansa-Main, E4 = Mutanda East, E5 = GART; [a]Means generated from standardized data

5.3.1.5 Root fresh yield

The genotypes had a mean RFY of 12.5 t ha^{-1}. Genotype G13 had the highest RFY with a mean of 17.5 t ha^{-1} across environments. The E5 environment had the highest mean RFY (20.4 t ha^{-1}) across genotypes while environment E2 had the lowest mean RFY (7.5 t ha^{-1}) (Table 5.2).

The G main effect and the G x E were highly significant ($p<0.001$) (Table 5.11). The IPCA1 and the IPCA2 accounted for 47.3% and 37.8%, respectively, of the G x E SS and were highly significant ($p<0.001$) (Table 5.11). The most stable genotypes with IPCA1 scores close to zero combined with above average performance (>12.5 t ha^{-1}) across environments were G6, G10, G9, G8, and G2 (Figure 5.5). Genotype G13 was the highest yielding but was less stable (IPCA1 = 0.95). It did not perform very well in

environment E5, though it was the best performing genotype in the rest of the environments. Among the low yielding genotypes, G12 and G15 with IPCA1 scores of 0.1 and -0.39, respectively, were the most stable (Figure 5.5 and Table 5.12). Environment E2 was the most stable environment (IPCA1 = 0.27) but had the lowest mean (7.5 t ha^{-1}) yield across genotypes. Conversely, environment E5 was very unstable (IPCA1 = -2.58) (Figure 5.5).

Table 5.11 AMMI mean squares root fresh yield (t ha^{-1}) of 15 genotypes of sweetpotato evaluated at five environments in Zambia

Source	**df**	**SS[a]**	**Mean squares**	**F value**	**Probability**	**% SS of:**	
						Treatment	**G x E**
Treatments	74	884.7	11.956	11.97	0.00000	100.00	
Genotypes (G)	14	399.1	28.510	28.53	0.00000	45.11	
Environment (E)	4	0.0	0.000	0.00	1.00000	0.00	
G x E	56	485.6	8.671	8.68	0.00000	54.89	
IPCA 1	17	229.7	13.511	13.52	0.00000		47.30
IPCA 2	15	183.3	12.221	12.23	0.00000		37.75
Residual	24	72.6	3.025	3.03	0.00003		14.95
Error	138	137.9	0.999				
Total	224	1051.7	4.695				

[a]SS = Sum of squares

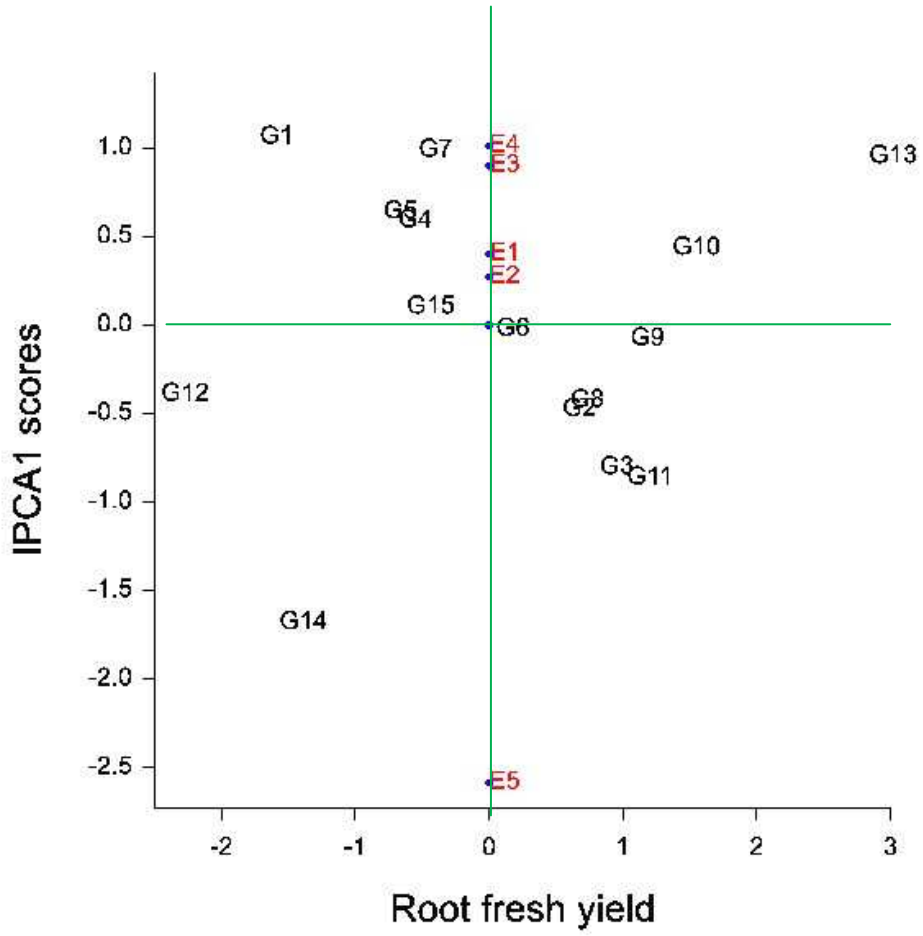


Figure 5.5: Biplot of mean root fresh yield (t ha^{-1}) and IPCA1 scores of 15 genotypes planted at five locations in Zambia. Grand mean = 12.5 t ha^{-1}. Data standardized.

Table 5.12 Genotypes ranked per environment on the basis of mean performance. Environments ranked by IPCA1 score for root fresh yield (t ha^{-1})

Genotype rank	Environments*				
	E1	**E2**	**E3**	**E4**	**E5**
1	G13	G13	G13	G13	G3
2	G7	G9	G10	G10	G11
3	G9	G11	G3	G3	G14
4	G15	G10	G8	G8	G8
5	G10	G7	G1	G2	G2
6	G11	G2	G2	G6	G9
7	G6	G8	G4	G9	G13
8	G2	G15	G6	G4	G10
9	G5	G6	G5	G7	G6
10	G8	G3	G7	G5	G12
11	G4	G5	G9	G11	G15
12	G3	G4	G12	G1	G4
13	G1	G14	G11	G15	G5
14	G14	G1	G15	G12	G7
15	G12	G12	G14	G14	G1
Mean[a]	0.001	-0.003	0.0001	-0.001	-0.0001
Environment rank and (IPCA 1 score)	3 (0.40)	4 (0.27)	2 (0.90)	1 (1.01)	5 (-2.58)

*E1 = Mansa-Mufulira, E2 = Mutanda West, E3 = Mansa-Main, E4 = Mutanda East, E5 = GART; [a]Means generated from standardized data

5.3.2 Spearman's rank correlations

5.3.2.1 β-carotene content

Rank correlation between environment E1 and E2 was significant ($p<0.05$). The rank correlations between E1 and E3, E1 and E4, E2 and E4, and E2 and E5 were highly significant at $p<0.01$. The correlations of the remaining pairs were highly significant ($p<0.001$) (Table 5.13).

Table 5.13 Spearman's correlations between environments of the ranking of 15 genotypes within each environment for β-carotene content (mg 100 g^{-1})

	Environment[a]				
Environment	**E1**	**E2**	**E3**	**E4**	**E5**
E1	1				
E2	0.529*	1			
E3	0.700**	0.900***	1		
E4	0.686**	0.586**	0.804***	1	
E5	0.775***	0.729**	0.914***	0.95***	1

*,**,***Significant at p<0.05, 0.01, 0.001, respectively. [a]E1 = Mansa-Mufulira, E2 = Mutanda West, E3 = Mansa-Main, E4 = Mutanda East, E5 = GART

Rank correlation between the genotypes indicated that some genotypes were highly positively correlated and some highly negatively correlated. For example, genotype G1 was highly, positively correlated with G10, G11, G12, and G15 but highly, negatively correlated with G3, G8, and G9 (Table 5.14). There were other genotypes with highly, positive correlations. For example, G5 was positively, highly correlated with G6, G11, G12, and G14.

5.3.2.2 Root dry mass composition

The rank correlations were highly significant (p<0.001) between all pairs of environments. Environment E4 with E5 were perfectly correlated (Table 5.15). Most of the genotypes were not significantly correlated with each other (Table 5.16). Among those that were significantly (p<0.05) correlated, only four were negatively correlated, namely: G10 with G4, G10 with G5, G10 with G6, and G12 with G10. Genotype G1 was positively, highly correlated with the most genotypes (six) followed by G12 (five).

Table 5.14 Spearman's correlations between 15 genotypes of their ranks in each of five environments for β-carotene content (mg 100 g^{-1})

	Genotype														
Genotype	**G1**	**G2**	**G3**	**G4**	**G5**	**G6**	**G7**	**G8**	**G9**	**G10**	**G11**	**G12**	**G13**	**G14**	**G15**
G1	1														
G2	0.3	1													
G3	-0.9**	-0.1	1												
G4	0.5	0.6	-0.3	1											
G5	0.3	0.3	-0.4	-0.4	1										
G6	0.3	0.8*	-0.1	0.1	0.7*	1									
G7	0.1	0.9**	0.0	0.2	0.6	0.9**	1								
G8	-0.8*	0.3	0.9**	-0.1	-0.2	0.2	0.4	1							
G9	-0.8*	0.3	0.9**	-0.1	-0.2	0.2	0.4	1.0	1						
G10	1.0***	0.3	-0.9**	0.5	0.3	0.3	0.1	-0.8*	-0.8*	1					
G11	0.7*	0.0	-0.9**	-0.1	0.7*	0.2	0.1	-0.8*	-0.8*	0.7*	1				
G12	0.7*	0.3	-0.6	-0.1	0.8*	0.7*	0.4	-0.5	-0.5	0.7*	0.7*	1			
G13	-0.3	0.7*	0.6	0.4	-0.2	0.5	0.6	0.8*	0.8*	-0.3	-0.7*	-0.2	1		
G14	-0.1	0.1	0.0	-0.7*	0.9**	0.6	0.5	0.1	0.1	-0.1	0.4	0.6	-0.1	1	
G15	1.0***	0.3	-0.9**	0.5	0.3	0.3	0.1	-0.8*	-0.8*	1.0***	0.7*	0.7*	-0.3	-0.1	1

*,**Significant at p<0.05, 0.01, respectively.

Table 5.15 Spearman's correlations between environments of the ranking of 15 genotypes within each environment for root dry mass (%)

	Environment				
Environment	**E1**	**E2**	**E3**	**E4**	**E5**
E1	1				
E2	0.754***	1			
E3	0.986***	0.761***	1		
E4	0.925***	0.796***	0.968***	1	
E5	0.925***	0.796***	0.968***	1.000***	1

***Significant at p<0.001; [a]E1 = Mansa-Mufulira, E2 = Mutanda West, E3 = Mansa-Main, E4 = Mutanda East, E5 = GART

5.3.2.3 Harvest index

Environments E2 and E3 were not correlated for HI (Table 5.17). Environments E1 with E3, and E3 with E5 were positively, highly correlated. The correlations between E5 and E1, and E5 and E4 were positive and significant at p<0.01. The correlations between the remaining pairs of environments were positive and highly significant (p<0.001). Genotypes G4 and G15 were each positively correlated with nine other genotypes (Table 5.18). The significant (p<0.05) positive correlation between G1 and G14 was the only one that was negative.

Table 5.16 Spearman's correlations between 15 genotypes of their ranks in each of five environments for root dry mass (%)

	Genotype														
Genotype	**G1**	**G2**	**G3**	**G4**	**G5**	**G6**	**G7**	**G8**	**G9**	**G10**	**G11**	**G12**	**G13**	**G14**	**G15**
G1	1														
G2	0.6	1													
G3	0.7*	0.6	1												
G4	0.8*	0.1	0.7*	1											
G5	0.9**	0.5	0.9**	0.9**	1										
G6	0.9**	0.2	0.5	0.9**	0.8*	1									
G7	0.4	0.5	-0.1	-0.1	0.0	0.3	1								
G8	0.4	0.5	-0.1	-0.1	0.0	0.3	1	1							
G9	0.7*	0.6	0.3	0.3	0.4	0.6	0.9**	0.9**	1						
G10	-0.5	0.2	-0.6	-0.9**	-0.7*	-0.7*	0.3	0.3	-0.1	1					
G11	-0.2	0.6	0.2	-0.5	-0.1	-0.6	-0.1	-0.1	-0.2	0.6	1				
G12	0.9**	0.5	0.9**	0.9**	1.0***	0.8*	0.0	0.0	0.4	-0.7*	-0.1	1			
G13	0.5	0.9**	0.8*	0.2	0.6	0.1	0.1	0.1	0.3	0.0	0.7*	0.6	1		
G14	0.7*	0.6	0.3	0.3	0.4	0.6	0.9**	0.9**	1.0***	-0.1	-0.2	0.4	0.3	1	
G15	0.3	0.1	-0.3	0.0	-0.1	0.4	0.9**	0.9**	0.8*	0.1	-0.5	-0.1	-0.3	0.8*	1

*,**,***Significant at p<0.05, 0.01, 0.001, respectively.

Table 5.17 Spearman's correlations between environments of the ranking of 15 genotypes within each environment for harvest index

	Environment[a]				
Environments	**E1**	**E2**	**E3**	**E4**	**E5**
E1	1				
E2	0.882***	1			
E3	0.532*	0.296^{NS}	1		
E4	0.932***	0.775***	0.757***	1	
E5	0.582**	0.804***	0.386*	0.575**	1

*,**,***Significant at p<0.05, 0.01, 0.001, respectively. [a]E1 = Mansa-Mufulira, E2 = Mutanda West, E3 = Mansa-Main, E4 = Mutanda East, E5 = GART.

Table 5.18 Spearman's correlations between 15 genotypes of their ranks in each of five environments for harvest index

	Genotype														
Genotype	**G1**	**G2**	**G3**	**G4**	**G5**	**G6**	**G7**	**G8**	**G9**	**G10**	**G11**	**G12**	**G13**	**G14**	**G15**
G1	1														
G2	0.7*	1													
G3	0.9**	0.9**	1												
G4	0.1	0.4	0.3	1											
G5	0.4	0.9**	0.7*	0.7*	1										
G6	0.1	0.5	0.2	0.7*	0.7*	1									
G7	0.1	0.5	0.2	0.7*	0.7*	1	1								
G8	0.0	0.3	0.1	0.9**	0.6	0.9**	0.9**	1							
G9	-0.4	0.1	-0.2	0.8*	0.5	0.8*	0.8*	0.9**	1						
G10	0.5	0.6	0.7*	0.8*	0.7*	0.3	0.3	0.5	0.3	1					
G11	0.0	0.3	0.1	0.9**	0.6	0.9**	0.9**	1	0.9**	0.5	1				
G12	0.1	0.4	0.3	1.0***	0.7*	0.7*	0.7*	0.9**	0.8*	0.8*	0.9**	1			
G13	0.3	0.8*	0.5	0.6	0.9**	0.9**	0.9**	0.7*	0.6	0.4	0.7*	0.6	1		
G14	-0.7*	-0.3	-0.6	0.5	0.1	0.6	0.6	0.7*	0.9**	-0.1	0.7*	0.5	0.3	1	
G15	0.0	0.3	0.1	0.9**	0.6	0.9**	0.9**	1.0***	0.9**	0.5	1.0***	0.9**	0.7*	0.7*	1

*,**,***Significant at p<0.05, 0.01, 0.001, respectively.

5.3.2.4 Vine fresh yield

All the correlations between environments were positive but the significance levels varied. Environment E2 and E3 were correlated at $p<0.05$. All the other environments were positively, significantly ($p<0.01$) correlated with E5. The remaining correlations between environments were highly significant ($p<0.001$) (Table 5.19). Also, all the correlations between the genotypes were positive with high correlations, the majority of which were highly significant ($p<0.001$) (Table 5.20).

Table 5.19 Spearman's correlations between environments of the ranking of 15 genotypes within each environment for vine fresh yield (t ha^{-1})

	Environment[a]				
Environment	**E1**	**E2**	**E3**	**E4**	**E5**
E1	1				
E2	0.818***	1			
E3	0.843***	0.407*	1		
E4	0.968***	0.775***	0.818***	1	
E5	0.718**	0.679**	0.554**	0.564**	1

*,**,***Significant at $p<0.05$, 0.01, 0.001, respectively. [a]E1 = Mansa-Mufulira, E2 = Mutanda West, E3 = Mansa-Main, E4 = Mutanda East, E5 = GART

Table 5.20 Spearman's correlations between 15 genotypes of their ranks in each of five environments for vine fresh yield (t ha^{-1})

	Genotype														
Genotype	**G1**	**G2**	**G3**	**G4**	**G5**	**G6**	**G7**	**G8**	**G9**	**G10**	**G11**	**G12**	**G13**	**G14**	**G15**
G1	1														
G2	0.9**	1													
G3	0.9**	1.0***	1												
G4	1.0***	0.9**	0.9**	1											
G5	1.0***	0.9**	0.9**	1	1										
G6	0.9**	1.0***	1.0***	0.9**	0.9**	1									
G7	0.9**	1.0***	1.0***	0.9**	0.9**	1.0***	1								
G8	0.9**	1.0***	1.0***	0.9**	0.9**	1.0***	1.0***	1							
G9	1.0***	0.9**	0.9**	1.0***	1.0***	0.9**	0.9**	0.9**	1						
G10	1.0***	0.9**	0.9**	1.0***	1.0***	0.9**	0.9**	0.9**	1.0***	1					
G11	1.0***	0.9**	0.9**	1.0***	1.0***	0.9**	0.9**	0.9**	1.0***	1.0***	1				
G12	0.9**	1.0***	1.0***	0.9**	0.9**	1.0***	1.0***	1.0***	0.9**	0.9**	0.9**	1			
G13	0.9**	1.0***	1.0***	0.9**	0.9**	1.0***	1.0***	1.0***	0.9**	0.9**	0.9**	1.0***	1		
G14	0.9**	1.0***	1.0***	0.9**	0.9**	1.0***	1.0***	1.0***	0.9**	0.9**	0.9**	1.0***	1.0***	1	
G15	1.0***	0.9**	0.9**	1.0***	1.0***	0.9**	0.9**	0.9**	1.0***	1.0***	1.0***	0.9**	0.9**	0.9**	1

,*Significant at p<0.01, 0.001, respectively.

5.3.2.5 Root fresh yield

All the correlations involving environment E5 were not significant. Correlations where E3 was involved were also not significant except with E4. Two pairs of environments, E2 with E1, and E4 with E3 were positively and highly correlated (Table 5.21). All the correlations between genotypes that were high were positive (Table 5.22). Rank correlations involving genotype G11 were all not significant. Similarly, most of the correlations that involved genotype G7 were not significant. Otherwise, most of the correlations between genotypes were positive and significant ($p<0.05$).

Table 5.21 Spearman's correlations between environments of the ranking of 15 genotypes within each environment for root fresh yield (t ha^{-1})

	Environment[a]				
Environment	**E1**	**E2**	**E3**	**E4**	**E5**
E1	1				
E2	0.886***	1			
E3	0.111^{NS}	0.236^{NS}	1		
E4	0.429*	0.593**	0.854***	1	
E5	-0.071^{NS}	0.321^{NS}	0.039^{NS}	0.304^{NS}	1

*,**,***Significant at $p<0.05$, 0.01, 0.001, respectively. NS = Not significant. [a]E1 = Mansa-Mufulira, E2 = Mutanda West, E3 = Mansa-Main, E4 = Mutanda East, E5 = GART

Table 5.22 Spearman's correlations between 15 genotypes of their ranks in each of five environments for root fresh yield (t ha^{-1})

	Genotype														
Genotype	**G1**	**G2**	**G3**	**G4**	**G5**	**G6**	**G7**	**G8**	**G9**	**G10**	**G11**	**G12**	**G13**	**G14**	**G15**
G1	1														
G2	0.9**	1													
G3	0.9**	1	1												
G4	0.8*	0.9**	0.9**	1											
G5	0.8*	0.9**	0.9**	1.0***	1										
G6	0.8*	0.9**	0.9**	1.0***	1.0***	1									
G7	0.4	0.3	0.3	0.6	0.6	0.6	1								
G8	0.9**	1.0***	1.0***	0.9**	0.9**	0.9**	0.3	1							
G9	0.5	0.7*	0.7*	0.9**	0.9**	0.9**	0.7*	0.7*	1						
G10	0.9**	1.0***	1.0***	0.9**	0.9**	0.9**	0.3	1.0***	0.7*	1					
G11	-0.3	0.1	0.1	0.3	0.3	0.3	0.1	0.1	0.6	0.1	1				
G12	0.9**	1.0***	1.0***	0.9**	0.9**	0.9**	0.3	1.0***	0.7*	1.0***	0.1	1			
G13	1.0***	0.9**	0.9**	0.8*	0.8*	0.8*	0.4	0.9**	0.5	0.9**	-0.3	0.9**	1		
G14	0.5	0.7*	0.7*	0.9**	0.9**	0.9**	0.7*	0.7*	1.0***	0.7*	0.6	0.7*	0.5	1	
G15	0.5	0.7*	0.7*	0.9**	0.9**	0.9**	0.7*	0.7*	1.0***	0.7*	0.6	0.7*	0.5	1.0***	1

*,**,***Significant at p<0.05, 0.01, 0.001, respectively.

5.3.3 Correlations among five traits

Root dry mass was negatively correlated with β-carotene content, VFY, and RFY whereas it was positively correlated with HI. Beta-carotene content was negatively correlated with HI and positively correlated with VFY. HI was negatively correlated with both VFY and RFY while VFY and RFY were positively correlated (Table 5.23)

Table 5.23 Phenotypic correlations among five traits measured on 15 genotypes in five environments

	Traits				
Traits	**Root dry mass (%)**	**β-carotene content (mg 100 g^{-1})**	**Harvest index**	**Vine fresh yield (t ha^{-1})**	**Root fresh yield (t ha^{-1})**
Root dry mass (%)	-				
β-carotene content (mg 100 g^{-1})	-0.404***	-			
Harvest index	0.223***	-0.234***	-		
Vine fresh yield (t ha^{-1})	-0.172*	0.162*	-0.687***	-	
Root fresh yield (t ha^{-1})	-0.152*	0.033^{NS}	-0.136*	0.739***	-

*,***Significant at p<0.05, 0.001, respectively. NS = Not significant.

5.4 Discussions and conclusion

The mean squares for the G x E were highly significant (p<0.001) for β-carotene content, RDM, HI, VFY, and RFY, indicating differential response of genotypes relative to each other across the five environments. The G x E interactions are revealed by the changes in the rank order of the genotypes across the environments for the five traits (Tables 5.4, 5.6, 5.8, and 5.10). The AMMI analysis identified genotypes that were stable across environments and these are discussed for each trait.

Spearman's rank correlations between environments were positive and high for β-carotene content, RDM, HI, and VFY (Tables 5.13, 5.15, 5.17, and 5.19; , respectively). These correlations can be attributed to a number of genotypes maintaining consistent rankings across environments. For example, for the trait RDM, genotypes G9, G14, and

G13 had consistently high values while others, G10, G4, and G5, had consistently low values (Table 5.6).

Mean β-carotene content ranged from 0.09 to 9.4 mg 100 g^{-1} indicating that β-carotene content was highly variable among the genotypes. The mean RDM (33.8%) of the 15 genotypes was high relative to the popular local, cultivar with genotype G9 recording the highest mean RDM of 42%. The mean HI was above 50% for all the genotypes indicating that most of the photosynthates were partitioned to the roots. Genotype G6 and G8 had the highest VFY and may be considered either as a vegetable or livestock feed depending on their palatability. The mean RFY ranged from 7.9 to 17.5 t ha^{-1}. The overall mean RFY of the 15 progeny selected from the polycross was 12.5 t ha^{-1} and was higher than the average of the germplasm collected (detailed in Chapter 3) which was 8.9 t ha^{-1}. This is a remarkable increase in yield for this polycross derived set of genotypes.

5.4.1 β-carotene content

The subdivision of G x E for β-carotene content in roots indicated that the first two IPCA axes accounted for 96% of the total variability. However, the high G (65% of treatment SS) and the relatively low G x E (35% of treatment SS) for β-carotene content may indicate that the evaluation for high, stable performance can be done using well chosen environments. This result concurs with that of Grüneberg *et al.* (2005) and Manrique and Hermann (2002) who reported the SS for G x E for β-carotene smaller than that for the main effects of genotype. Similar results were obtained for cassava for total carotenoids (Ssemakula *et al.*, 2007). The relatively high stability of the genotypes for β-carotene content may indicate that this trait is less influenced by the environment than, for example, RFY. This suggests that prospects for improving β-carotene content in sweetpotato are favourable. Eight genotypes, namely G1, G2, G4, G6, G8, G10, G11, and G12 performed above average and were stable across environments. Genotypes with high β-carotene can be identified early in the breeding programme and a few, well chosen environments can be used. For example, genotype G3 was the best performer and was best adapted to three environments, E3 (8.9 mg 100 g^{-1}), E4 (10.4 mg 100 g^{-1}), and E5 (9.8 mg 100 g^{-1}), but its performance was lower in E2 (7.5 mg 100 g^{-1}).

5.4.2 Root dry mass composition

Root dry mass is a very important trait for consumers in Zambia. The 15 selected polycross progeny recorded RDM above 30% which is the preferred level among consumers. This is an indication that the objective of breeding high β-carotene and high RDM genotypes is achievable. For example, genotypes G2, G6, and G8 were stable across all five environments with above average performance for both β-carotene content (5.0, 4.7, and 4.7 mg 100 g^{-1}, respectively) and RDM (37, 37, and 35%, respectively). These three genotypes can consequently be recommended for all five environments (Figure 5.5). Genotype G3, which had the highest mean β-carotene level of 9.4 mg 100 g^{-1}, was, however, more stable for RDM with above average performance (35%) (Figure 5.2). Genotype 3 had the third highest mean yield across environments (14.7 t ha^{-1}). It was the top performer in environment E5 (30 t ha^{-1}) and is therefore recommended for this specific environment.

5.4.3 Harvest index

Grüneberg *et al.* (2005) found that genotypes with high yield and high yield stability tend to also have high HI and high HI stability. In this study, only two genotypes, G9 and G10, conformed to this finding (Figures 5.3 and 5.5). Therefore, an ideal genotype will need to balance the allocation of photosynthates between the development of harvestable roots and adequate vine production.

Genotype G6 had the highest VFY (7.6 t ha^{-1}) across environments and its mean HI (0.66) was low and stable but the RFY was average. The genotype can be considered for forage production for livestock or for vegetable production depending on the palatability. In addition, it provides sufficient quantities of vines for propagation.

5.4.4 Root fresh yield

The significant ($p<0.001$) G x E mean square and its high relative proportion of Treatment SS (55%) for RFY is expected because yield is a polygenic trait (Easwari and Sheela, 1998; Cach *et al.*, 2006) and, therefore, influenced by the environment (Table 5.11). Other G x E studies (Collins, *et al.*, 1987; Bacusmo *et al.*, 1998; Naskar and

Singh, 1992; Ngeve, 1993; Manrique and Hermann, 2002; Grüneberg *et al.*, 2005) have reported that in sweetpotato, RFY is sensitive to G x E. The strong influence of the environment on RFY makes the potential genetic gain in RFY unpredictable. Hence, early testing of genotypes in multi-locations to identify those with specific versus general stability is necessary. The G x E (55% of Treatment SS) for RFY was larger than the G (45% of Treatment SS) main effect. This implies that higher yields could be attained by improving crop management practices in environments suited to the crop besides emphasising the improvement of genotypes.

5.4.5 Correlations among five traits

Negative correlation between RDM and β-carotene content confirmed previous results (Hernandez *et al.,* 1967; Jones, 1977). RDM was also negatively correlated with VFY and RFY indicating that selecting for higher RDM may compromise the yield of both the roots and the vines. There were positive associations among VFY and RFY suggesting that breeding for any of these traits would not reduce the desired level of the other.

5.4.6 General conclusion

The magnitude of the G x E for β-carotene content, RDM, and HI was small and selection for these traits may be conducted in a few, well selected environments. Conversely, RFY and VFY yield may require early testing in varied environments to select genotypes with either wide or specific adaptation. It can be concluded that it is possible to breed for high β-carotene, high RDM and high yield sweetpotato genotypes with wide or specific adaptation in Zambia as the AMMI analysis identified genotypes G2, G6, and G8 as stable across environments for both β-carotene content and RDM. They performed above average for both traits. Therefore, G2, G6, and G8 qualify as genotypes with above average yield that would do well in all the environments with acceptable β-carotene content and RDM. Genotype G3 was best suited for environment E3, E4, and E5 and had the highest mean β-carotene content (9.4 mg 100 g^{-1}), and high mean RDM (35.5%), and high mean RFY of 14.7 t ha^{-1} across the environments. Also it had above average mean RFY (14.7 t ha^{-1}) meeting the basic criteria for a genotype preferred by consumers (as determined in the PRA study detailed in Chapter 2). These

identified genotypes will undergo further evaluation that may culminate in their release for production by Zambian farmers.

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Appendices

Appendix 5.1 Number of seed produced from each parental genotype in two polycrosses (12 x 12, and 30 x 8) conducted at Mansa Research Station.

ID	Parent	Source	Number of seeds	
			12 parent	30 parent
1	Excel	CIP Kenya	2,395	
2	Kabalenge	Local	292	544
3	Matembele 3K	Local	221	18
4	W-119	CIP Kenya	3,095	888
5	L2-4/20/5	Local	268	54
6	15/1	Local	1,320	280
7	Unknown 2/1	Local	1,670	32
8	L3-199084/1	Local	2,822	1,500
9	No name 13K	Local		272
10	Zambezi/1	Local		112
11	Kakamega	CIP Kenya		3,380
12	L3-L0-4/10/6	Local		234
13	Munwe umo	Local		228
14	Carrots Mwewa	Local		3,696
15	Kasompe	Local		50
16	No name 14N	Local		76
17	Katansha	Local		1014
18	Zambezi	Local		934
19	L3-Mugamba 3/1	Local		104
20	Lukusashi	Local		56
21	199047/4	Local		22
22	Carrot-C	Local		3,476
23	Resisto	CIP Kenya		1066
24	1998-12-3	ARC - VOPI South Africa		2,715
25	1999-1-7	ARC - VOPI South Africa		1,738
26	1997-14-17	ARC - VOPI South Africa		334
27	Mulungushi	Local		686
28	Chingovwa	Local	3,190	
29	199062.1	CIP Kenya	1,350	
30	L4-138/3	Local	6,595	
	Total		23,218	23,509

Appendix 5.2 Field layout of a 12 x 12 sweetpotato polycross arranged in a randomised complete block with eight replications
DOP*: 16/12/2005

1	2	12	3	11	4	10	5	9	6	8	7
2	3	1	4	12	5	11	6	10	7	9	8
12	1	11	2	10	3	9	4	8	5	7	6
3	4	2	5	1	6	12	7	11	8	10	9
11	12	10	1	9	2	8	3	7	4	6	5
4	5	3	6	2	7	1	8	12	9	11	10
10	11	9	12	8	1	7	2	6	3	5	4
5	6	4	7	3	8	2	9	1	10	12	11
9	10	8	11	7	12	6	1	5	2	4	3
6	7	5	8	4	9	3	10	2	11	1	12
8	9	7	10	6	11	5	12	4	1	3	2
7	8	6	9	5	10	4	11	3	12	2	1

1 = Zambezi/1/1, 2 = Excel, 3 = L4-138/3, 4 = 55/1, 5 = L0-103/2, 6 = W-119, 7 = 199062.1, 8 = L2-4/20/5, 9 = 15/1, 10 = Unknown 2/1, 11 = Chingovwa, 12 = L3-199084/1; *DOP = Date of planting

Appendix 5.3 Field layout of a 30 x 30 sweetpotato polycross arranged in a randomised complete block design with eight replications
DOP*: 5/12/2005

	Plots																													
Reps	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**	**30**
1	15	25	22	14	17	2	6	28	16	12	30	4	27	13	10	18	5	20	8	11	7	3	9	21	23	26	19	29	24	1
2	1	27	6	4	14	18	21	29	10	22	3	23	8	13	26	12	20	16	19	5	25	11	15	17	9	2	24	28	7	30
3	18	22	4	30	16	8	21	23	3	7	1	28	24	29	15	10	25	9	12	27	13	26	20	19	5	2	6	17	14	11
4	23	27	9	5	13	1	12	30	8	2	6	7	22	11	18	4	20	15	21	16	3	24	25	17	19	29	28	10	14	26
5	29	9	16	14	21	8	12	7	10	1	2	19	20	4	24	17	3	26	22	11	23	27	13	25	5	18	30	15	28	6
6	24	19	25	1	21	11	23	29	5	15	12	16	9	7	20	10	22	28	30	3	4	6	26	13	2	17	14	8	18	27
7	8	17	5	18	16	9	12	28	15	29	22	26	7	1	19	20	10	21	2	3	25	4	6	30	14	11	24	13	27	23
8	23	29	22	4	13	27	30	26	10	20	18	6	25	9	19	15	2	28	7	14	1	12	8	16	3	11	5	24	17	21

*DOP = Date of planting

Spacing between plants was 2 m x 2 m. Planting was done on ridges raised 30 cm off the ground.
The genotypes are numbered as detailed in Appendix 5.1

Appendix 5.4 Progeny selections from the 12 x 12 and 30 x 30 polycrosses

No	Genotype	Root shape	Root Surface defects	Colour Chart	PSC	Flowering Habit	RDM (%)	UMRN	UMRM (g)	MRN	MRM (g)	VFM (g)	CK	SP	WD
1	L7-Chingovwa/36	obvate		RHS:9/2 1355U	brownish orange	none	35.18	3	50	1	120	25	1	1	2
2	L7-Unknown 2/1/49	curved		RHS:9 137U	orange	sparse	35.95	3	85	1	120	50	1	2	3
3	L7-W-119/107	elliptic		RHS:9 137U	purple	none	36.98	2	100	1	130	90	1	1	2
4	L7- Chingovwa/103	curved	contrictions	RHS:9/3 7507U	copper	none	36.35	1	25	1	130	45	1	1	3
5	L7-W-119/13	elliptic		RHS 9/2 1355U	copper	moderate	39.34	2	5	1	135	140	1	1	2
6	L7-Chingovwa/50	obvate		RHS:9/2 1355U	cream	profuse	37.49	1	15	1	150	80	1	1	5
7	L7-Chingovwa/86	elliptic		RHS:9/2 1355U	cream	none	35.64	1	15	1	170	20	1	1	3
8	L7-Unknown 2/1/48	long elliptic		RHS:9/2 1355U	brown	sparse	39.11	4	140	1	190	115	1	1	3
9	L7-Chingovwa/84	long elliptic		RHS:9/3 7507U	cream	sparse	36.73	2	95	1	195	30	1	1	2
10	L7-Unknown 2/1/109	elliptic		RHS:9/3 1355U	cream	none	39.48	3	110	1	200	50	1	1	1
11	L7-Chingovwa/62	elliptic		RHS:9/2 1355U	brownish orange	profuse	34.98	0	0	2	205	20	1	1	1
12	L7-Chingovwa/64	long elliptic		RHS:9/3 750U	cream	none	40.64	1	25	1	205	25	2	1	4
13	L7-W-119/61	curved		RHS 9 137U	purple	moderate	37.68	0	0	2	225	30	1	1	3
14	L7-Chingovwa-c/58	round elliptic		RHS:9/2 1355U	copper	sparse	35.83	0	0	2	235	40	1	1	3
15	L7-Unknown 2/1/110	round		RHS:9/1 123U	copper	none	38.79	2	15	2	240	70	1	1	1
16	L7-Excel/118	long elliptic		RHS:9 137U	orange	none	37.66	1	30	1	265	35	1	1	2
17	L7-Unknown 2/1/158	obvate		RHS:9 137U	copper	sparse	48.63	3	40	2	300	140	1	1	1
18	L7-Chingovwa-c/66	obvate		RHS:9 137U	pink	moderate	38.99	0	0	1	300	55	1	1	3
19	L7-Unknown 2/1/40	elliptic		RHS:9 137U	orange	sparse	37.25	1	5	1	305	40	1	1	2
20	L7-199062.1/17	round		RHS:9 137U	orange	profuse	36.65	5	171.2	1	337.5	205.3	1	1	5
21	L7-Chingovwa/16	ovate		RHS:9/2 1355U	cream	profuse	36.32	2	40	2	355	95	1	1	3
22	L7-Unknown 2/1/5	long elliptic		RHS:9 137U	pink	sparse	44.28	6	200	1	370	140	1	1	4
23	L7-W119-c/63	elliptic		RHS:9 137U	orange	profuse	53.21	2	65	2	375	120	1	1	3
24	L7-Unknown 2/1/95	obvate	grooves	RHS:9/2 1355U	copper	none	39.35	3	100	2	495	85	1	1	1
25	L7-W119-c/22	obvate	contriction	RHS:9/1 1233U	pink	profuse	36.10	8	300	3	540	135	1	1	2

PSC = Predominant skin colour, RDM = Root dry mass, UMRN = Number of unmarketable roots. UMRM = mass of unmarketable roots, MRN = Number of maketable roots, MRM = mass of marketable roots, VFM = Vine fresh mass, CK = Cracking, SP = Sprouting, WD = Weevil damage

Appendix 5.4 (Continued)

No	Genotype	Root shape	Root Surface defects	Colour Chart	PSC	Flowering Habit	RDM (%)	UMRN	UMRM (g)	MRN	MRM (g)	VFM (g)	CK	SP	WD
26	L7-199062.1/95	elliptic		RHS:9/2 1355U	copper	moderate	35.65	0	0	2	555	85	1	1	3
27	L7-Unknown 2/1/66	obvate	grooves	RHS:9 137U	copper	none	40.00	4	265	2	610	180	1	2	2
28	L7-15/1/17	obvate	alligator skin	RHS:9 137U	orange	none	35.15	0		3	635	220	1	1	3
29	L7-Chingovwa/55	obvate		RHS:9 137U	copper	profuse	41.46	3	110	3	700	230	1	1	2
30	L7-Chingovwa-c/24	elliptic	constrictions	RHS:9/3 750U	cream	moderate	36.25	1	10	2	725	120	1	1	2
31	L7-Chingovwa/83	obvate		RHS:9/3 7507U	brownish orange	sparse	36.55	0	0	1	745	105	1	1	1
32	L7-W-119/89	round		RHS 9/2 1355U	copper	profuse	35.95	2	95	1	810	275	1	1	2
33	L7-Chingovwa-c/56	round	grooves	RHS:9/2 1355U	copper	moderate	37.95	6	15	3	890	130	2	1	3
34	L7-W119-c/65	elliptic		RHS:9 137U	copper	moderate	35.60	11	315	4	940	330	1	1	2
35	L7-Chingovwa-c/36	ovate	alligator skin	RHS:9 137U	copper	moderate	38.25	2	85	4	1210	325	4	1	4
36	L7-Chingovwa/22	obvate		RHS:9/2 1355U	cream	none	36.30	2	40	5	1265	235	1	1	5

PSC = Predominant skin colour, RDM = Root dry mass, UMRN = Number of unmarketable roots. UMRM = mass of unmarketable roots, MRN = Number of maketable roots, MRM = mass of marketable roots, VFM = Vine fresh mass, CK = Cracking, SP = Sprouting, WD = Weevil damage
*Scores for mole damage, weevil damage, and cracking were as follows: 1 = No symptom, 2 = 1-5 roots affected in a plot of 20 plants, 3 = Many roots affected slightly (5-10% of root area), 4 = All roots affected moderately (11 - 25% of root area), and 5 = All roots affected severely (>25% of root area). Flesh colour was scored as follows: 0 = white, 1 = cream, 2 = light orange, 3 = medium orange, 4 = orange, and 5 = dark orange.

Appendix 5.5 Soil nutrient analysis of the five experimental sites for the G x E trial

Environment	Designation	pH	Soil nutrients*											
			P	Ca	Mg	Na	K	Cu	Zn	Mn	Fe	%N	%C	CEC
Mansa-Mufulira	E1	4.6	4	25	22	-	5	7	trace	22.2	39.1	0.11	1.5	-
Mutanda-West	E2	4.3	11	32	10	-	17	-	1.8	-	16.7	-	0.88	-
Mansa-Main	E3	4.1	10	53	19	2.2	26.8	0.4	2.5	12	41.4	0.8	1.17	3.84
Mutanda-East	E4	4.3	7	85	19	2.1	24.6	1	1.3	23	42	0.8	1.08	2.44
GART	E5	4.1	2	30	14.7	-	6	-		14.7		0.7	1.02	

*Units are ppm where not indicated

Chapter 6: Overview of the research findings

6.1 Introduction

Sweetpotato is generally regarded as one of the crops with the potential to alleviate vitamin A deficiency in humans because of the moderate to high levels of β-carotene in orange to deep orange coloured root flesh. Presently, however, most of the genotypes grown in Zambia are white fleshed, hence low in β-carotene. A breeding programme with the overall objective of incorporating β-carotene expression in consumer-preferred local genotypes with high root dry mass (RDM) was initiated at Mansa Research Station, Zambia in 2005. The research outcomes of this breeding programme which have been presented in this thesis, effectively constitute the first step toward contributing to the alleviation of vitamin A deficiency in Zambia through the bio-fortification of sweetpotato. These first steps were achieved by pursuing the following main objectives:

- Understanding, through a participatory rural appraisal, consumer preferences for sweetpotato genotypes for specific purposes;
- Collecting and analyzing sweetpotato germplasm for yield and nutritional traits, thereafter selecting parents for a β-carotene breeding programme;
- Identifying the gene action that influences root yield and secondary traits for the development of efficient breeding strategies for generating sweetpotato genotypes with high β-carotene and RDM; and
- Evaluating sweetpotato genotypes across locations to determine the magnitude of G x E interaction for β-carotene content, RDM, harvest index (HI), vine fresh yield (VFY), and root fresh yield (RFY), and to identify stable and high performing genotypes.

6.2 Sweetpotato production constraints and end-user preferences

In order to ensure the products of the proposed breeding programme would be acceptable to farmers, farmers were involved in the formulation of the selection criteria to be employed in developing new genotypes with improved β-carotene expression. To this end a survey was conducted to understand consumer preferences for sweetpotato in three districts of Zambia. An interdisciplinary team used participatory rural appraisal (PRA) research tools to collect data from

three agricultural camps in each district. Ten households were targeted per agricultural camp. Pairwise comparisons were employed for ranking preferred products or attributes.

The respondents identified a number of sweetpotato attributes they preferred. The most common preference was root sweetness (listed by about 35 % of respondents) followed by the root yield (listed by 23% of respondents). The third most common preference was a tie between early maturity and good storage ability (both listed by 9% of respondents). Other prominent preferences were for additional taste attributes and storability of both roots and vines. Many of the selection criteria used subsequently in the breeding programme (such as good root storage, good taste, low fibre, high dry mass, leaves that make a good vegetable and resistance to pest and diseases) were identified by means of a survey. These farmer and consumer preferences identified during the PRA will continue to guide breeding objectives in developing orange fleshed sweetpotato cultivars with further desirable traits.

6.3 Evaluation of sweetpotato germplasm for yield and β-carotene based on farmer preferences

Sixty four germplasm accessions collected in four districts of Luapula Province in Zambia were evaluated at Mansa Research Station in an 8 x 8 triple lattice field trial. Considerable phenotypic variation was noted for the traits of interest: RDM, HI and β-carotene. Such sufficient phenotypic variation, preferably coupled with preferably high heritability, increases the likelihood of obtaining genetic gain for the traits under selection.

A selection index for HI, RDM, and good storage traits was used to select 10 best performing accessions for further evaluation and possible release but also for use as parents in a polycross. The mean RDM composition of the 10 selected parents was 32%, higher than the 28% of the popular cultivar, Chingovwa. The HI of all 10 selected parents was greater than 80% and their mean marketable root yield was 3 t above the grand mean (8.9 t ha^{-1}).

The selection index greatly facilitated the identification of genotypes that had desirable combinations of the important traits under consideration. Increasing the quantitative expression of any one of these traits without adversely affecting the expression of the other traits necessitated co-selecting all the traits. The 10 selected parents were subsequently used in a

polycross conducted at Mansa Research Station in 2006 and 2007. Some of the resultant progeny have expressed the desired high β-carotene content in combination with high RDM.

6.4 Gene action controlling β-carotene content, root dry mass, and root fresh yield

A study of the quantitative inheritance of important traits in sweetpotato was conducted by means of 5 x 5 full diallel (excluding selfs). Twenty crosses with 20 F_1 progeny per cross and their five parents, were evaluated in a 5 x 5 triple lattice field trial.

The cross mean squares of the four traits were highly significant ($p<0.001$). The general combining ability (GCA) and specific combining ability (SCA) mean squares were significant for β-carotene content ($p<0.001$), RDM ($p<0.001$), HI ($p<0.001$), and RFY ($p<0.001$). The ratios of GCA to SCA variances were 0.76 for both β-carotene content and HI, 0.68 for RFY and 0.92 for RDM indicating that additive gene action was predominant in the inheritance of the traits. The two high β-carotene parents used in this study exhibited high, positive GCA effects, indicating that additive gene action was predominant in the inheritance of β-carotene. However, high β-carotene parents (1 and 3) with high, positive GCA effects did not necessarily result in desirable progeny in every cross as some of their progeny were low in β-carotene. Therefore, parents to be used in specific crosses should also be selected on the basis of their SCA effects and the actual performance of the cross. In support of this argument, high RDM parents that had positive and highly significant ($p<0.001$) GCA effects produced only one cross, 5x1, with positive (0.6) and significant ($p = 0.01$) SCA effects. The best performing progeny for RDM were, however, obtained from this cross.

The estimates of narrow sense heritability were 20.9% for β-carotene content, 29.1% for HI, 34.9% for RFY and 76.3% for RDM, suggesting that rapid genetic gains should be possible with mass selection breeding techniques based on the phenotype of the parent for RDM but progress will be slow for β-carotene content HI, and RFY. From the above results, it can be concluded that GCA or SCA effects alone or in combination cannot be used for selecting parents for a hybrid programme without considering the actual performance of the progeny within a cross.

6.5 Evaluation of G x E interaction for beta-carotene content and root dry mass

The effect of G x E interaction on β-carotene content, RDM, HI, and RFY of 15 sweetpotato progeny from selected two polycrosses was investigated in five diverse locations in Zambia. The locations represented the major sweetpotato growing agroecologies in the country. The two locations evaluated in the 2007/8 season and the three locations evaluated in the 2008/9 season were collectively considered as five environments. A randomised complete block design with three replications was used to evaluate the 15 progeny at each location.

The G x E analysis was conducted using the additive main effects and multiplicative interaction (AMMI) model. The performance of genotypes was dependant on the environment for all the traits considered. The high G effects and relatively low G x E for β-carotene content and high G effects for RDM, imply that evaluation and selection can be accomplished in fewer environments to identify genotypes with high and stable performance. From the AMMI analysis, progeny G2, G6, and G8 were identified as stable across environments for both β-carotene content and RDM. Genotype G3 was specifically adapted to environments E3, E4, and E5 for RFY, and had the highest mean β-carotene content (9.4 mg 100 g^{-1}) and high mean RDM (35%) across the environments. The results suggest that it is possible to breed sweetpotato genotypes for cultivation in Zambia that have high and stable performance for β-carotene and RDM. This study has revealed how important it is to have a range of test environments that is broadly representative of the target environments. Information on the nature of the G x E is necessary to decide whether to breed for specific or general adaptation to environments

6.6 Breeding progress achieved

With the help of farmers, 10 genotypes were selected as being acceptable for use as parents for the sweetpotato breeding programme at Mansa Research Station in Mansa. Progeny from the 5x5 diallel that were superior to their parents will be further evaluated in multilocational trials for their adaptability. From the AMMI analysis three progeny from the polycross were identified with stable and high performance for both β-carotene content and RDM. One other polycross progeny was best suited to three of the five test environments and had the highest β-carotene content and high RDM. The superior polycross progeny are currently being multiplied for further evaluation in on-farm trials during the 2009/10 season using different farming systems before they are recommended for release.

6.7 The way forward

Once the performance of the selected genotypes has been verified through multilocational and, on-farm trials they will be recommended for release in the target environments. Meanwhile, conclusions drawn from the statistical analyses will be employed to provide guidance in the planning of future breeding trials. More hand and open pollinated crosses will be made in the continued endeavour to develop new cultivars that are even more superior for the important traits, particularly β-carotene content and root dry mass.