FARMERS' PERCEPTIONS AND COPING STRATEGIES WITH SWEET POTATO WEEVIL AND CHARACTERIZATION OF SWEET POTATO GENOTYPES FOR DIVERSITY AND RESISTANCE TO *Cylas puncticollis* BOHEMAN IN KENYA

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Farmers' perceptions and coping strategies with sweet potato weevil and characterization of sweet potato genotypes for diversity and resistance to *Cylas puncticollis* Boheman in Kenya

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DECLARATION

This thesis is my original work and has not been presented for a degree in any other university

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DEDICATION

This thesis is dedicated with deepest appreciation to my late mother Theresa and my siblings (Jackline, Calvine and Bobrayan) for their love and support that was always my inspiration during many years of hard work.

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LIST OF ABBREVIATIONS AND ACRONYMS

AACC	Association of American Cereal Chemists
AFLP	Amplified fragment length polymorphism
ARS	Agricultural Research Service
ATC	Agriculture Training College
AVRDC	Asian Vegetable Research and Development Center
CABI	Centre of Agriculture and Bioscience International
CIAT	International Center for Tropical Agriculture
CIP	International Potato Center
CTAB	Cetyl Trimethyl Ammonium Bromide
DAP	Diammonium phosphate
DNA	Deoxyribonucleic Acid
EDTA	Ethylenediaminetetraacetic acid
GOK	Government of Kenya
ISSR	Inter-simple sequence repeat
KALRO	Kenya Agriculture and Livestock Research Organization
LD	Lethal Dose
LSD	Least Significant Difference
MAB	Marker Assisted Breeding
NaCRRI	National Crops Resources Research Institute
OFSP	Orange Fleshed Sweet Potato
PCR	Polymerase Chain Reaction
RAPD	Random Amplified Polymorphic DNA
RCBD	Randomized Complete Block Design
RFLP	Restriction Fragment Length Polymorphism
SSR	Simple Sequence Repeats
UPGMA	Unweighted Pair-Group Method with Arithmetic Average
USDA	United States Department of Agriculture

ABSTRACT

Sweet potato (*Ipomoea batatas* (L.) Lam.) contributes significantly to food security and income of subsistence farmers in Kenya. However, productivity of the crop is constrained by several biotic, abiotic and socio-economic factors. Amongst the biotic constraints, insect pests such as the sweet potato weevil (*Cylas* spp.) cause significant yield losses. However, in Kenya, there is limited information on farmers' perception and management of *Cylas* spp. and on diversity among cultivated sweet potato genotypes. The objectives of this study were to: (i) Assess farmers' perceptions and coping strategies to the sweet potato weevil; (ii) Analyze variation among selected sweet potato genotypes using agro-morphological, molecular and nutritional characters, and; (iii) Screen selected sweet potato (*Ipomea batatas* L.) genotypes for resistance to the sweet potato weevil. Firstly, participatory rural appraisal approach was conducted in the year 2012 in Homa Bay County where 269 farmers were interviewed on farmers' perceptions and coping strategies against the sweet potato weevil (*Cylas* spp.). This study revealed that *Cylas* spp. was the most problematic (93.3%) pest. Many farmers (90.7%) were not aware of sweet potato genotypes that had field resistance to *Cylas* spp. The most commonly used methods by farmers to manage *Cylas* spp. were re-ridging during weeding (21.2%) followed by covering exposed roots with soil (12.6%). Secondly, field experiments were conducted on-station in 2014 at two sites (ATC -Miyare and -KALRO Embu) using 68 sweet potato genotypes arranged in a Randomized Complete Block Design. Data were recorded on variation in agro-morphological, molecular and nutritional characters. On the basis of quantitative agro-morphological traits, Analysis of variance revealed significant ($p \leq 0.05$) differences among sweet potato genotypes. Genotypes Nyautenge (16.82 t/ha) and Kemb 10 (17.04 t/ha) had the highest average root yield at ATC Miyare and KALRO Embu respectively while, genotypes 56682-03 (0.84 t/ha) and K/KA/2004/215 (1.07 t/ha) had the least average root yield at ATC -Miyare and KALRO -Embu respectively. The genotypes were variable in respect to all qualitative traits studied. Both quantitative and qualitative based dendrograms did not group the genotypes according to geographical area of origin or shared names. On molecular approach, 13 simple sequence repeat (SSR) markers were used to determine genetic relationship among the sweet potato genotypes. The SSR markers were highly polymorphic (0.2723) and cluster analysis divided the genotypes into two major groups. However, the genotypes did not form specific groups according to geographic regions or shared names. Nutrionally, the genotypes significantly ($p \leq 0.0001$) differed in dry matter, root protein, root carotenoids, root sucrose and root starch contents but dendrograms did not group the genotypes in relation to their origin or shared names. Genotype Nyautenge had a stable high yield (16.82 t/ha at ATC -Miyare and 15.23 t/ha at KALRO -Embu) and high dry matter content (40.14% at ATC -Miyare and 32.26% at KALRO -Embu) at both sites. However, the same genotype rated very low in other equally important nutrients like total carotenoids and sucrose contents at ATC -Miyare and KALRO -Embu. Genotypes Kenspot 1, Saly boro, 91/2187, 9 Nduma, Kenspot 3 and Kenspot 2 had high dry matter contents at both sites and hence recommended for inclusion in future breeding

programmes. Thirdly, fifty-one selected sweet potato genotypes were evaluated for their resistance to *Cylas punticollis* Boheman (Coleoptera: Brentidae) in a controlled experiment of no-choice arena from November, 2015 to February, 2016. The 51 evaluated genotypes were significantly ($p \leq 0.0001$) different in their resistance to *C. puncticollis* damage. The study revealed that no genotype was completely resistant to weevils but genotypes Obugi (5.00 adults) and 5 Nyandere (5.00 adults) were the highly resistant to *C. puncticollis* while genotypes Tainung (25 adults), Naspot 1 (24.33 adults), Kenspot 5 (22.67 adults) and Fundukhusia (22.67 adults) were the most susceptible to *C. puncticollis* damage. Resistance to weevils was negatively correlated (-0.71) to dry matter content and positively correlated to starch (0.46) and sucrose (0.48) contents. In conclusion, genotype Obugi is a stable high yield performer (9.21 t/ha and 9.55 t/ha in ATC -Miyare and KALRO -Embu respectively) and has a high resistance to *C. puncticollis* as compared to Naspot 1 (susceptible check) and Santo Amaro (resistant check). Other genotypes rated in this study as medium resistant to *C. puncticollis* and had earlier recorded high yields at KALRO -Embu are Santo Amaro (11.49 t/ha) and Wera (9.22 t/ha). However, these genotypes recorded low yields in ATC -Miyare and thus may not be suitable for ATC -Miyare site and its surrounding. Genotype Tainung was found to be the most inadequate since it was the most susceptible (25 adults) to weevils, low performing in yield (1.44 t/ha at ATC -Miyare and 5.70 t/ha at KALRO -Embu) and was low in dry matter content (21.40% at ATC -Miyare and 24.39% at KALRO -Embu) as compared to others. All the above-mentioned traits can make the genotype not to be preferred by many farmers. Nonetheless, the genotype has got a high carotenoid content (27.55 µg/g at ATC Miyare and 30.57 µg/g at KALRO Embu) as compared to other genotypes and thus suitable for addressing vitamin A defficiency in the society.

CHAPTER ONE
INTRODUCTION

1.1 Sweet potato

Sweet potato is one of the world's most important food crops (Tortoe, 2010). The crop is the world's sixth most important food crop, after rice (*Oryza sativa* L.), wheat (*Triticum aestivum* L.), maize (*Zea mays* L.), potato (*Solanum tuberosum* L.), and cassava (*Manihot esculenta* Crantz) (CIP, 2010a). It is grown as a starchy root crop throughout the tropical, sub-tropical and frost-free temperate climate zones in the world (ICAR, 2007) where it supports more people per unit area than any other crop (Okada *et al*., 2002). The crop has flexible planting and harvesting periods such that it can be harvested within 4 months of planting, and roots store well when left in the ground for a period of six to twelve months (Kapinga *et al.*, 1995; Karyeija *et al*., 1998).

1.2 Sweet potato utilization

Sweet potato is grown for food, feed and income generation in many countries in sub-Saharan Africa (Fugile, 2007; Low *et al*., 2009; Khalid *et al.,* 2013; Pedrosa *et al.*, 2015). It is an important food security crop, often crucial during famine periods due to its excellent drought tolerance and rapid production of storage roots (Kapinga *et al*., 2003; Mukhopadhyay *et al*., 2011). All plant parts have economic and nutritional utility (Antiaobong and Bassey, 2009). The vine tips and leaves constitute an important source of vegetable proteins, minerals and vitamins (Alghali and Munde, 2001); the vines are used as green fodder for cattle (Nedunchezhiyan *et al*., 2012); while the tuberous roots are an excellent source of carbohydrates in the human diet. The orange fleshed sweet potato has recently attracted attention since its roots are naturally biofortified with β-carotene (Ezeocha, *et al.,* 2010), an important component of combating vitamin A deficiency in children (Korieocha *et al*., 2009). Other benefits of sweet potato roots include its use as a raw material for industrial production of bio-degradable plastics and bio-fuel (Kozai *et al*., 1996a, b).

1.3 Sweet potato production

China is the world's biggest sweet potato producer, and had an output of over 70 million tones in 2016 (Table 1.1). The average annual sweet potato (*Ipomoea batatas* L.) production worldwide was 105.19 million tones in the year 2016 (Table 1.1). Africa's average annual sweet potato production in 2016 was 21.32 million tonnes (20% of the global harvest) cultivated in an area of 4.18 million hectares (Table 1.1). About 58% of the sweet potato produced in Africa in the same year was from Eastern Africa (FAOSTAT, 2018). In East Africa, Tanzania was the largest producer (3.82 million tonnes), followed by Uganda (2.12 million tones), then Kenya (0.73 million tonnes) (Table 1.1). Tanzania and Uganda have also bigger hectarage of land under sweet potato production as compared to Kenya (FAOSTAT, 2018). In Kenya, sweet potato production is practiced in the western, central and coastal areas of the country. Out of this, over 80% is grown in the Lake Victoria basin with Kakamega, Bungoma, Busia, Homa Bay, and Kisii Counties having high acreages of this crop.

Although the productivity of sweet potato in Kenya (14.78 t/ha) was higher than that of Tanzania (5.03 t/ha) and Uganda (4.41 t/ha) in the year 2016 (Table 1.1), it is still low compared with the productivity in China (21.51 t/ha) (FAOSTAT, 2018). This means that there is still room for improvement of sweet potato production in Kenya which will increase food security and farmers' incomes in the country. In order to further improve the crops' productivity in Kenya, there is need to analyse the factors that limit sweet potato production.

Table 1.1: Sweet potato production in some selected countries/regions for 2016

Region/Country	Average area harvested (ha)	Average production (tonnes)	Productivity (tonnes/ha)
World	8,623,973	105,190,501	12.20
Africa	4,187,768	21, 316,860	5.09
China	3,291,048	70,793,704	21.51
Kenya	47,184	697,364	14.78
Uganda	482,241	2,126,989	4.41
Tanzania	759,542	3,822,872	5.03

Source: FAOSTAT, 2018.

1.4 Constraints to sweet potato production

Most sweet potato genotypes grown in Africa are low yielding landraces that are white, cream, yellow or orange fleshed (Loebenstein and Thottappilly, 2009). Yields vary greatly according to cultivars, local climatic conditions and cultural techniques (Antiaobong, 2007). Sweet potato production is constrained by several factors namely: socio-economic (shortage of improved varieties, shortage of clean planting materials), abiotic (drought, poor soil fertility, heat) and biotic stresses (pests and diseases) (Carey *et al.*, 1997; Karyeija *et al.*, 1998; Gibson and Aritua, 2002; and Aritua *et al.*, 2007).

Sweet potato weevil (*Cylas* spp.) is one of the most devastating biotic factors limiting sweet potato production in Eastern Africa (Okonya *et al.*, 2016a; Okonya and Kroschel, 2013). Although different sub-species of sweet potato weevils can be found in different geographical locations, their mode of feeding remains the same (Capinera, 2001). *Cylas* spp. cause serious damage to all parts of sweet potato plant throughout their life cycle, from egg to adult. When laying eggs, female weevils excavate cavities and create egg-laying punctures in the roots (Hue and Low, 2015). The eggs are laid below the surface of the roots and covered with dark colour excrement from the female adults (Capinera, 2001). As a result of the unsightly punctures, the appeal of the roots and market price of sweet potato become greatly reduced, resulting in food insecurity and major economic losses. In Kenya there is no documented information on farmers' awareness on sweet

potato in regard to the weevil. Furthur there is scarcity of information on how farmers in Kenya manage the sweet potato weevil.

Use of resistant genotypes is one of the most effective and cheapest weevil control method that can be used by small-scale farmers (Ngailo *et al*, 2016). Although there is some documention on weevil resistant sweet potato genotypes grown in Kenya (Kivuva *et al.,* 2015; Gruneberg *et al.,* 2015; Kwach et al., 2008), most commonly grown genotypes in the country have not yet been evaluated for their resistance to the weevil. This calls for further screening of sweet potato genotypes for their resistance to the sweet potato weevil.

1.5 Sweet potato genetic diversity

Sweet potato germplasm is estimated at more than 1,000 accessions in the world but genetic studies as a basis for the development of cultivars is still limited. A number of scientists including Gichuki *et al.,* (2003); Karuri *et al.,* (2010); Tumwegamire *et al.,* (2011); and Koussao *et al.,* (2014) have used different approaches including agro-morphological, biochemical and molecular markers to characterize sweet potato and its close relatives. However, information on many traits of economic importance is still scanty. In addition, even though sweet potato genotypes have been characterized in relation to their reaction to pests, diseases and drought (Karuri *et al.,* 2009; Makanginya, 2012) there are limited studies on the reaction of sweet potato genotypes to weevil infestation.

1.6 Statement of the problem

Sweet potato is consumed as a staple food in some parts of Kenya thus contributing to food and nutrition security. The crops' production in Kenya has been constrained by lack of varieties that can give high yields, high dry matter, high starch and high β-carotene with adequate resistance to sweet potato weevils. Production loss due to infestation by sweet potato weevil (*Cylas* spp.) has been shown to reach up to 100%. In

Kenya, there is no documented information on farmers' awareness on sweet potato in regard to the weevil. Also, there is limited information on sweet potato genotypes available in Kenya in response to weevil infestation and mode of infestation. Further, sweet potato germplasm in the country has not been adequately characterized for variation in characters that would be useful in breeding programmes. Such characters could either be directly selected for by the plant breeders or used for indirect selection of desirable genotypes. It is therefore important to evaluate existing sweet potato genotypes on the basis of variation in agro-morphological, molecular and nutrition traits and screen for their resistance to the sweet potato weevil.

1.7 Justification of the study

Sweet potato (*Ipomoea batatas*) is grown throughout the tropical, sub-tropical and frost-free temperate climate zones (ICAR, 2007). The crop is one of the world's most important versatile yet underutilized food crop grown for its storage roots (Tortoe, 2010). It is a short cycle crop which usually matures in 3 to 4 months (Anyaegbunam *et al.,* 2008), and may be grown two or three times in a year (Okonkwo, 2002).

Over 300 sweet potato lines are maintained in various KALRO stations in Kenya. These lines are either landraces collected from farmers' fields or breeding lines obtained from International Center for Tropical Agriculture (CIAT). Traditional naming systems of the landraces are often based on traits that are perceived subjectively and therefore in so doing it is not uncommon to find confusion between varieties or use of different names for the same cultivar (Elias *et al.,* 2001). This calls for proper identification of the existing sweet potato varieties through characterization so as to avoid such confusion that results in the traditional naming of varieties. Further, the variation within the collection of sweet potato germplasm available in Kenya is largely unknown since only a few accessions have been characterized in previous studies (Gichuru *et al.,* 2006; Karuri *et al.,* 2010). If the germplasm is to be utilized in breeding programmes, or if

potential duplicates within it has to be identified, then there is need to undertake further characterization studies.

Both improved varieties and landraces that are grown succumb to several pests, including the most devastating sweet potato weevil. As a pest, the sweet potato weevil severely reduces yields and greatly affects the quality of damaged roots. This has led to a potential decrease in sweet potato production which has become a threat to food security in the country. Continued use of susceptible genotypes and lack of effective control measures to *Cylas* spp. contribute to low yields. Both chemical and cultural control methods have been reported to be ineffective against *Cylas* spp. Therefore, use of resistant genotypes remains the most effective and cheapest method for small-scale farmers.

Host plant insect resistance in sweet potato has been documented in the literature but complete resistance to weevils remains non-existent in commercially acceptable cultivars despite years of research and breeding (Low *et al.,* 2009; Okonya *et al.,* 2016a). Genotypes do vary in susceptibility and the environment greatly affects resistance to the sweet potato weevil (Mao *et al.,* 2004). Several approaches have been used over the years by several institutions to screen and select varieties for weevil resistance. The need is pressing for weevil-resistant sweet potatoes (*Ipomoea batatas*) that meet traditional and market preferences and the demands of commercial handlers and processors. The use of local genetic resources is necessary since they are well-adapted to local agro-ecologies and possess farmers-preferred traits.

This study sought to contribute to the existing literature on sweet potato weevil by assessing farmers perceptions, coping strategies and characterizing sweet potato genotypes for diversity and resistance to the pest. This will be undertaken through a survey, field trials at two locations and laboratory experiments.

1.8 Objectives

1.8.1 Overall objective

To assess farmers' perceptions and coping strategies to the sweet potato weevil; and to characterize and screen selected sweet potato (*Ipomea batatas* (L) Lam). genotypes for their resistance to the sweet potato weevil (*Cylas puncticollis* Boheman).

1.8.2 Specific objectives

1. To assess farmers' perceptions and coping strategies against the sweet potato weevil in Homa bay County.
2. To analyze variation among selected sweet potato *(Ipomea batatas* L.) genotypes using agro-morphological, molecular and nutritional characters.
3. To screen selected sweet potato (*Ipomea batatas* L.) genotypes for resistance to the sweet potato weevil (*Cylas puncticollis*).

1.9 Hypotheses

1. Farmers in Homabay County are not aware of and have no coping strategies against the sweet potato weevil.
2. No variation exists among sweet potato genotypes in relation to agro-morphological, molecular and nutritional characters.
3. Sweet potato genotypes do not differ in their resistance to the sweet potato weevil (*Cylas puncticollis*).

CHAPTER TWO
LITERATURE REVIEW

2.1 Description, origin and agro-ecological requirements of sweet potato

Sweet potato (*Ipomoea batatas* L. is an important food security crop in many developing countries (Korada *et al.*, 2010). The crop is a dicotyledonous plant that belongs to the family *Convolvulaceae* (Tortoe, 2010). The family includes 50 genera and over 1000 species of which *Ipomoea batatas* is the only species of economic importance as food. The genus *Ipomoea* consists of about 600 to 700 species including sweet potato (Cao *et al.*, 2009; Vaeasey *et al.*, 2008). *Ipomoea* spp. has been mentioned as a leaf vegetable in Ethiopia. Sweet potato is hexaploid with 2n = 6x = 90 chromosomes (Prakash *et al*., 1996). Central America has been documented as the origin and the primary centre of diversity of the currently cultivated sweet potato (Srisuwan *et al.,* 2006; Low *et al.,* 2009). Sweet potato is believed to have been introduced to Africa by Portuguese during the 16^{th} and 17^{th} century and East Africa is one of the secondary centres for sweet potato diversity (Gichuki *et al.,* 2003).

Although sweet potato has an outcrossing mating system, it is propagated vegetatively with each cultivar considered a clone (Prakash *et al*., 1996). Self-incompatibility in the flowers results in allogamy, inceasing genetic heterozygosity (Thompson *et al*., 1997). Sexual compatibility is related to a multiallelic sporophytic self-incompatibility system expressed in the stigma (Diaz *et al*., 1996). The growth habit of sweet potato is typically herbaceous and perennial. However, it is grown as an annual plant by vegetative propagation using either storage roots or stem cuttings. The crop is predominantly prostrate with a vine system that expands rapidly horizontally on the ground. Variations from this include the erect, semi-erect, spreading, and extremely spreading types (Huaman, 1999).

Sweet potato is grown from 48°N to 40°S of the equator with altitudes ranging from 0 to 3000 m above sea level (Woolfe, 1992; Vaeasey *et al.,* 2008; Low *et al.,* 2009; Troung *et al.,* 2011). However, Stathers *et al*. (2013) reported that varieties growing at ≥2,500m above sea level have poorer taste and low dry matter. This is because low temperatures at high altitudes impact upon sweet potatoes growth negatively by reducing their photosynthetic ability and rate of translocation of carbohydrates from shoots to the roots. Sweet potato being a tropical (warm weather) crop, dry matter and sugar production is usually related to ambient temperature. The crop can grow at temperatures of between 15 – 35 ^{o}C with an optimum of 20 – 25 ^{o}C (Stathers *et al*., 2013). Temperatures below 12 °C and above 35 ^{o}C retard sweet potato growth (Kuo, 1991). Dry matter production increases with increasing temperatures from 20 ^{o}C to 30 ^{o}C, but declines at temperatures beyond 30 ^{o}C (Kuo, 1991). The crop grows best with a well distributed annual rainfall of 600-1600mm (Low *et al.,* 2009). Excess rainfall at early stage of establishment may aggravate weed problem resulting in low yield (Harrison and Jackson, 2011). Prolonged and frequent drought and erratic rainfall cause substantial yield reduction of the crop (Low *et al.,* 2009; Schafleitner *et al.,* 2010). Further, the crop requires full sun light (Troung *et al.,* 2011). Sweet potato can be grown in many types of soils but does best on deep, moderately fertile, sandy loam soils, which produce high quality storage roots with an attractive shape and appearance (Stathers *et al*., 2013). Sweet potato does best on well-drained, slightly acid soils, with optimal pH 5.6-6.6, but can tolerate soils with higher and lower pH (Stathers *et al*., 2013).

2.2 Socio-economic, abiotic and biotic constraints to sweet potato production

2.2.1 Socio-economic constraints

There are several socio-economic constraints which affect sweet potato production. These include inadequate availability of high yielding, disease resistant planting materials, poor crop management (e.g. inappropriate or no fertilizer application and

weeding) and lack of post-harvest technologies (Kulembeka *et al.,* 2005; Tairo *et al.,* 2005; Ndunguru *et al.,* 2009).

According to FAOSTAT (2018), Kenya's sweet potato productivity (14.78 t/ha) is still low compared to the productivity of other countries like China (21.51 t/ha). This means that there is still room to improve sweet potato productivity in Kenya in order to address food insecurity and increase farmers' income. Further, among the East African countries, Kenya has the lowest average production of the crop (697,364 tonnes) compared to Uganda (2,126,989 tonnes) and Tanzania (3,822,872 tonnes) (FAOSTAT, 2018). This means that many farmers in Kenya are not willing to invest in growing this crop. Low production of sweet potato in Kenya is contributed by lack of high yielding varieties with farmers' preferred traits (Karuri *et al.,* 2009). High yielding and farmers preferred varieties are the basis for increased productivity and sustainable development of the crop. Currently, most farmers use local landraces because such genotypes are well adapted to the local agro-ecological environments (He *et al.,* 2006). Though adapted to local agro-ecologies, most landraces are low yielding and late maturing (Masumba *et al.,* 2005). Also, several attempts have been made to use exotic varieties in various agro-ecologies to improve low productivity and evade pest and disease damage (Kapinga *et al.,* 2009; Gasura *et al.,* 2010). However, the exotic varieties have shown relatively poor performance compared to landraces which are well adapted to the farming systems (Gasura *et al.,* 2010). For instance, Mwanga and Ssemakula (2011) reported almost 100% failure of the newly introduced orange-fleshed sweet potato in Uganda. Similar studies in Tanzania indicated that, some of the introductions were rejected by farmers due to low dry matter content, low yields and poor production of vines during recurrent droughts (Kulembeka *et al.,* 2005). A report by Ruto (2017) indicated that Kemb 10, Kemb 23, SPK 013, SPK 004 and 'Japanese 420009 pumpkin' were some of the recently developed high yielding sweet potato varieties introduced in Kenya by KALRO in collaboration with CIP.

Inadequate post-harvest technologies such as poor storage facilities and improper processing technologies severely affect production and sustainability of the crop (Fugile, 2007; Waddington *et al.,* 2010). Many farmers store sweet potato roots in the ground for a period of six to twelve months (Karyeija *et al*., 1998) which exposes the crop to weevil infestation hence reducing crop yields.

Inadequate extension services limits dissemination and adoption of improved crop husbandry practices. Consequently, farmers continue growing informally disseminated inferior planting materials, which lead not only to persistence of pests and diseases but also negatively affect productivity of the crop (Fugile, 2007; Namanda *et al.,* 2011). Also, poor linkage between farmers and other stakeholders coupled with undeveloped and fragmented infrastructures in rural areas, significantly lowers the productivity of the crop (Kapinga and Carey, 2003; Waddington *et al.,* 2010).

2.2.2 Abiotic constraints

Abiotic constraints which significantly affect sweet potato production include drought and low soil fertility (Fugile, 2007; Namanda *et al.*, 2011). Drought is a significant abiotic constraint that limits the productivity of sweet potato affecting both the quality and quantity of yields (Cattivelli *et al.,* 2008; Namanda *et al.,* 2011). In a participatory rural appraisal, Oduro (2013) reported that drought was among the highly ranked constraints in sweet potato production in Ghana. Although it is documented that sweet potato is drought tolerant, prolonged and frequent dry spells and erratic rainfall cause substantial yield reduction (Johanson and Ives, 2001). Drought not only affects crop growth and development, but also root yield, dry matter content and composition, and pests and disease incidences (Ekanayake and Collins, 2004; Masumba *et al.*, 2005). For instance, during periods of drought weevils infest the crop, roots are not able to form a lot of tubers (yield becomes low), the drying of crop takes place and also there is feeding on the crop by other pests like moles increase since there exists little or no alternative source of food for them.

An *et al.* (2003) reported lower sweet potato yields during the hot-dry season compared to cool-wet season; however, the response varied with genotypes. Genotypes that are susceptible to drought typically do not survive drought or prolonged dry seasons, do not produce volunteer plants, and thus do not provide planting material for the next crop. Besides low dry matter content and susceptibility to viral diseases, the newly introduced orange fleshed sweet potato (OFSP) are unable to withstand drought, which leads to low productivity and unacceptability to farmers (Mwanga and Ssemakula, 2011; Makanginya., 2012). Gibson (2005) reported that their participatory sweet potato breeding and selection trials were ruined by drought and farmers rejected the less drought tolerant varieties. Therefore, drought significantly affects and lowers sweet potato production and productivity.

Majority of the subsistence farmers do not apply both inorganic and organic fertilizers during the crop production. Declining soil fertility constrains sweet potato production as its replenishment is limited by unaffordable high prices of inorganic fertilizers (Elliott and Hoffman, 2010) and unavailability of organic fertilizers. Continuous cropping without addition of organic and inorganic manures has led to a decline in soil fertility and consequently a decline in productivity (Saleh and Zahor, 2007).

2.2.3 Biotic constraints

The production of sweet potato is affected by several biotic constraints such as weeds, diseases and insect pests (Harrison and Jackson, 2011; Lou *et al.,* 2010; Ndunguru *et al.,* 2009; Schafleitner *et al.,* 2010). Weeds may cause severe yield loses when high rainfall occurs early in the growing season (Harrison and Jackson, 2011). However, they can be managed by weeding at six weeks after planting.

Diseases and insects of economic importance are sweet potato virus diseases and sweet potato weevils, respectively (Kivuva *et al.,* 2014). Sweet potato virus disease (SPVD) is distributed worldwide (Gibson *et al.,* 1998; Mukasa *et al.,* 2006). It is the most

devastating disease-causing reduction in plant growth and storage root yields (Gibson, 2005; Gibson *et al.,* 2004; Gibson *et al.,* 1997; Kapinga *et al.,* 2009; Karyeija *et al.,* 2000). The damage caused by SPVD ranges from 50 to 98% (Gibson *et al.,* 1998; Njeru *et al.,* 2004; Tairo *et al.,* 2004). The disease causes strap-shaped leaves, vein-clearing, puckering, chlorosis and stunting in susceptible sweet potato genotypes and yields are much reduced. Additionally, SPVD limits the length of time the roots can be kept in the ground and shorten the storage duration of the harvested crop (Engoru *et al.,* 2005; Tsakama *et al.,* 2010).

The sweet potato weevils (*Cylas* spp.) are considered to be the most important insect pests of the crop (Lebot, 2010). Under field conditions, the two species of African sweet potato weevils, *Cylas bruneus* (Fabricius) and *Cylas punticollis* (Boheman), have been reported to cause yield loss of up to 100% in Uganda, 50% in Tanzania, and 90% in Kenya (Musana *et al.,* 2016). The differences in the reported yield loss due to *Cylas* spp. is attributed by the differences in the abundance of the pest in these countries. The weevils' tunnel and feed on vines and storage roots thereby reducing the quality and yield of the crop (Stathers *et al.,* 1999). Damage to sweet potato by *Cylas* spp. is particularly severe during the dry conditions; as the pest cannot dig in the soil but gains access to sweet potato roots through cracks that appears in the soil as the soil dries out under moisture stress (Muyinza *et al.,* 2007). The use of infected, low yielding planting materials significantly contributes to persistence of insect pests like weevils. A crop that has been in the field for a long time has higher chances of the vines being infected with insect pest.

Other biotic constraints such as sweet potato butterfly (*Acraea acerata* Hewitson), sweet potato whitefly (*Bemisia tabaci* Gennadius), *Alternaria* leaf spot, bacterial rot, black rot, stem blight, *Fusarium* rot, nematodes, millipedes and vertebrate pests such as rats are also a threat to sweet potato production (Ebregt *et al.,* 2004; Johanson and Ives, 2001; Kapinga *et al.,* 1995; Okonya *et al.,* 2016b; Gamarra *et al.,* 2016).

2.3 Diversity of sweet potato genotypes

The cultivated species of *I. batatas* includes plants that are very variable in their morphology (Huaman, 1999) and in their genetic constitution (Koussao *et al.,* 2014; Karuri *et al.,* 2010). The crop exhibits phenotypic diversity as reflected by the skin and flesh colour of the tubers, the shape of roots, leaves and branches, the depth of rooting and maturity period, resistance to pests and diseases and dry matter content of the tubers (Austin and Huaman, 1996).

2.3.1 Importance of genetic diversity

Plant genetic diversity is a prerequisite for an effective plant-breeding programme. In plant breeding programmes, assessment of levels and patterns of genetic diversity is often carried out in order to analyze genetic variability in cultivars and identification of diverse parents for crosses (Barret and Kidwell, 1998). It is a useful and essential tool for parents' choice in hybridization to develop high yield potential cultivars (Haydar *et al*., 2007; Gaur *et al*., 1978) and to meet the diversified goals of plant breeding (Haydar *et al*, 2007).

Genetic diversity is also used to study the taxonomic relationship among genotypes and to choose varieties with good qualities and incorporate them into breeding programmes (Escribano *et al*., 1991; Cartea *et al*., 2003; Balkaya and Ergun, 2008). Hornokova *et al*. (2003) stated that the knowledge of genetic diversity's extent and the identification, differentiation and characterization of genotypes and populations, respectively, provides an informative tool for the detection of duplicates in the collection.

2.3.2 Charaterization of plant germplasm

Sweet potato has a fairly high diversity and is generally distinguished on the basis of agro-morphological traits. Agro-morphological characterization is routinely conducted with internationally standardized agro-morphological descriptors (Lebot, 2010). The usual approach to characterization and evaluation of population involves cultivation of

sub-samples and establishing their morphological and agronomic description (Hayward *et al.,* 1993). Morphological characters have been used to identify the centre of origin and evolution of *Ipomoea batatas* L., (Zhang *et al*., 1996) duplicates in sweet potato collections in Kenya and Burkina Faso (Karuri *et al.,* 2009; Koussao *et al.,* 2014) and in establishment of core collections in Indonesia (Mok and Schmiendiche, 1999).

Morphological/Phenotypic characterization in sweet potato is done by assessing variations in the vine, leaf, flower and storage root characteristics (Huaman, 1991). Despite the environmental influences on plant morphology, this direct inexpensive and easy to use method of estimations was perceived as the strongest determinant of the agronomic value and taxonomic classification of plants (Li *et al.*, 2009). The agronomic characters coupled with reaction to pests, diseases and other stresses have also been used to characterize sweet potato. However, limited success has been achieved with morphological diversity analysis alone (Yada *et al*., 2010a). Therefore, to optimize the characterization efficiency, morphological characterization has now been combined with molecular techniques.

According to La Bonte (2002), when trait expression is environmentally unstable or difficult to evaluate, molecular markers become more useful than the traditional morphological evaluations. Molecular markers (segments of DNA markers) can be used as tools to detect the extent and structure of genetic variation, providing insights into the diversity of crop varieties and potential contributions offered by their wild relatives (Naylor *et al.,* 2004). Hu *et al*. (2003) used inter-simple sequence repeat (ISSR) to investigate the genetic relationships between cultivated sweet potato and its wild relatives. Amplified fragment length polymorphism (AFLP) has been used for studying the historic dispersal of sweet potato (Zhang *et al*., 2004) as well as for assessing the genetic diversity of cultivars and landraces (Zhang *et al*., 2000; Fajardo *et al*., 2002). Microsatellite or simple sequence repeats (SSR) are considered to be the most efficient markers for genetic diversity studies in many plants (Rakoczy-Trojanowska and

Bolibok, 2004) including sweet potato (Zhang *et al*., 2000; Karuri *et al.*, 2010). This is because they are abundant in plant genomes and they demonstrate high levels of polymorphism and are adaptable to automation (Donini *et al*., 1998). In addition, SSR markers are highly co-dominant and can easily be detected on high-resolution gels. Several such markers have been developed for sweet potato (Jarret and Bowen, 1994; Buteler *et al*., 1999; Hu *et al*., 2004) and used successfully for determining the genetic relationship between cultivars derived from hybrid or polycross breeding programs (Hwang *et al*., 2002). For instance, Gichuru *et al.* (2006) and Karuri *et al*. (2010) analysed the diversity among sweet potato cultivars from distinct agro-ecological zones using morphological and SSR markers. However, there is still a large collection of sweet potato germplasm in Kenya and the diversity within it is largely unknown since only a few accessions have been characterized in previous studies (Gichuru *et al*., 2006, Karuri *et al*., 2010, Yada *et al*., 2010b)

2.4. Participatory Rural Appraisal (PRA)

Participatory Rural Appraisal (PRA) is an interactive approach in research that emphasizes local participation, which enables local people to contribute in their own appraisal, analysis and plans (Abdullah *et al.,* 2012). This approach has been widely used to collect information on farmers' needs and challenges to venture in breeding new sweet potato cultivars (Kiiza *et al.,* 2012). PRA is beneficial as it emphasises co-learning, through learning alongside local communities and involving project stakeholders from a variety of backgrounds (Pretty *et al.,* 1995). PRA is useful in identifying the needs, aspirations and constraints of rural indigenous communities (Binns *et al.,* 1997); aims to facilitate information sharing among stakeholders (Abdullah *et al.,* 2012); and increases the possibility that development projects will thrive by tailoring them to local situations (Chambers, 1994). Gibson *et al.* (2011), Mwanga *et al.* (2011) and Kiiza *et al.* (2012) suggested the need to consider farmers and consumers in sweet potato cultivar development and selection for enhanced adoption. The common tools in PRA are semi-structured interviews, focus group

discussions, mapping and modeling, seasonal calendars and activity profiles, matrix scoring and pairwise ranking, local histories and Venn diagrams (Abdullah *et al.,* 2012).

2.5 Sweet potato nutritional characters

Sweet potato (*Ipomoea batatas* L.) is planted widely in tropical and sub-tropical regions. Information about quality attributes of African sweet potato germplasm is very limited. Sweet potato is rich in carbohydrate, starch, mineral, vitamin, protein and β-carotene contents (Ziska *et al*., 2009; Rose and Vasanthakaalam, 2011; Maria and Rodica, 2015). These characters can be used to characterize sweet potatoes since different genotypes vary in their contents.

Sweet potato genotypes vary in colour and carotenoid concentration. Orange flesh sweet potato is high in carotenoids pigments (Jakahata *et al.,* 1993). The white colour in sweet potato roots is due to the presence of lycopene and yellow orange colour is due to the presence of β-carotene (Dauthy, 1995). Yellow flesh cultivars contain higher amounts of β-carotene than white types (Salunke and Kadam, 1998). More than 60 mg total carotenoids in 100 g dry matter has been reported (Woolfe, 1992). The primary vitamin A forming carotenoid in sweet potato is β-carotene (Bengtsson *et al*., 2008; Wu *et al.,* 2008; USDA ARS, 2010), although small amounts of α-carotene and β-cryptoxanthin can be found in some varieties.

The concentration of β-carotene varies among sweet potato genotypes (Hagenimana *et al*., 1999a; Kidmose *et al*., 2006; Kidmose *et al*., 2007; Kidmose *et al*., 2009; Bengtsson *et al*., 2008; Wu *et al*., 2008; USDA ARS, 2010). There is a very wide (1100-fold) range of β-carotene concentrations among sweet potato genotypes such that, the more orange the colour is, the higher the carotenoid content (Ameny and Wilson, 1997; Takahata *et al*., 1993). β-carotene concentrations also vary with growing, harvesting, and storage conditions (Bengtsson *et al*., 2008, Hagenimana *et al*., 1999a), farming site (K'osambo *et al*., 1998), season (Liu *et al*., 2009), root age (K'osambo *et al*., 1998;

Hagenimana *et al*., 1999b), drought (vanHeerden and Laurie, 2008), and virus infestation (Kapinga *et al.*, 2009).

The average storage root dry matter of the cultivated sweet potato genotypes of the world is about 30% but varies widely depending on factors such as genotypes, environment (location, climate, day length, and soil pest diseases), seasons and cultivation practices (Bradbury and Holloway, 1988; Woolfe, 1992; Tsakama *et al.*, 2010). For instance, the application of farm yard manure and green leaf manure in sweet potato production yielded high storage root with high dry matter content compared to application of inorganic fertilizer (Nedunchezhiyan *et al.*, 2010). Also, a large number of storage roots might reduce dry matter content as the plant may not be able to supply enough photosynthetic assimilates to all storage roots (Gasura *et al*., 2010). Slafer and Savin (1994) and Mwanga *et al.* (2007) reported high dry matter content as an important characteristic of a good sweet potato genotype preferred by consumers and processors. For instance, in sub-Sahara Africa, small-scale farmers prefer sweet potato genotypes that have a high dry matter content (Mwanga *et al.*, 2007; Cervantes-Flores *et al.*, 2010). Also, high dry matter content, low fibre, and good taste are the most preferred traits of the crop by women farmers' (Gruneberg *et al.*, 2009; Mwanga *et al.*, 2010). A dry matter content >25% is an important component for acceptability of a new sweet potato genotype by farmers (Shumbusha *et al.*, 2010). Further, storage roots with high starch and low hexoses (glucose and fructose) contents are important characteristics preferred by the sweet potato industry (Slafer and Savin, 1994). High starch and low soluble sugar contents decrease the cost of sweet potato processing due to the absence of oxidation reactions (McKibbin *et al.*, 2006).

Approximately 80 – 90% of sweet potato storage root dry matter is made up of carbohydrates, mainly starch (60 – 70% of dry matter) and sugars (15 – 20% of dry matter) and lesser amounts of pectins, hemicelluloses and cellulose (Woolfe, 1992). Usually white- and cream-fleshed varieties have higher starch (about 50 – 80% of dry

matter) and lower sugar contents (about 5 – 15% of dry matter) compared with Orange fleshed sweet potato genotypes, which have lower starch (45 – 55% of dry matter) and higher sugar contents (10 – 20% of dry matter) (Woolfe, 1992). Sucrose is the most dominant sugar in raw sweet potato roots with smaller amounts of glucose and fructose (Bouwkamp, 1985; Lai *et al*., 2013). During storage of the tubers some starch are converted into reducing sugars and subsequently into sucrose (Salunke and Kadam, 1998).

Sweet, low dry-matter content (about 20%) orange flesh sweet potatoes (OFSP) are the predominant types of genotypes produced in the United States, but in much of sub-Saharan Africa (SSA) the preferred types have cream or white-flesh colour, high dry-matter content (28–30%) and little to no sweetness (Mwanga *et al.*, 2007). Because of their reduced carotenoid content, these types are not as nutritious as the orange-fleshed types. Therefore, much breeding work in SSA is focusing on the development of higher dry-matter, semi-sweet OFSP to address the vitamin A deficiency needs of women and children in order to prevent malnutrition and enhance nutrition and food security (CIP, 2010b).

Sweet potato could be a good source of protein ingredient for food processing as it possesses good solubility and emulsifying properties (Mu *et al.,* 2009). The average total protein content of sweet potato is low (1.5% on fresh weight basis and 5% dry weight basis) though values of up to 18% have been reported. For example, Gayoum and Rahman (2012) reported protein values of 12.22 to 17.9%, Salami *et al*. (2006) 13.76 to 18.18% and Salunkhe and Kadam (1998) 0.30 to 10.00%. The difference in protein content among sweet potato genotypes could be attributed to effects of genotypes, environments or genotype-environment interactions. The difference in protein content among genotypes implies that it could be possible to breed and produce sweet potato with high protein content.

2.6 Sweet potato weevil

Cylas puncticollis (Boheman) (Coleoptera: Brentidae) and *Cylas bruneus* (Fabricius) (Coleoptera: Brentidae) are restricted to Africa while *Cylas formicarius* (Fabricius) (Coleoptera: Brentidae) is found throughout the tropical regions of North America, the Caribbean, Europe, Africa, Asia and Oceania (Hue and Low, 2015). Although different sub-species of sweet potato weevil can be found in different geographical locations, their mode of feeding remains the same (Capinera, 2001). *Cylas* spp. cause serious damage to all parts of sweet potato plant throughout their life cycle, from egg to adult. When laying eggs, female weevils excavate cavities and create egg-laying punctures in the roots or stem (Hue and Low, 2015; Okonya *et al*, 2016a; Musana *et al.*, 2016). The eggs are laid below the surface of the roots and covered with dark colour excrement from the female adults (Capinera, 2001). As a result of the unsightly punctures, the appeal of the roots and market price of sweet potato become greatly reduced, resulting in major economic losses.

2.6.1 Description of sweet potato weevil

Sweet potato weevil belongs to coleoptera order and brentidae family. They are of three types i.e. *Cylas brunneus* (Fabricius), *Cylas punticollis* (Boheman) and *Cylas formicarius* (Fabricius) (Lebot 2010). *Cylas brunneus* is brown and smaller than the larger, black *Cylas puncticollis*, while *Cylas formicarius* is as small as *Cylas brunneus* but has a bluish-black abdomen and a red thorax (Ames *et al*., 1997). The male and female adult sweet potato weevils can be distinguished by the shape of their antennae. The antennae of the males are straight while those of the female are club-shaped at the end (Ames *et al.*, 1997; Stathers *et al*., 2013). After mating, the female sweet potato weevil lays eggs singly in holes that she chewed into either the vines or exposed and easily accessible storage roots. While the female weevil can survive for up to 4 months, she typically lays all her eggs (50 – 250) within the first two months (Stathers *et al*., 2013). Whilst the development period will be affected by the temperature, the egg typically hatches 3 – 7 days after it has been laid (Stathers *et al*., 2013). The larva that

emerges is legless, curved and whitish with a dark brown head. It will start feeding and, as it does so, it tunnels through the vine or root into which it was placed as an egg (Stathers *et al*., 2013). It is this tunneling that is so destructive to the sweet potato crop, causing the holes and black tunnels. Low levels of infestation can reduce the root quality and marketable yield as the root produces a bitter terpenes and phenolic compounds, in response to the sweet potato weevil's feeding which make roots unsuitable for both human and animal consumption (Chalfant *et al*., 1990; Ames *et al*., 1996). This damage can continue even after the roots have been harvested (Stathers *et al*., 2013). The larvae live for 11–33 days before they pupate (Stathers *et al*., 2013). Pupation occurs within the larval tunnels, and lasts for 3 – 28 days after which the adult beetle emerges (Stathers *et al*., 2013). Adults may remain an average of 6 days within the root before they eat their way out (Eulitz, 1974). The adult is initially light brown but, after about a week, its cuticle hardens and becomes dark brown in colour. The adult then leaves the root zone and starts search for a mate (Stathers *et al*., 2013). The whole cycle from egg to adult typically takes 32 days (Stathers *et al*., 2013). The two African *Cylas* species (*C. puncticollis* and *C. brunneus*) often occur together in fields and cause huge yield losses of up to 100% (Girma 1994; Smit 1997; Chalfant *et al*., 1990).

2.6.1.1 Biology of *Cylas puncticollis*

Cylas puncticollis can easily be distinguished from the other two species (*C. brunneus* and *C. formicarius*) because the adult is all black and larger than the other two. Egg to adult development of *C. puncticollis* is possible at temperatures of 17.5–35 °C but not at <15 °C or >40 °C (Okonya *et al.*, 2016a). Okonya *et al.* (2016a) reported that the total development of *C. puncticollis* is almost 6.4 times longer at 17.5 ºC (86 days) than at 35 ºC (16 days). Optimal temperature for survival of eggs and pupae is between 25°C and 30ºC (Okonya *et al.*, 2016a). Smit and van Huis (1999) and Anota and Odebiyi (1984a) reported that *C. puncticollis* has a total development time (from egg to adult) of 20-28 days. According to Smit and van Huis (1999), the first adult weevils of *C. puncticollis* emerged from the infested roots 24 days after exposure of the roots to oviposition while

Stathers *et al.*, (2003a) reported that *C. puncticollis* adults started emerging from roots of all cultivars 22-23 days after set up. These results contrasted with those of other researchers. For instance, according to Eulitz (1974) total development time of *C. puncticollis* was 4 – 5 days shorter than that reported by Smit and van Huis (1999) while Nwana (1979) reported 2 – 4 days longer development period than that reported by Smit and van Huis (1999). Consequently, Ames *et al*., (1997) reported a developmental period of 32 days.

There are contradictory reports about the life span of *C. puncticollis* and the number of eggs laid by the female adult. For instance, Ames *et al*. (1997) reported that females lay 90 – 140 eggs in their lifetime. However, according to Okonya *et al.* (2016a), an individual female lays a maximum of 17 eggs per day and a total of up to 545 eggs in 178 days. They further reported that the maximum number of days an adult weevil can live is 309. On the other hand, Sathula *et al*. (1997) reported 115 eggs per female and a lifespan of 143 days. Further, according to Smit and van Huis (1999) females have a life span of 93 – 113 days and each female lays at least one egg per day (103 eggs in a lifetime) at 27°C. He further reported that the survival percentage of the eggs laid by the females is at 87 – 95%. At 27 °C the first adult weevils emerged from infested roots 24 days after exposure of the roots to oviposition (Smit and van Huis, 1999).

2.6.1.2 Biology of *Cylas bruneus*

C. brunneus adults are small and not uniform in colouring. The most common type can easily be confused with *C. formicarius*. Development of all *C. brunneus* live stages is possible at 17.5–32°C (Musana *et al.*, 2016). At 27 °C, *C. brunneus* completes development (from egg to adult) in about 44 days (Ames *et al*., 1997). Mullen (1981) reported that the development period of *C. bruneus* was 12 to 13 days longer than that of *C. formicarius* and 3 – 5 days longer than that of *C. puncticollis*. Adult dies after about 2 months (Ames *et al.*, 1997). *C. brunneus* females lay 80 – 115 eggs in their lifetime (Ames *et al*., 1997). According to Smit and van Huis (1999) females have a life

span of 80 – 104 days and each female lays at least one egg per day at 27 ^{o}C. He further reports that the survival percentage of the eggs laid by the females is at 84 – 90%. At 27 ^{o}C the first adult weevils emerged from infested roots 34 days after exposure of the roots to oviposition (Smit and van Huis, 1999).

2.6.1.3 Biology of *Cylas formicarius*

C. formicarius has a bluish black abdomen and a reddish-brown thorax. At optimal temperatures of 27 – 30 °C, *C. formicarius* completes development (from egg to adult) in about 33 days (Ames *et al*., 1997). Females lay between 100 and 250 eggs in this period (Ames *et al*., 1997), but Jansson and Hunsberger (1991) and Mullen (1981) reported 122 and 88 eggs respectivey. At sub-optimal temperatures, development takes longer (Ames *et al*., 1997). Adults live an average of 100 days (Ames *et al*., 1997). Adult longevity is 2½ – 3½ months (Ames *et al*., 1997). However, Jansson and Hunsberger (1991) and Mullen (1981) reported a life span of 76 and 79 days respectively for the females. The differences between the results of different studies mentioned above are as a result of carrying out the experiments in different environments (Smit and van Huis, 1999). The more stressful the environment (e.g. non-optimal temperature), the lower the eggs produced and the longer the development period.

2.6.2 Economic Importance of sweet potato weevil

Cylas spp. is known to cause crop yield losses of up to 100% especially during extended dry seasons (Smit, 1997; Ebregt *et al*., 2005; Fuglie, 2007; Nderitu *et al*., 2009; Okonya *et al.*, 2016a). *Cylas* spp. have been reported as a major pest in Uganda (Muyinza *et al*., 2007; Mwanga *et al*., 2009; Smit, 1997), Kenya (Nderitu *et al*., 2009; Smit and Matengo, 1995), Nigeria (Tewe *et al*., 2003) and are also present within 20 other countries in Africa (CABI, 2005). Both *C. puncticollis* and *C. brunneus* are of importance in Western Kenya (Magenya and Smit, 1991). Weevil distribution patterns

within the crop change during the growing season (Jansson *et al*., 1990) where they are more abundant in vines early in the season and move to fleshy roots as the crop mature.

Weevils are more abundant and injurious during the dry season. This is because of the high temperatures and low moisture that favour high weevil population build up and the soil cracks which expose fleshy roots to the weevils (Malinga, 2000). Adult *Cylas* spp. feed on leaves whilst larvae feed on stems and storage roots. Stem damage is thought to be the main reason for yield loss, although damage to the vascular system caused by feeding, larval tunneling and secondary rots substantially reduce storage root yields (Sorensen, 2009). The nature of attack and hidden feeding habit by *Cylas* spp. reduces the effectiveness to control them by chemical and biological insecticides or natural enemies (Smit *et al*., 2001). Despite years of intensive conventional plant breeding research, no varieties with complete resistance to *Cylas* spp. have been found until now (Stevenson *et al*., 2009).

Accessibility to the roots by the weevil determines infestation with deep-rooted varieties being less infested by the weevil (Burdeos and Gaspasin, 1980; Stathers *et al.*, 2003b). Soil type highly determines the weevil infestation (Malinga, 2000) with highly eroded soils likely to face severe damage. Crop debris left on farmer's field after harvesting serve as source of infestation for the new crop (Smit, 1997). Planting of a new crop adjacent to infested crop may aggravate pest infestation on the new crop (Magenya and Smit, 1991), unless a barrier like a sorghum crop lies between them (Smit, 1997). Dispersal is mainly through vine cuttings as adults hide beneath the leaves thus serving as a source of infestation on new fields, (Alcazar *et al*., 1997). The maximum dispersal distance of sweet potato by either crawling or flying is 120 m per day for *C. puncticollis*, 80 m per day for *C. brunneus* and 55 m per day for *C. formicarius* (Miyatake *et al*., 1995).

2.6.3 Management of sweet potato weevil

When sweet potato weevil populations are high, no single control method provides adequate protection. The integration of different techniques, with emphasis on the prevention of infestation, provides sustainable protection (Ames *et al*., 1997; Okonya *et al.,* 2016a).

2.6.3.1 Sex pheromone trap

Research has been conducted on the use of commercially produced sex pheromone traps to reduce the male weevil population (Pillai *et al.,* 1993; Smit, 1997). The trap is usually designed with synthetic pheromone lure such as (Z)-3-dodecen-1-ol and (E)-2 butenoate together with ethyl acetate and is usually placed at ground level to facilitate the entrance of adult weevils, which will then be killed by the insecticide inside the trap (Hue and Low, 2015). The sex pheromone trap of the sweet potato weevil is hung in the field above a container of soapy water with the insecticide. When the male adults arrive, attracted by the pheromone, they fall into soapy water with the insecticide and die. However, in Uganda, use of pheromone did not lead to a reduction in weevil damage of roots (Stathers *et al*., 2013). In a separate study, Reddy *et al*. (2014) reported that sweet potato roots damage decreased when a synthetic pheromone trap with (Z)-3-dodecen-l-ol and (E)-2-butenoate was used proving that pheromone traps are effective in reducing the damage done by sweet potato weevil.

2.6.3.2 Biological control

Numerous studies and laboratory experiments have proven that entomopathogenic fungi are useful in the control of sweet potato weevil. Reddy *et al*. (2014) conducted a field study to compare the effectiveness of entomopathogenic fungi, insecticides, and combination of both entomopathogenic fungi and insecticide in controlling sweet potato weevil by determining the adult weevils' mortality. The authors showed that *Metarhizium brunneum* with insecticide and *Beauveria bassiana* with insecticide caused 100% adult weevil mortality at 48 hours after treatment, while *M. brunneum* and *B.*

bassiana alone required 168 to 192 hours after treatment to cause 100% mortality. Besides, Ondiaka *et al.* (2008) showed that spraying of *B. bassiana* or *M. anisopliae* caused adult mortality between 62.5% and 89.2% respectively. However, use of the entomopathogenic fungus like *B. bassiana* as biological control measure is limited to areas with constantly moist climate (Ames *et al.*, 1997). Biological control methods using entomopathogenic nematodes has been found to have beneficial interaction with sweet potato and offers a promising way to suppress sweet potato weevil population (Kaya and Gaugler, 1993)

2.6.3.3 Chemical control

Various synthetic chemical insecticides are currently used in sweet potato plantation to prevent or treat sweet potato weevil infestation. Organophosphates and imidacloprid, which are chloronicotinyl insecticides, act primarily on the insect central nervous system by binding irreversibly to insect nicotinic receptor, leading to nicotinergic neuronal pathway obstruction and eventually failure in production of acetylcholinesterases (Hue and Low, 2015). Acetylcholinesterases are required to break down or deactivate acetylcholine in chemical synapse. The lack of this enzyme will result in accumulation of acetylcholine, overstimulation of cholinergic synapses, paralysis, and eventually the death of the insect (Giesy *et al*., 2014). Insecticides can be used for treatment of vines at planting and early in the growing season, at 1 and 2 months after planting (Okonya *et al.*, 2016a). Insecticides applied late in the growing season (after storage root formation) may not be very effective (Okonya *et al.*, 2016a).

Mason and Jansson (1991) conducted an experiment to compare the toxicity of five insecticides: parathion, carbamate methomyl, chlorpyrifos, chlorinated hydrocarbon endosulfan, and carbamate carbaryl, against adult *Cylas formicarius* using Petri dish bioassays in laboratory. The results showed that organophosphates (parathion and chlorpyrifos) were the most toxic as they had the lowest LD_{50} values (1.97 and 5.12 μg/g of wet biomass), followed by methomyl (6.03μg/g of wet biomass), endosulfan

(57.44 μg/g of wet biomass), and lastly carbaryl (297.41 μg/g of wet biomass). Due to their higher toxicity, chlorpyrifos and parathion were suggested for the control of sweet potato weevils.

According to Collins and Mandoza (1991) and Stathers *et al*. (2013), sweet potato weevils are difficult to control using chemical pesticides as the egg; larval and pupal stages of their life cycle are protected within the stems and roots and not easily reached by insecticides. Further, use of chemical insecticides in Africa is, still very low, possibly because most farmers are unfamiliar with the biology and behavior of the weevil or even its presence (Okonya *et al.*, 2016a).

2.6.3.4 Cultural control

Many farmers use cultural measures to control weevils such as: use of weevil-free planting materials, keeping distance between old and newly planted fields, flooding or regular irrigation, crop rotation, mulching, removal of nearby alternate hosts, field sanitation, incorporation of ashes into the soil before planting, adjustment of the planting dates, earthing up or filling of soil cracks and harvesting as soon as the tubers mature (Smit, 1964; Martin and Leonard, 1967; Onweueme and Sinha, 1991; Daiber *et al.*, 1994; Skoglund and Smit, 1994; Fielding and Van Crowder, 1995; Smit, 1997; Stathers *et al*., 2013, Okonya *et al.,* 2016a). The above-mentioned cultural control methods have not provided a satisfactory solution to the problem yet.

2.6.3.5 Host plant resistance

Host plant resistance plays an important role in the management of serious insect pests (Rao, 2005). Farmers have reported some sweet potato varieties that suffer less damage from sweet potato weevil than others suggesting some quantifiable level of resistance (Stathers *et al*., 1999; Mao *et al*., 2001). Breeders have not yet developed any sweet potato varieties that are completely resistant to weevils (Stathers *et al*., 2013). Identification of a potential source of resistance to *Cylas* spp. in sweet potato (*Ipomoea*

batatas L.) or its wild relatives is of paramount importance for successful development of insect-resistant plants. An approach to ascribing particular cultivars is to start by eliciting the locally important characteristics themselves through open-ended interviews (Prain and Mok, 1992).

Varieties with immunity or a high level of resistance are not available but some varieties have low to moderate levels of resistance (Ames *et al*., 1997). Varying levels of resistance have been reported in both field and laboratory evaluations (Mullen *et al*., 1980; Mullen *et al.*, 1985; Story *et al*., 1996; Story *et al*., 1999a, b, c; Thompson *et al*., 1999; Stathers *et al.*, 2003a, b; Muyinza *et al.*, 2012). However, inconsistent performance by selected breeding lines between years and within years at different locations is often encountered, limiting the successful development of commercially useful resistant sweet potato genotypes (Collins *et al*., 1991). Varieties seem resistant to sweet potato weevil in areas of low infestation pressure but succumb to high infestation pressure in areas where weevils are indigenous (Cockerham and Harrison, 1952; Jansson *et al.*, 1987).

The mode of resistance to sweet potato weevils is believed to be both biochemical and morphological. Proposed mechanisms of resistance in sweet potato include antibiosis, antixenosis, escape and tolerance (Barlow and Rolston, 1981). The mechanism of resistance through escape may be due to some attribute of the variety such as early maturity. Host plants that express non-preference (anti-xenosis) affect the way an insect pest perceives the desirability of the host plant. Non-preference plants either provide stimuli that are unattractive to the pest (colour, odor, texture such as downy hairs) or fail to provide stimuli that are attractive to the pest. In this way, non-preference plants affect the behavior of pests. Antibiosis is a type of resistance in which the host plant causes injury, death, reduced longevity, or reduced reproduction of the pest. Plants that express antibiosis affect the biology of pests. Barlow and Rolston (1981) reported that antibiosis due to inhibition of feeding and oviposition is independent of preference,

non-preference or a combination of two or more of these general types of resistance. Often, both a resistant and susceptible variety will have the same basic response to a pest, but the resistant variety will respond more quickly or more dramatically than the susceptible variety, reducing the amount of damage the pest causes. Host plants that express tolerance are resistant to pest damage because they can remain healthy and yield well despite the damage. These plants must also be able to heal wounds and fight diseases that enter through wounds.

Polygenic basis for resistance has been suggested with important plant traits in weevil resistance being fleshy root density, high dry matter and starch content (Hahn and Leuschner, 1982), rooting depth, vine thickness, (Burdeos and Gaspasin, 1980) and high levels of caffeic acid (Stevenson and Mwanga, 2006). Deep-rooting and early maturing varieties (90 to 120 days) are about four times less susceptible to infestation than shallow-rooting and late maturing varieties (180 days or more). As a result, both deep storage roots and early maturing varieties tend to decrease the severity of weevil damage (Lima and Morales, 1992).

Latex is a sticky emulsion that exudes upon damage from specialized canals in about 10% of flowering plant species. Latex has no known primary metabolic function and has been strongly implicated in defense against herbivorous insects (Agrawal and Konno, 2009). The potential of latex produced by the sweet potato as a defense mechanism against the sweet potato weevil, *C. formicarius* (F.) was investigated by Data *et al.* (1996). The authors reported that young vine material produced more latex and had less weevil feeding damage than older more mature portions of the vine. Also, application of latex to the surface of root cores reduced feeding and oviposition (Data *et al.*, 1996). The latex excreted by varieties less preferred by weevils contains high concentrations of Z-esters than those found in varieties heavily attacked by weevils (Snook *et al.*, 1994). By further exploiting this finding in breeding, resistance to weevils may be improved. Several lines of evidence suggest that latex production in plants is

phenotypically plastic (that is, responsive to environmental conditions). For example, work on the rubber tree (*H. Brasiliensis*) and sweet potato (*I. batatas*) shows that light levels, drought, and soil moisture conditions determine the amount of latex production (Data *et al.,* 1996, Raj *et al.,* 2005).

According to Wang and Kays (2002), host-plant phytochemicals play critical roles in insect behavior, modulating a cross-section of key behavioral decisions. The authors found out that volatile extracts from storage roots (site of oviposition) and aerial plant parts of sweet potato were attractive to female sweet potato weevil, the former being substantially greater. Three oxygenated monoterpenes (nerol, Z-citral, and methyl geranate), found in storage roots but not aerial plant parts, were identified as attractants while the sesquiterpene volatile fraction was repellent to female sweet potato weevil (Wang and Kays, 2002). Thus, selection of clones with decreased volatile attractants and/or increased deterrents using an analytical means of quantification may significantly facilitate developing resistance to the sweet potato weevil (Wang and Kays, 2002).

CHAPTER THREE

ASSESSMENT OF SWEET POTATO PRODUCTION CONSTRAINTS, FARMERS' PERCEPTIONS AND COPING STRATEGIES WITH THE SWEET POTATO WEEVIL IN KENYA; A CASE STUDY OF HOMA BAY COUNTY.

3.1 Introduction

Sweet potato (*Ipomoea batatas* L.) is the world's sixth most important food crop, after rice (*Oryza sativa* L.), wheat (*Triticum aestivum* L.), maize (*Zea mays* L.), potato (*Solanum tuberosum* L.) and cassava (*Manihot esculenta* Crantz) (CIP, 2010b). It is the third most important root crop grown in eastern Africa after cassava and potato (FAO, 2011). It is an important food security crop in Kenya, often crucial during famine periods due to its excellent drought tolerance and rapid production of storage roots (Mukhopadhyay *et al.,* 2011). In addition to serving as an important complementary food crop, sweet potato supplements household income through formal and informal trading at both rural and urban markets, thereby contributing to the alleviation of widespread food shortages and poverty for the majority of rural communities who are dependent on this crop in Africa (Mwanga and Ssemakula, 2011). In Kenya, sweet potato production is practised in the western, central and coastal areas of the country. Out of this, over 80% is grown in the Lake Victoria basin (Gruneberg *et al.,* 2004) with Kakamega, Bungoma, Busia, Homa bay, and Kisii Counties having high acreages of this crop. However, its production is limited due to several abiotic (drought, low rainfall, poor soils) (Carey *et al.,* 1997), biotic (insect pests and diseases), (Karyeija *et al*., 1998; Gibson and Aritua, 2002) and socio-economic factors. Among the major biotic constraints for sweet potato production insect pests are recorded as the most important (FAOSTAT, 2013).

The most serious and commonly reported insect pests for sweet potato in Africa are the sweet potato weevils (*C. brunneus* and *C. punticollis*), caterpillars of the sweet potato butterfly (*Acraea acrerata* Hew.,), the clearwing moth (*Synanthedon sp*p.), the sweet

potato hornworm (*Agrius convolvuli* L.) and the sweet potato whitefly (*Bemisia tabaci*) (Nderitu *et al.,* 2009). The two African *Cylas* spp. (*C. puncticollis* and *C. brunneus*) usually appear together in fields and cause huge yield losses of up to 100% especially during dry periods (Nderitu *et al*., 2009).

Assessing farmers' observations on constraints affecting crop production has been used as a tool for documenting pest status and designing pest management options suitable for a particular community (Obopile *et al*., 2008). Such information could be obtained using various approaches such as participatory rural appraisal (PRA) and diagnostic questionnaire surveys. Participatory rural appraisal is a flexible and time saving approach used to collect and analyze information involving farmers and researchers (Bhandari, 2003). The approach enables communities to share and enhance their experiences, plan and act together with external agents to enrich their livelihoods (Bar-On and Prinsen, 1999). PRA approach is an effective method that has been used to collect data from farmers which would help in understanding the pest status and possible management strategies in various crops (Mukanga *et al.,* 2011; Tounou *et al*., 2013).

Even though the sweet potato weevil (*Cylas* spp.) is an economically important pest of sweet potato in the world (Okonya *et al.,* 2016a), comprehensive studies on *Cylas* spp. in Kenya are scanty. However, some reports suggest that sweet potato weevils cause appreciable damage to the crop annually on farmers' fields (Nderitu *et al.,* 2009). There is no information available on the status of sweet potato weevil infestation in Homa bay County. The present study sought to assess sweet potato production constraints and farmers opinions and coping strategies employed in managing the sweet potato weevil in Homa Bay County, Kenya. The findings are of great importance in the development of management strategies that are appropriate for resource poor farmers.

3.2 Materials and methods

3.2.1 Study area

The study was conducted between February and April, 2012 in two sub-Counties (Rachuonyo and Ndhiwa) of Homa Bay County of Kenya (Figure 3.1). Ndhiwa sub-County lies on the geographical co-ordinates of 0° 44′ 0″ South and 34° 22′ 0″ East. Ndhiwa is administratively divided into five Divisions which include Riana, Ndhiwa, Nyarongi, Kobama and Pala. Ndhiwa sub-County receives long rains during the months of February to May (500 – 1000 mm) and short rains during the months of August to November (250 – 400 mm) with an average range of between 500 – 1650 mm p.a. (GOK, 2009a). The agro-ecological zone of the region is within the lower midlands (LM1 – LM3). Altitude ranges between 1200 – 1400m above sea level and average annual temperatures are 20.5 – 21.7 °C. The area has three types of soils; black soils (vertisols– cotton soils), silt loam and clay loam (luvisols) (GOK, 2009a).

Rachuonyo sub-County lies on the geographical co-ordinates of 0° 26′ 24″ South and 34° 44′ 20″ East. Rachuonyo is divided into two agro-ecological zones: the medium-high potential "upper midland" (found in Kasipul and Kabondo Divisions), and the drier "lower midland" found close to Lake Victoria (in Karachuonyo East and West Divisions) (GOK, 2009b). The region receives an average annual rainfall of 800 -1800 mm. The site has an elevation ranging between 1180 - 1900m above sea level (GOK, 2009b). Kasipul and Kabondo Divisions have deep, well drained relatively fertile soils. The main food crops grown in this region include maize, cassava, beans, groundnuts and sweet potatoes; while the main cash crops are tea and coffee (GOK, 2009b). Karachuonyo East and West Divisions on the other hand have soils of poor fertility and drainage. The food crops grown in this region include maize, sorghum, millet, sweet potato, cassava, groundnuts, beans and yams while cotton is the main cash crop in the region (GOK, 2009b).

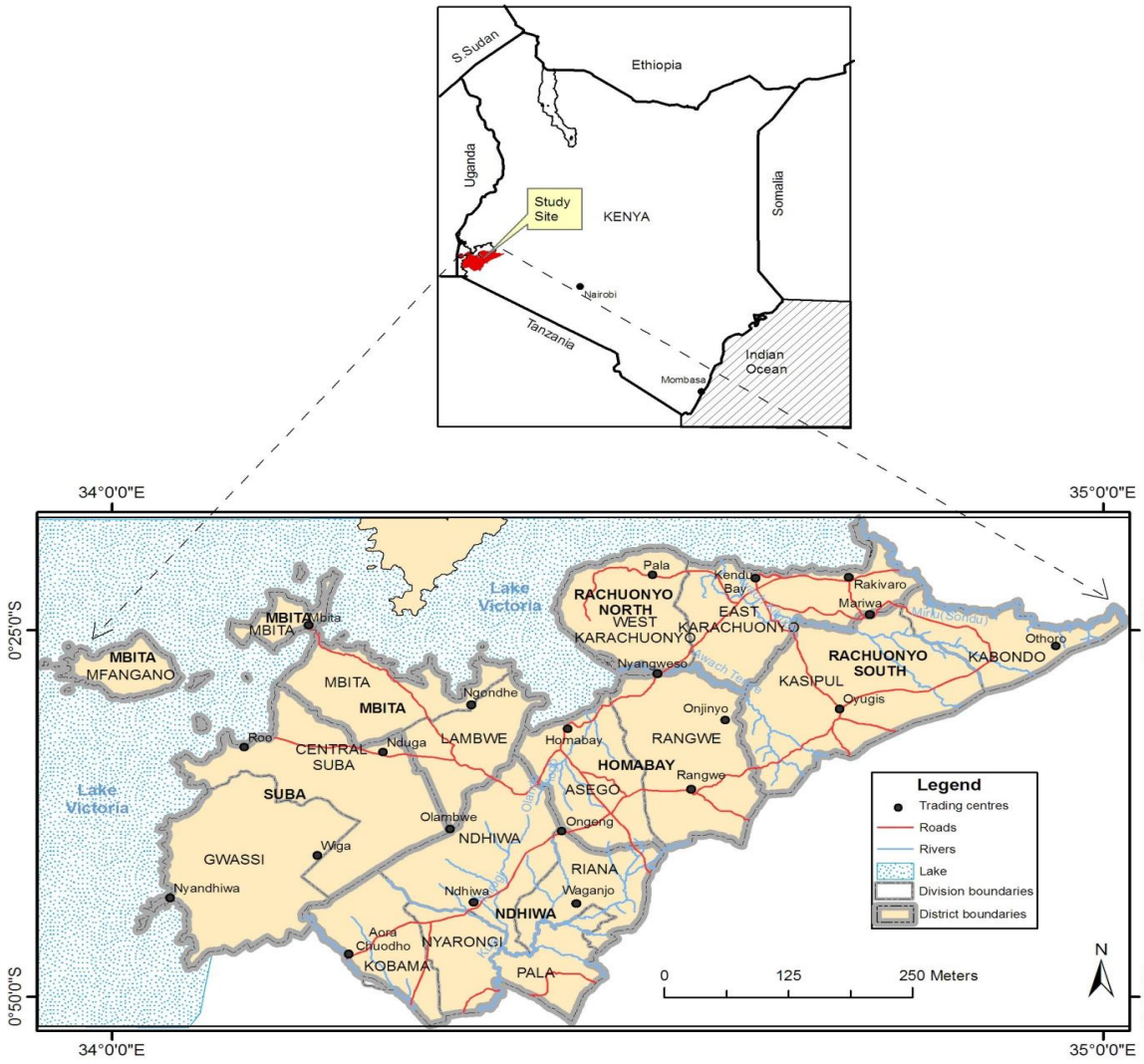

Figure 3.1: Location of Ndhiwa and Rachuonyo sub-Counties

3.2.2 Research design

The study was conducted using a Participatory Rural Appraisal (PRA) approach in which a reconnaissance survey preceded a detailed survey of the area. Participatory Rural Appraisal is a set of participatory and largely visual techniques for assessing group and community resources, identifying and prioritizing problems and appraising strategies for solving them. In this study, the approach aimed at incorporating the

knowledge and opinions of rural people in developing an integrated pest management strategy that is appropriate for resource poor farmers.

3.2.3 Target population, sample size and sampling techniques

With the assistance of agricultural extension workers, a preliminary survey was done to obtain information on the total number of sweet potato farmers in the area. Based on this information the number of interviewees per sub-County was determined. The study population was 900 farmers. These were farmers who had been growing sweet potato for atleast the last five years. A sample size of 269 farmers was arrived at using the table on sample size selection and standardization equation (Israel, 2003; Krejcie and Morgan, 1970).

$$n = \left[\frac{n_0}{1 + \left(\frac{n_0 - 1}{N}\right)}\right]$$

Where; *N* is the known population; *n* is sample size; and n_0 is the unknown population.

$$n_0 = \frac{Z^2 pq}{e^2}$$

Where n_0 is the sample size; Z^2 is the abscissa of the normal curve that cuts off an area α at the tails $(1.96)^2$; *e* is the desired level of precision (0.05); *p* is the estimated proportion of an attribute that is present in the population (0.5); and *q* is 1-*p*.

In this study, n_0 was calculated using the above formula and was found to be 385 farmers.

Individual farmers (269) filled the questionnaires while six farmer groups participated in focus group discussions. Out of the 269 farmers who participated in this study, 145 were selected purposively from Rachuonyo sub-County whereas 124 were selected from Ndhiwa sub-County. This comprised 80 male and 189 female participants from the two sub-Counties (Table 3.1). The qualification of the selected focus discussion

group was based on the fact that there were more than 25 members who had been actively growing sweet potatoes for more than five years. The respondents were purposively identified through the help of extension officers in the County. Transect walks were done with the focus discussion groups and with the help of extension officers. The participants walked to different farms so as to make observations in the field on infestation of sweet potato roots by weevils and other challenges faced by farmers in the fields. The tools validity in this study was enhanced by piloting in the non-target area of Suba sub-county with the help of extension officers. This helped in identifying the accuracy and the usefulness of the tools and acted as a basis for adjusting them so as to improve their efficiency.

3.2.4 Data collection methods

Data was collected using a semi-structured questionnaire and focus group discussions. The questionnaire was designed and used to collect data from individual respondents. A sample of the questionnaire is shown in Appendix 1. The questionnaire was pre-tested in Suba sub-County while the actual survey was conducted in Homa Bay County. During the interviews, farmers were shown coloured photographs of respective insect pests and effects of weevil damage on the sweet potato roots.

More information was collected using focus group discussions with farmers and pairwise ranking. All these were done within purposively selected groups with the help of extension officers. Two and four groups from Rachuonyo and Ndhiwa respectively were involved in the focus group discussions. Data was collected from the farmers using names of sweet potato genotypes that were known to be resistant to the sweet potato weevil, constraints affecting sweet potato production and strategies used for managing the sweet potato weevil.

3.2.5 Data analysis techniques

Quantitative data collected was analysed using cross tabulation descriptive statistical techniques (i.e. frequencies and percentages) and standard error. This was done using Statistical Package for Social Sciences (SPSS) version 16. Correlation of the respondents reporting on the most problematic pest in Rachuonyo and Ndhiwa sub-Counties was done using Pearson's correlation. This was to test the hypothesis that there was no significance difference in the perception of sweet potato weevil as the most problematic pest between sweet potato farmers in the two sub-Counties. Further, correlation of the genotypes reported to have resistance to *Cylas* spp. in Rachuonyo and Ndhiwa sub-Counties was done using Pearson's correlation. This was to test the hypothesis that there was no significance difference on the reported genotypes having resistance to *Cylas* spp. by farmers in the two sub-Counties. The relationship between farmers demographic profile (age, gender, level of education and occupation) and selected variables (farmers' perception on the most problematic pest of sweet potato, farmers' control strategies of the sweet potato weevil, farmers knowledge on existing sweet potato genotypes resistant to weevil and farmers unadoption of resistant weevil genotypes) was determined using multiple regression analysis.

For the qualitative data, the farmers were initially given an opportunity to list all the problems they encountered during the production of the crop and thereafter, the standard pair wise ranking was done. Pairwise ranking was used as a means of prioritizing or ranking lists of constraints encountered by farmers during sweet potato production. To make matrix tables, each constraint was compared in turn with each of the other constraints. The constraint with the highest frequency in the matrix was considered to be the most important and hence ranked as number one.

3.3 Results

3.3.1 Demographic profile and characteristics of the sweet potato farmers in Homa Bay County

Information concerning the occupation, gender, sub-County of residence, level of education and age, of 269 farmers who participated in this study is shown in Table 3.1. Of all the respondents, 92.2% were farmers, 2.6% were casual workers and 1.5% were salaried workers in non-agriculture areas. It was further established that majority (70.3%) of the respondents were female whereas only 29.7% were male. The data was collected from the respondents in Ndhiwa and Rachuonyo sub-counties, where 53.9% (145) were from Rachuonyo and 46.1% (124) were from Ndhiwa sub-Counties. Concerning the educational level of the respondents, majority (66.2%) had completed primary school education whereas 15.2% (41) had completed secondary school education. However, 11.9% (32) never attended any formal education and the rest had attained A-level, middle level or university education. This implies that majority of the respondents were at least able to read and write. The findings also showed that 26.8% (72) of the respondents were 41-50 years old while 26.0% (70) were aged 31-40 years old. There were 17.1% (46) of the respondents who were aged below 30 years while the rest of the respondents were over 50 years old.

Table 3.1: Demographic profile of the respondents in Homa Bay County, Kenya (N=269)

	Number	%
AGE		
Below 30 yrs	46	17.1
31 - 40 yrs	70	26.0
41-50 yrs	72	26.8
Above 50	81	30.1
GENDER		
Female	189	70.3
Male	80	29.7
LEVEL OF EDUCATION		
Primary	179	66.2
Secondary	41	15.2
Never attended	32	11.9
Tertiary	17	6.3
SUB-COUNTY		
Rachuonyo	145	53.9
Ndhiwa	124	46.1
OCCUPATION		
Farmer	248	92.2
Casual worker	7	2.6
Salaried workers in non-agriculture	4	1.5
Salaried workers and doing Business	10	3.8

3.3.2 Sweet potato production constraints

Among the production constraints identified by farmers, infestation of crop by *Cylas* spp. was ranked number one by three focus groups (two from Ndhiwa and one from Rachuonyo) (Table 3.2). Erratic rains were reported by two groups each in Ndhiwa and Rachuonyo as the most limiting factor of sweet potato production (Table 3.2). They explained that erratic rains lead to loss of soil moisture leading to soil cracking which enhances the weevils to attack the crop. The least threatening factors in both sub-Counties to sweet potato production reported by farmers in groups were infestation of crop by disease and lack of capital (Table 3.2). However, the study established that infestation by porcupines, too much rain, difficulty in land preparation and infestation

by couch grass (*Elymus repens*) among others were sweet potato constraints that were unique to Ndhiwa sub-County (Table 3.2).

Table 3.2: Major Constraints to sweet potato production in Homa Bay County

SUB-COUNTY	Division	RANK 1	2	3	4	5	6	7
Rachuonyo South	Kasipul	Infestation by SPW and Mole rats	Lack of market	Lack of healthy vines	*	*	*	*
	Kabondo	Erratic rains	Lack of healthy vines	Lack of capital	Lack of market	Infestation by Mole rats	Infestation by SPW	Infestation by disease
Ndhiwa	Kobama	Lack of healthy vines	Erratic rains	Infestation by SPW	Lack of market	Weeds (couch grass)	Late maturity of variety	Difficulty in land preparation
	Nyarongi	Infestation by SPW	Infestation by Mole rats	Infestation by disease	Too much rains	Lack of market	Erratic rains	*
	Ndhiwa Group 1	Infestation by SPW	Lack of healthy vines	Erratic rains	(i) Infestation by disease (ii) Road inaccessibility	(i) Lack of capital (ii) degraded soils	Infestation by porcupines	Infestation by Mole rats
	Ndhiwa Group 2	Erratic rains	Lack of healthy vines	Lack of capital	Lack of market	Infestation by Mole rats	Infestation by SPW	Infestation by disease

* There was no ranking of any constraint; SPW means Sweet potato weevil

3.3.3 Most problematic pests of sweet potato varieties

About 93.3% (250) of the respondents who participated in this study stated that sweet potato weevil was the most problematic pest that affects sweet potato (Table 3.3). Moreover, the results indicated that 90.3% of the respondents from Rachuonyo sub-County stated that sweet potato weevil was the most problematic pest while 96.8% of the respondents from Ndhiwa stated that sweet potato weevil was the most problematic pest (Table 3.3). Another 3.4% (9) of farmers identified moles as an equally

problematic pest (Table 3.3). Additionally, the findings of this study revealed that large animals like cattle were also considered as a threat to the production of sweet potatoes as stated by 1.5% (4) of the respondents (Table 3.3). Other pests mentioned were potato clearwing moth (0.7%), stainer (0.4%), porcupine (0.4%) and grain borer (0.4%).

Table 3.3: Most problematic pests/predators of sweet potato

S/N	Name of most problematic Pest/Predator	Number of respondents			Percentage of respondents Within the sub-County			Within the the two sub-Counties		
		SB1 (m)	SB2 (n)	∑ SB1 + SB2 (p)	SB1 (u) u =m/144 * 100	SB2 (v) v =n/124 * 100	∑ SB1 + SB2 (w) w =p/268 * 100	SB1 (x) x =m/p * 100	SB2 (y) y =n/p * 100	∑ SB1 + SB2 (z) z =p/p * 100
1	Sweet potato weevil	130	120	250	90.3	96.8	93.3	52.0	48.0	100
2	Potato clearwing moth	2	0	2	1.4	0.0	0.7	100	0.0	100
3	Livestock	4	0	4	2.8	0.0	1.5	100	0.0	100
4	Moles	6	3	9	4.2	2.4	3.4	66.7	33.3	100
5	Stainer	1	0	1	0.7	0.0	0.4	100	0.0	100
6	Porcupine	1	0	1	0.7	0.0	0.4	100	0.0	100
7	Grain borer	0	1	1	0.0	0.8	0.4	0.0	100	100

Key:

SB1 means Rachuonyo sub-County;

SB2 means Ndhiwa sub-County;

m is the number of farmers in Rachuonyo sub-County reporting on a pest;

n is the number of farmers in Ndhiwa sub-County reporting on a pest;

p is the number of farmers in both Rachuonyo and Ndhiwa sub-Counties reporting on a pest; **u** is the percentage of farmers in Rachuonyo sub-County reporting on a pest;

v is the percentage of farmers in Ndhiwa sub-County reporting on a pest;

w is the percentage of farmers in both Rachuonyo and Ndhiwa sub-Counties reporting on a pest;

x is the percentage of farmers in Rachuonyo sub-County reporting on a pest out of the total farmers in both sub-counties that had reported on the same pest.

y is the percentage of farmers in Ndhiwa sub-County reporting on a pest out of the total farmers in both sub-counties that had reported on the same pest;

z is the total percentage of farmers in both sub-Counties reporting on a pest.

A significance level of 0.05, a p-value of 0.160 was obtained which implied that there was no significant relationship between the sub-County and the respondents' perception on the most problematic pest (Table 3.4).

Table 3.4: Correlation of respondents reporting on the most problematic pest in Rachuonyo and Ndhiwa sub-Counties

Symmetric Measures					
		Value	Asymp. Std. Error[a]	Approx. T[b]	Approx. Sig.
Interval by Interval	Pearson's R	-0.086	0.061	-1.411	0.160[c]
N of Valid Cases		268			

a. Not assuming the null hypothesis.
b. Using the asymptotic standard error assuming the null hypothesis.
c. Based on normal approximation.

3.3.4 Sweet potato genotypes with field resistance to *Cylas* spp.

The study established that majority of the farmers from Rachuonyo (89.6%) and Ndhiwa (91.9%) were not aware of any sweet potato genotype that had field resistance to *Cylas* spp. (Table 3.5). However, some farmers in Rachuonyo (10.4%) and Ndhiwa (8.1%) reported nine genotypes which had shown some level of field resistance to root damage by *Cylas* spp. (Table 3.5). The genotypes reported by farmers in Rachuonyo (Kalamb Nyerere, Tombra, Sinia, Odinga, Kemb 10, Wera, Zapallo) were different from those reported in Ndhiwa (Amina, Mugande and Ndege oyiejo (Table 3.5).

Table 3.5: Farmers views on sweet potato genotypes with field resistance to *Cylas* spp.

S/N	Name of weevil resistant variety	Number of respondents			Percentage of respondents Within the sub-County			Within the the two sub-Counties		
		SB1 (m)	SB2 (n)	∑ SB1 + SB2 (p)	SB1 (u)	SB2 (v)	∑ SB1 + SB2 (w)	SB1 (x)	SB2 (y)	∑ SB1 + SB2 (z)
					u =m/144 * 100	v =n/124 * 100	w =p/268 * 100	x =m/p * 100	y =n/p * 100	z =p/p * 100
1	Not applicable	129	114	243	89.6	91.9	90.7	53.1	46.9	100
2	Kalamb Nyerere	1	0	1	0.7	0.0	0.4	100	0.0	100
3	Tombra	3	0	3	2.1	0.0	1.1	100	0.0	100
4	Sinia	2	0	2	1.4	0.0	0.7	100	0.0	100
5	Odinga	6	0	6	4.2	0.0	2.2	100	0.0	100
6	Odinga and Kemb 10	1	0	1	0.7	0.0	0.4	100	0.0	100
7	Odinga, Kemb 10 and Zapallo	1	0	1	0.7	0.0	0.4	100	0.0	100
8	Tombra and Wera	1	0	1	0.7	0.0	0.4	100	0.0	100
9	Amina and Mugande	0	9	9	0.0	7.3	3.4	0.0	100	100
10	Ndege oyiejo	0	1	1	0.0	0.8	0.4	0.0	100	100

Key:

SB1 means Rachuonyo sub-County; **SB2** means Ndhiwa sub-County;

m is the number of farmers in Rachuonyo sub-County reporting on a resistant genotype;

n is the number of farmers in Ndhiwa sub-County reporting on a resistant genotype;

p is the number of farmers in both Rachuonyo and Ndhiwa sub-Counties reporting on a resistant genotype;

u is the percentage of farmers in Rachuonyo sub-County reporting on a resistant genotype;

v is the percentage of farmers in Ndhiwa sub-County reporting on a resistant genotype;

w is the percentage of farmers in both Rachuonyo and Ndhiwa sub-Counties reporting on a resistant genotype;

x is the percentage of farmers in Rachuonyo sub-County reporting on a resistant genotype out of the total farmers in both sub- counties that had reported on the same resistant genotype.

y is the percentage of farmers in Ndhiwa sub-County reporting on a resistant genotype out of the total farmers in both sub-counties that had reported on the same resistant genotype;

z is the total percentage of farmers in both sub-Counties reporting on a resistant genotype.

This study established that only a small percentage of the farmers from Rachuonyo (1.4%) and Ndhiwa (4.0%) who were aware of genotypes that had field resistance to *Cylas* spp. were still growing them (Table 3.6). However, the rest of the farmers gave different reasons as to why they no longer grew the resistant genotypes even though they were aware of them (Table 3.6). Some of the reasons that were given by farmers to justify why they did not grow the resistant genotypes known to them are presented in Table 3.6. The reasons included unsuitable genotype characteristics like high fibre content (0.7%), not tasty/sweet (2.6%), poor storage potential (1.5%), low yielding (0.4%), late maturity (0.4%), susceptibility to water logging (0.4%) and unmarketability (2.2%). The results of this study show that the genotypes reported by farmers for resistance to *Cylas* spp. were region specific (Table 3.6).

Table 3.6: Reasons that contributed to farmers unadoption of sweet potato genotypes with field resistance to Cylas spp.

S/N	Reason given by farmer for not growing weevil resistant genotype	Number of respondents			Percentage of respondents					
					Within the sub-County			Within the the two sub-Counties		
		SB1 (m)	SB2 (n)	∑ SB1 + SB2 (p)	SB1 (u) u =m/144 * 100	SB2 (v) v =n/124 * 100	∑ SB1 + SB2 (w) w =p/268 * 100	SB1 (x) x =m/p * 100	SB2 (y) y =n/p * 100	∑ SB1 + SB2 (z) z =p/p * 100
1	Not applicable (since farmer was not aware of any sweet potato resistant genotype)	129	114	243	89.6	91.9	90.7	53.1	46.9	100
2	Not applicable (since farmer still grows the resistant sweet potato genotype)	2	5	7	1.4	4.0	2.6	28.6	71.4	100
3	Lack of planting vines	5	3	8	3.5	2.4	3.0	62.5	37.5	100
4	Genotype not marketable	6	0	6	4.2	0.0	2.2	100	0.0	100
5	Genotype has high fibre content	2	0	2	1.4	0.0	0.7	100	0.0	100
6	Genotype not tasty/sweet	5	2	7	3.5	1.6	2.6	71.4	28.6	100
7	Poor storage potential	4	0	4	2.8	0.0	1.5	100	0.0	100
8	Suceptible to water logging	1	0	1	0.7	0.0	0.4	100	0.0	100
9	Genotype is low yielding	1	0	1	0.7	0.0	0.4	100	0.0	100
10	Genotype is late maturing	1	0	1	0.7	0.0	0.4	100	0.0	100

Key: **SB1** means Rachuonyo sub-County; **SB2** means Ndhiwa sub-County;

m is the number of farmers in Rachuonyo sub-County reporting on a reason;

n is the number of farmers in Ndhiwa sub-County reporting on a reason;

p is the number of farmers in both Rachuonyo and Ndhiwa sub-Counties reporting on a reason;

u is the percentage of farmers in Rachuonyo sub-County reporting on a reason; **v** is the percentage of farmers in Ndhiwa sub-County reporting on a reason;

w is the percentage of farmers in both Rachuonyo and Ndhiwa sub-Counties reporting on a reason;

x is the percentage of farmers in Rachuonyo sub-County reporting on a reason out of the total farmers in both sub-counties that had reported on the same reason.

y is the percentage of armers in Ndhiwa sub-County reporting on a reason out of the total farmers in both sub-counties that had reported on the same reason;

z is the total percentage of farmers in both sub-Counties reporting on a reason.

Even though the genotypes reported by farmers for resistance to *Cylas* spp. were region specific, the results of this study show that the correlation between Rachuonyo and Ndhiwa sub-Counties on the resistant genotypes to *Cylas* spp. was not significant (Table 3.7). A correlation value of 0.108 and at significance level of 0.05, p-value of 0.077 was obtained (Table 3.7) which implied that there was no significant relationship between the two sub-Counties and the genotypes that had field resistance to *Cylas* spp.

Table 3.7: Correlation of varieties reported to have resistance to *Cylas* spp. in Rachuonyo and Ndhiwa sub-Counties

Symmetric Measures					
		Value	Asymp. Std. Error[a]	Approx. T[b]	Approx. Sig.
Interval by Interval	Pearson's R	0.108	0.054	1.776	0.077[c]
N of Valid Cases		268			

a. Not assuming the null hypothesis.
b. Using the asymptotic standard error assuming the null hypothesis.
c. Based on normal approximation.

3.3.5 Farmers' management practices of *Cylas* spp.

It was evident from this study that different methods of *Cylas* spp. management were engaged in the two sub-Counties. The findings are shown in Table 3.8. *Cylas* spp. management methods used by farmers in Rachuonyo included earthing-up of ridges (re-ridging) during weeding (26.2%), early harvesting (14.5%), removal of exposed roots from the ground (11%), disposal of infested roots at harvest (11.7%), early planting (12.4%), planting on ridges (19.3%), use of clean planting vines (15.2%), covering of exposed roots with soil (23.4%), minimizing movement in the field once the crop is ready for harvest (20%), intercropping sweet potato with other crops (0.7%), crop rotation (2.8%), use of pesticides (2.1%), practicing field sanitation (2.1%) and growing the crop in a field that is situated far away from an old sweet potato crop (4.1%). In Ndhiwa, sweet potato management practices included re-ridging during weeding

(15.3%), disposal of infested roots at harvest (12.1%), early planting (0.8%), early harvesting (6.5%), crop rogueing (7.3%), use of pesticides (0.8%) and use of wood ash (0.8%).

Table 3.1: Control methods for *Cylas* spp. on sweet potato crop by farmers in Homa Bay County

S/N	Control Method(s) as practised by respondents	Numbers of respondents			Percentage of respondents					
					Within the sub-County			Within the two sub-Counties		
		SB1 (m)	SB2 (n)	∑ SB1 + SB2 (p)	SB1 (u) u =m/145 * 100	SB2 (v) v =n/124 * 100	∑ SB1 + SB2 (w) w =p/269 * 100	SB1 (x) x =m/p * 100	SB2 (y) y =n/p * 100	∑ SB1 + SB2 (z) z =p/p * 100
1	Not applicable (Don't control the weevils)	16	80	96	11.0	64.5	35.7	16.7	83.3	100
2	Early harvesting	21	8	29	14.5	6.5	10.8	72.4	27.6	100
3	Earthing up of the ridges during weeding (re-ridging)	38	19	57	26.2	15.3	21.2	66.7	33.3	100
4	Planting during rainy season (Early planting)	18	1	19	12.4	0.8	7.1	94.7	5.3	100
5	Use of Pesticides	3	1	4	2.1	0.8	1.5	75.0	25.0	100
6	Removal of exposed roots from the ground	16	0	16	11.0	0.0	5.9	100	0.0	100
7	Disposal of infested roots during harvesting	17	15	32	11.7	12.1	11.9	53.1	46.9	100
8	Planting on ridges	28	0	28	19.3	0.0	10.4	100	0.0	100
9	Use of clean planting vines	22	0	22	15.2	0.0	8.2	100	0.0	100
10	Planting in fields that are situated far away from old sweet potato fields	6	0	6	4.1	0.0	2.2	100	0.0	100
11	Field sanitation	3	0	3	2.1	0.0	1.1	100	0.0	100
12	Practice crop rotation	4	0	4	2.8	0.0	1.5	100	0.0	100
13	Covering exposed roots with soil	34	0	34	23.4	0.0	12.6	100	0.0	100
14	Intercropping sweet potato with other crops (cowpea or maize)	1	0	1	0.7	0.0	0.4	100	0.0	100
15	Farmer minimizes moving in the field once the crop is ready for harvest	29	0	29	20.0	0.0	10.8	100	0.0	100
16	Crop rogueing	0	9	9	0.0	7.3	3.3	0.0	100	100
17	Use of wood ash	0	1	1	0.0	0.8	0.4	0.0	100	100

Key: **SB1** means Rachuonyo sub-County;
SB2 means Ndhiwa sub-County;
m is the number of farmers in Rachuonyo sub-County reporting on a control method;
n is the number of farmers in Ndhiwa sub-County reporting on a control method;
p is the number of farmers in both Rachuonyo and Ndhiwa sub-Counties reporting on a control method;
u is the percentage of farmers in Rachuonyo sub-County reporting on a control method;
v is the percentage of farmers in Ndhiwa sub-County reporting on a control method;
w is the percentage of farmers in both Rachuonyo and Ndhiwa sub-Counties reporting on a control method;
x is the percentage of farmers in Rachuonyo sub-County reporting on a reason out of the total farmers in both sub-counties that had reported on the same control method.
y is the percentage of farmers in Ndhiwa sub-County reporting on a control method out of the total farmers in both sub-counties that had reported on the same control method;
z is the total percentage of farmers in both sub-Counties reporting on a control method.

3.3.6: The relationship between farmers demographic profile and selected variables

The relationship between farmers demographic profile and their perception on the most problematic sweet potato pest; knowledge on sweet potato genotypes resistant to *Cylas* spp.; reasons for their unadoption of the known sweet potato resistant genotype; and their control methods of *Cylas* spp. is shown below (Table 3.9). The results of this study show that farmers' age, gender, education level and occupation did not affect the manner in which they perceived the most problematic pest of sweet potato (Table 3.9). However, the relationship between the respondents' gender and the knowledge of sweet potato genotypes resistant to weevils was significant ($p \leq 0.05$) as shown in Table 3.9. Further, the relationship between the respondents' occupation and the knowledge of sweet potato genotypes resistant to weevils was significant ($p \leq 0.05$). The respondents' occupation also influenced their continual use of resistant genotypes to the sweet potato weevil (Table 3.9). The results of this study also revealed that the relationship between the level of education and weevil control strategies by the respondents was significant ($p \leq 0.05$) as shown in Table 3.9.

Table 3.9: The relationship between farmers' demographic profile and other selected variables

Variables	Age	Gender	Education level	Occupation
Most problematic pest of sweet potato genotypes as perceived by respondents.	0.776ns	0.082ns	0.260ns	0.135ns
Knowledge on sweet potato varieties with field resistance to *Cylas* spp. as perceived by respondents.	0.278ns	0.010*	0.425ns	0.001*
Control method(s) of the sweet potato weevil as practiced by respondents	0.102ns	0.563ns	0.020*	0.473ns
Reasons for unadoption of sweet potato genotypes with field resistance by the respondents.	0.816ns	0.215ns	0.494ns	0.012*

*Significant at $p \leq 0.05$ ns means not significant at $p \leq 0.05$.

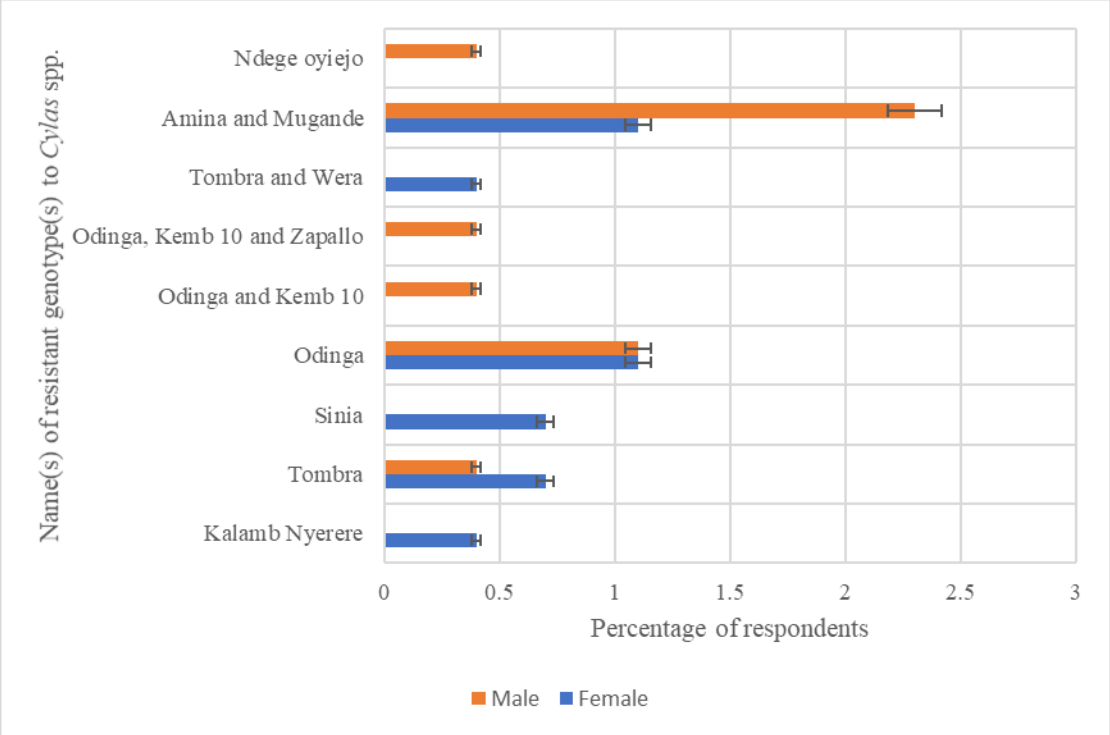

Figure 3:2: Relationship between gender of respondents and their knowledge on sweet potato genotypes resistant to weevils

According to the results of this study, gender of the farmer affected how farmers perceived the genotypes that were resistant to sweet potato weevils. Apart from, genotypes Odinga, Tombra, Kemb 10 and Zapallo, other genotypes were perceived differently by the two genders which was significant (Figure 3.2). For instance, out of the 269 farmers interviewed, genotypes Ndege oyiejo (0.4%), Kemb 10 (0.4%) and Zapallo (0.4%) were perceived by only males as resistant while genotypes Wera (0.4), Sinia (0.7%) and Kalamb Nyerere were perceived by females only as resistant (Figure 3.2).

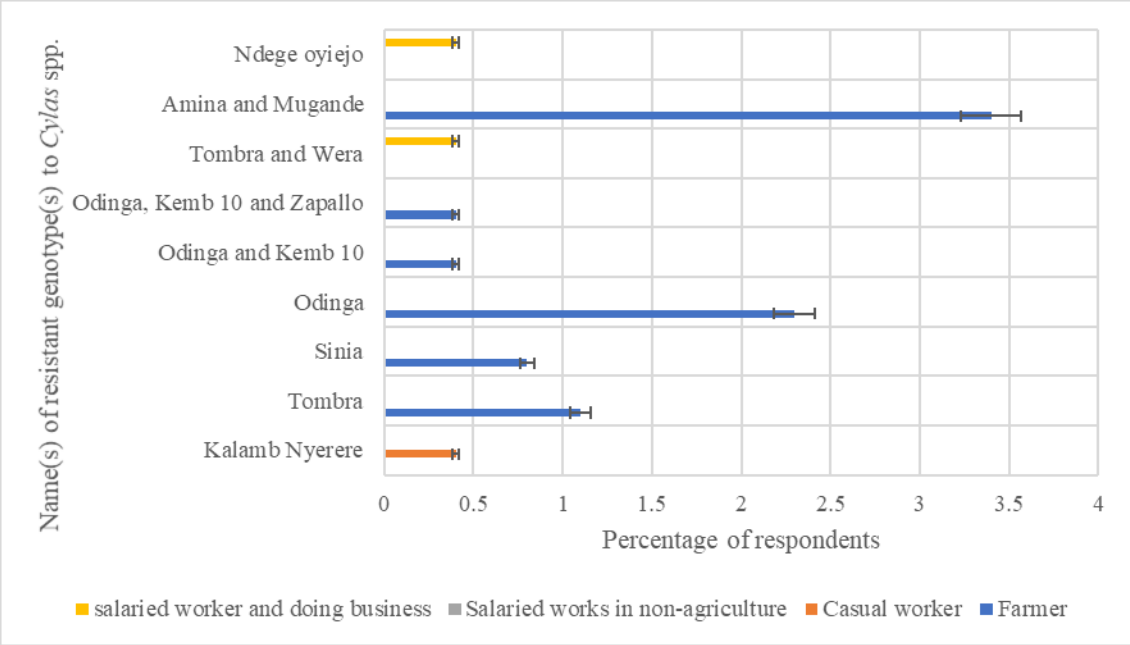

Figure 3:3: Relationship between occupation of the respondents and knowledge on sweet potato genotypes resistant to weevils

Results of this study show that the respondents whose occupation was farming were the people who reported many sweet potato genotypes that had resistance to weevils (Figure 3.3). They solely identified genotypes Amina, Mugande, Zapallo, Kemb 10, and Odinga as resistant genotypes to weevils (Figure 3.3). Genotype Ndege oyiejo was reported by a salaried worker who owns also a business enterprise as a resistant genotype to weevils, while genotype Kalamb Nyerere was reported by a casual worker as a resistant genotype to weevils (Figure 3.3).

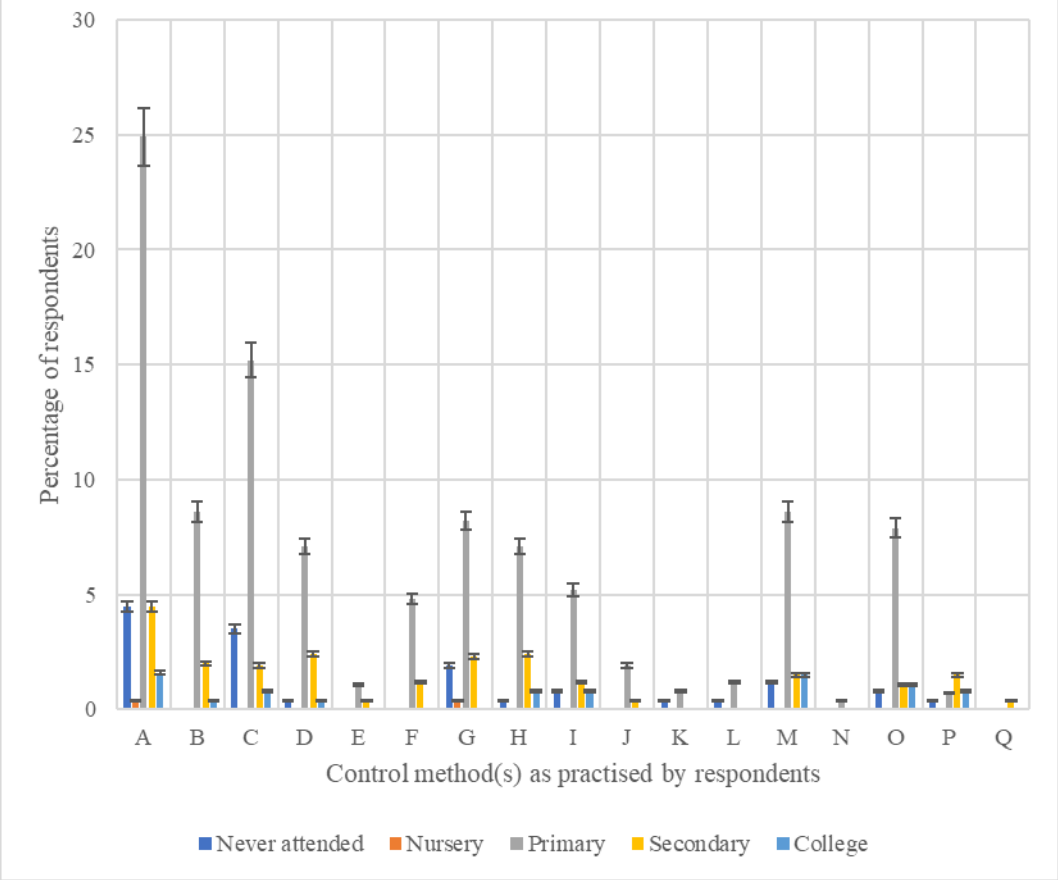

Figure 3:4: Relationship between level of education of the respondents and weevil control methods as practiced by farmers

Key:

A -Not applicabe (Respondent doesn't control the weevils)
B -Early harvesting
C -Earthing up of ridges during weeding (re-ridging)
D -Planting during rainy season (Early planting)
E -Use of pesticides
F -Removal of exposed roots from the ground
G -Disposal of infested roots during harvesting
H -Planting on ridges
I -Use of clean planting vines
J -Planting in fields that are situated far away from old sweet potato fields
K -Field Sanitation
L -Practice crop rotation
M -Covering exposed roots with soil
N -Intercropping sweet potato with other crops (cowpea and maize)
O -Farmer minimizes moving in the field once the crop is ready for harvest
P -Crop rogueing
Q -Use of wood ash

According to the results of this study, many of the control methods of *Cylas* spp. are practiced by respondents whose level of education was at primary level followed by those whose level of education was at secondary level (Figure 3.4). Sweet potato weevil control methods practiced by those who had attained education at primary level included re-ridging (15.2%), early havesting (8.6%) and covering of exposed roots with soil (8.6%) among others (Figure 3.4). The study also revealed that those respondents who had never gone to school controlled sweet potato weevils with an exception of 4.5% who did not control the weevils (Figure 3.4). There was also a case of a respondent who had attained tertiary education but did not control weevils (Figure 3.4).

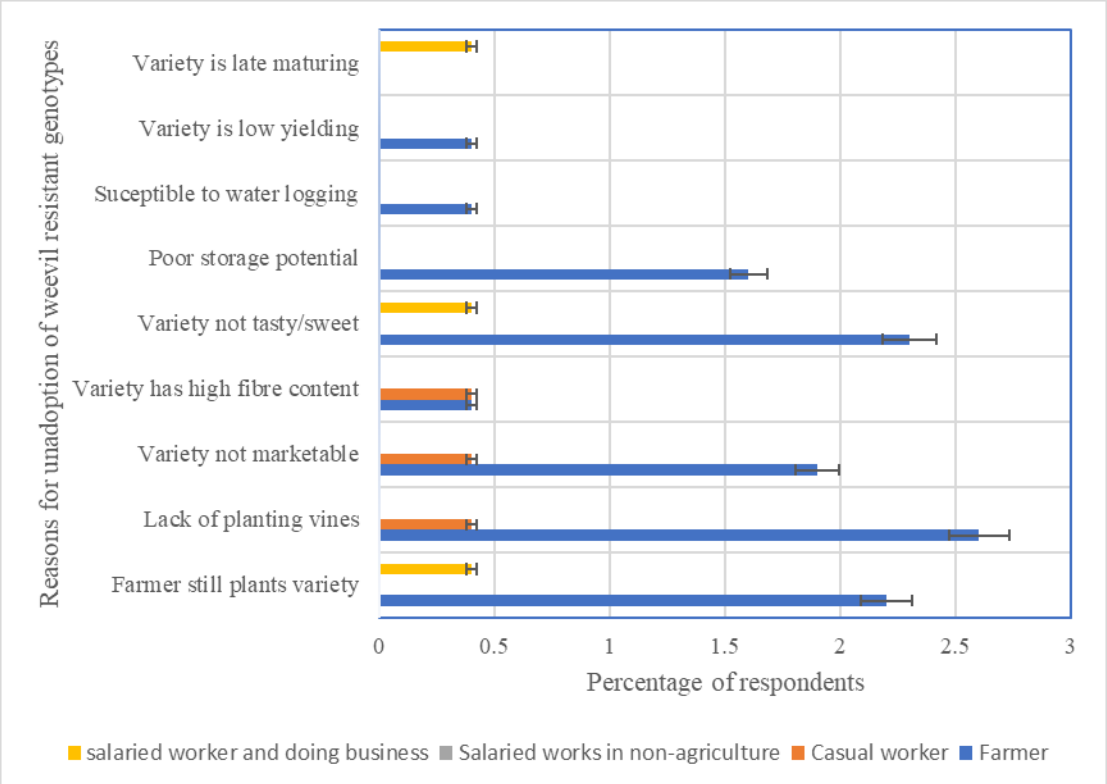

Figure 3:5: Relationship between occupation and respondents' reasons for unadoption of sweet potato genotypes resistant to weevils

Respondents had different reasons as to why the were not growing resistant genotypes to weevils in relation to their occupation. Farmers had many reasons of rejecting

genotypes known to them as weevil resistant more than any other group (Figure 3.5). Lack of planting vines and less sweet varieties were unfavorable traits cited by many farmers which were significantly different from other traits cited by other groups (Figure 3.5). This study revealed that it was only a portion of farmers (2.2%) and salaried workers with business enterprises (0.4%) that still grew weevil resistant genotypes known to them (Figure 3.5).

3.4 Discussion

The results from three out of six groups that rated the infestation of the sweet potato by *Cylas* spp. as the most serious problem emphasized the economic importance of the pest in the study region. Therefore, identification of factors limiting production and provision of environmentally-friendly options for integrated crop management is inevitable if sweet potato production among the small-scale farmers is to be increased (Okonya and Kroschel, 2013). The results that some sweet potato production constraints were reported by farmers in Ndhiwa and not by farmers in Rachuonyo could have been attributed to the differences in the agro-ecological conditions exhibited by the two regions (GOK, 2009a; GOK, 2009b). For instance, Ndhiwa sub-County in particular is noted for its heavy, difficult to manage vertisols, which occasionally are mixed with sandy loams or clay loams (GOK, 2009a). These soils are not suitable for sweet potato production because in case of the presence of much rain, they hold excess amounts of water resulting to rotting of the sweet potato roots. Rachuonyo on the other hand is covered by deep well drained soils that are easy to cultivate (GOK, 2009b). Such soils are suitable for sweet potato production since the crop does best on deep, moderately fertile, sandy loam soils (Stathers *et al*., 2013).

As established in this study, 93.3% of the farmers identified *Cylas* spp. as the most problematic pest that greatly affected sweet potato production in Homa Bay County. In some previous studies in Southern Ethopia, *Cylas* spp. was equally identified as the most problematic pest (Ashebir, 2006). For instance, in southern Ethiopia 68.3% of the

interviewed farmers identified *Cylas* spp. to be the most important pest in sweet potato production (Ashebir, 2006). The results of this study show that the genotypes reported by farmers for resistance to *Cylas* spp. were region specific. This could have been attributed to the fact that the planting varieties readily available to farmers are adapted to different agro-ecological conditions exhibited by the two sub-Counties (GOK, 2009a; GOK 2009b). Most of the genotypes adapted to the agro-ecological conditions in Rachuonyo sub-County and grown by farmers were different from most of the genotypes that were adapted to the agro-ecological conditions in Ndhiwa sub-County resulting to farmers from the two regions growing different genotypes and hence having different observations on the resistance to *Cylas* spp. The results of this study showing that the genotypes reported by farmers for resistance to *Cylas* spp. were region specific could also be caused by environmental effects on the grown genotypes making a genotype to be susceptible in one region but resistant in another region. For instance, Collins *et al.,* (1991) reported that inconsistent performance by selected breeding lines between years and within years at different locations is often encountered, limiting the successful development of commercially useful resistant sweet potato genotypes.

The resistant genotypes reported by farmers in Rachuonyo (Kalamb nyerere, Tombra, Sinia, Odinga, Kemb 10, Wera, Zapallo) were different from those reported in Ndhiwa (Amina, Mugande and Ndege oyiejo (Table 3.5). This is contrary to the findings from other studies where genotypes Kemb 10 and Zapallo were considered to be very susceptible to weevils in Western Kenya (Kwach *et al.,* 2008). According to these researchers, genotypes SPK 004 and Bungoma exhibited some degree of weevil resistance (Kwach *et al*., 2008) but in the current study, no farmer reported that. The reason behind these contradicting results on the resistance or susceptibility of genotypes could be attributed by the inconsistent performance of genotypes between years and within years at different locations which is usually encountered (Collins *et al.*, 1991).

Farmers observation on resistance of genotypes to *Cylas* spp. needs to be investigated further as they may provide potential sources of resistance to the pest. Some studies have reported differences in *Cylas* spp. damage among genotypes (Mwanga *et al*., 2003; Stathers *et al*., 2003a, b). However, complete sweet potato variety resistance to *Cylas* spp. has not been reported (Mwanga *et al*., 2003; Mwanga *et al*., 2009). Factors such as depth of rooting, quantity of root latex and amount of foliage, have been reported to contribute to reduced *Cylas* spp. sweet potato damage (Mwanga *et al*., 2003; Stathers *et al*., 2003a, b).

The most popular *Cylas* spp. management method in both Rachuonyo and Ndhiwa sub-Counties was found to be earthing-up of ridges (re-ridging) during weeding (Table 3.8). This is an important strategy to deter weevil infestation during drought conditions. It can be achieved by hilling (ridging) a small area around the sweet potato plant in order to prevent the entry of weevils into roots and oviposition by female weevils' (Hue and Low, 2015). However, re-ridging works best only when performed at the root formation stage. Therefore, the practice of some farmers (12.6%) covering already exposed roots with soil is not an effective management strategy.

A total of 8.2% respondents interviewed in this study use clean planting vines as a management strategy of *Cylas* spp (Table 3.8). This is an effective weevil management strategy. More than 95% oviposition occurs in the first 35 cm of vines especially when female weevils cannot access the roots and thus planting of infested vines is one of the ways of distributing weevils (Hue and Low, 2015). Nevertheless, farmers are cautioned against the use of older portions of vines as these are usually severely infested with weevils as compared to younger vines (AVRDC, 1990). Since planting of infested vines will spread weevil infestation, treatment of infested vines with insecticides is currently being recommended to reduce weevil infestation (Hue and Low, 2015).

The use of pesticides to control weevils as practiced by 1.5% of farmers can be effective depending on the type of insecticide used. Hwang and Hung (1994) conducted a field experiment to test the efficacy of five insecticides: chlorpyrifos, phorate, terbufos, fensulfothion, and carbofuran, in controlling sweet potato weevils, by applying the insecticide twice to soil before planting and during earthing up. In both studies, chlopryrifos demonstrated a high efficacy in suppressing sweet potato weevil infestation and hence it is widely used as one of the control methods during the integrated pest management of sweet potato weevils.

Intercropping of sweet potato with maize or cowpea, crop rotation and field sanitation as practiced by some farmers reduces the incidence of sweet potato weevils. It has been reported that intercropping sweet potato with cowpea resulted in up to tenfold reduction in the infestation of *Cylas* spp. compared to monocrop of sweet potato (Pillai *et al.*, 1987). Besides, effective crop rotations also resulted in lower tuber damage compared to monoculture of sweet potato (Pillai *et al.*, 1996). Further, sanitation practices play a vital role in protecting sweet potatoes from pests with limited flying capacity such as *Cylas* spp. (Hue and Low, 2015).

Other *Cylas* spp. management methods used by farmers such as early planting and harvesting as practiced by 7.1% and 10.8% of the total respondents (Table 3.8) can also reduce incidences of *Cylas* spp. (Hue and Low, 2015). This is because early planting ensures that the crop matures during rainy season which prevents soil cracking because of sufficient moisture in the soil (Hue and Low, 2015). Soil cracking due to drought will facilitate the entry of eggs into the roots. Besides, some studies reported that weevil associated damage increase by over four times if harvesting was delayed by 30 days (Cisneros and Gregory, 1994; Cisneros *et al.*, 1995). This means that it is necessary to harvest mature crops early enough to reduce weevil spread.

The results that individuals from the two genders (male and female) perceived different genotypes resistant to weevils could be attributed to their differences in the preference of genotypes grown. The results that those who are in farming career reported many sweet potato genotypes resistant to weevils as compared to other respondents could be attributed to the fact that the farmers in search of suitable genotypes for production, have been able to grow many genotypes through trial and error and hence have had a wider observation on how they react to weevils. Another probable reason could be that as farmers search on weevil resistant genotypes (sweet potato weevil being an economic pest), they have exchanged information amongst themselves with the help of extension officers. The fact that many respondents with primary level of education practiced many weevil management practices than any other group could be attributed to knowledge acquired through personal experience and informal education. The fact that only a few respondents who had tertiary education practiced a few weevil management strategies could be attributed to acquiring knowledge in a non-crop science field while in college hence there is need that they be trained on sweet potato production too.

3.5 Conclusion

The following are conclusions made from this study:

1. *Cylas* spp. was the most problematic pest by 90.3- 96.8% of households in Homa Bay County.
2. Many (35.7%) of the farmers in Homabay County did not use any strategies to manage *Cylas* spp with most (64.5%) from Ndhiwa sub-County.
3. The three most important coping strategies against the weevil in Homa bay County are earthing-up of ridges during weeding, covering of exposed roots with soil and disposal of infested roots during harvesting that are practiced by 21.2%, 12.6% and 11.9% of the farmers respectively.
4. Gender of the farmer influenced the reporting of resistsant genotypes to weevils in Homa Bay County.

CHAPTER FOUR

EVALUATION OF VARIATION AMONG SWEET POTATO (*Ipomea batatas*) GENOTYPES USING AGRO-MORPHOLOGICAL, MOLECULAR AND NUTRITIONAL CHARACTERISTICS

4.1 Introduction

A comprehensive analysis of the variation in sweet potato is essential for sound germplasm conservation strategies (e.g. sampling of existing genetic resources in germplasm collections and at successive stages of development in breeding programmes, identification of duplicates, selection for core collection and future exploration planning). The possibility of improvement in any crop is dependent on the variability available in the crop (Jindal *et al*., 2010). For instance, the wider the genetic variability in the traits, the better the chances of improvement through selection (Jindal *et al*., 2010). Das and Naskar (2008) pointed out that analysis of genotypes at genetic level gives more light on their genetic relationships along with morphological traits which will be of immense help in guiding the breeding programme in sweet potato for their improvement. Characterization is valuable for providing gene banks with complete information on the characteristics of a given germplasm, thereby contributing to an optimal ex-situ management of collections.

Studies by a number of scientists have shown strong variations existing in sweet potato plants, which include skin and flesh colour, depth of rooting, storage root shape and size, variations in the resistance to insect pests and diseases as well as partitioning of dry matter content, among others (Vimala and Hariprakash, 2011; La Bonte *et al*., 2000). The establishment of appropriate understanding of these variations would consistently contribute to the selection and improvement of the crop. Traditionally, sweet potato characterization has been based on morphological and agronomic traits as they are easy to evaluate and the methods are relatively cheap (Elameen *et al.*, 2011). However, the expression of these traits is subject to genetic constitution, environmental factors and their interactions. Most of the important characters including yield are

highly influenced by environment, since they are polygenically controlled (Amin and Singla, 2010). However, qualitative characters such as general outline of the leaf and shape of the central leaf lobe have been reported to be important in studying the crops diversity (Karuri *et al*., 2010), since these characters are not affected by the environment (Huaman, 1992). From evaluating 14 sweet potato accessions, Daros *et al.* (2002) reported high morphological variability. They noted that the most informative descriptors were the abaxial leaf vein pigmentation, shape of the roots and vine tip pubescence (Daros *et al.*, 2002). Morphological variation has been widely used to characterize sweet potato genotypes (Gichuru *et al*., 2006; Karuri *et al*., 2010; Koussao *et al*., 2014) and to eliminate duplicates among genetic accessions (Li *et al*., 2009; Karuri *et al*., 2009). Additionally, Jha (2011) and Beah *et al.* (2014) using agro-phenotypic characters reported wide diversity among sweet potato genotypes in India and Sierra Leone, respectively.

In order to optimize germplasm characterization efficiency, agro-morphological characterization has now been combined with molecular techniques (Koussao *et al*., 2014). The complex genome of sweet potato, and the fact that it is extremely heterozygous, exhibiting multiple combinations of chromosomes and genes due to its ploidy, contributes to its molecular diversity. According to Naylor *et al.* (2004), one can use molecular markers as tools to detect the extent and structure of genetic variation; provide insights into the diversity of crop varieties and potential contributions offered by their wild relatives; and to analyze the inheritance of key crop traits (including those that are subject to complex inheritance due to the involvement of numerous genes). Molecular markers concern the DNA molecule itself and, as such, are considered to be objective measures of variation. They are not subject to environmental influences; tests can be carried out at any time during plant development; and, best of all, have the potential of occurring in unlimited numbers, covering the entire genome (de Vicente and Fulton, 2003). Commonly used molecular markers include Restriction Fragment Length Polymorphism (RFLP), Random Amplified Polymorphic DNA (RAPD),

Amplified Fragment Length Polymorphism (AFLP), Inter-Simple Sequence Repeats (ISSR) and Simple Sequence Repeats (SSR) (Williams *et al*., 1990). Such markers are morphologically neutral, and not influenced by epistatic interactions (Koutita *et al*., 2005).

Use of microsatellites also called simple sequence repeats (SSR) can be of great help in genetic diversity studies. SSRs are highly variable and evenly distributed throughout the genome (Hajeer *et al.*, 2000). These are short, 2-8 nucleotide repeats such as CA or AGC, which are repeated in tandem up to hundreds of times at many independent loci, and are everywhere in eukaryote genomes (Lagarcrantz *et al.*, 1993).

These markers are easily automated, highly polymorphic, and have good analytical resolution, thus making them a preferred choice of markers (Matsuoka *et al*., 2002). These polymorphisms are identified by constructing PCR primers for the DNA flanking the microsatellite region (Hajeer *et al*., 2000; Godwin *et al*., 2001; Morgante *et al*., 2001). Since flanking DNA is more likely to be conserved, the microsatellite-derived primers can often be used with many varieties. Polymorphism is also based on the number of tandem repeat units (Godwin *et al*., 2001). These repeat motifs are flanked by conserved nucleotide sequences from which forward and reverse primers can be designed to PCR-amplify the DNA section containing the SSR (FAO/IAEA, 2002). SSRs can be exchanged easily between laboratories and multiple reactions can be run to speed up the assay, where the products have non-overlapping size ranges. It is also possible to amplify SSRs using smaller amounts of DNA.

Sweet potato (*Ipomoea batatas* L.) is rich in carbohydrate, starch, mineral, vitamin, protein and β-carotene contents (Ziska *et al*., 2009; Rose and Vasanthakaalam, 2011; Maria and Rodica, 2015). Different sweet potato genotypes have different contents of dry matter, carbohydrate, starch, protein and carotene contents. In sweet potato, the skin as well as the flesh contains carotenoids and anthocyanin pigments which determines its

colour. The combination and intensity of these pigments vary to produce varying intensities of yellow, cream, orange, pink or purple skin and flesh colour. Some researchers have studied the variety differences in sweet potato roots with regard to nutrition characters (Tumwegamire *et al*., 2011). Whereas levels of root β-carotene and dry matter contents are fairly well documented for African germplasm, there is scarce information about other quality traits, thus making results of this study unique. In Kenya, there is a large collection of sweet potato germplasm available but only a few genotypes have been studied in regard to nutrition characters. If the germplasm is to be utilized in breeding programmes, or if potential duplicates within it has to be identified, then there is a need to undertake characterization studies. The objective of this study was to characterize a range of sweet potato genotypes using agro-morphological characters, microsatellite markers and nutrition characters.

4.2 Materials and methods

4.2.1 Plant material

A total of 68 sweet potato genotypes collected in 2013 as vine cuttings from different sources (in Kenya and Uganda) were used in the study. Out of these, 57 genotypes were from KALRO -Embu comprising of 29 landraces, 28 improved clones while eleven F_1 hybrids were from National Crops Resources Research Institute (NaCRRI), Uganda (Table 4:1). The genotypes from KALRO had earlier been collected from Western (Kakamega, Homa Bay, Migori and Kisii Counties) and Eastern (Embu County) regions. The 68 sweet potato genotypes were multiplied at KALRO- Embu to increase their numbers.

Table 4.1: List of the 68 sweet potato genotypes collected for agro-morphological, molecular and nutrition characterization

Serial No.	Genotype name	Source*	Flesh colour
1	Kenspot 1	Eastern (Kenya)	Yellow
2	Saly boro	Western (Kenya)	Orange
3	91/2187	Western (Kenya)	Yellow
4	Oduogo jodongo	Western (Kenya)	White
5	5 Nyandere	Western (Kenya)	Cream-Yellow
6	Odinga	Western (Kenya)	Yellow
7	Naspot 1	Western (Kenya)	Yellow
8	Kenspot 3	Eastern (Kenya)	Orange
9	Naspot x New Kawogo 2	NaCRRI (Uganda)	Cream
10	Nyamuguta	Western (Kenya)	Cream-white
11	Nyautenge	Western (Kenya)	Cream
12	Ejumula x New Kawogo 4	NaCRRI (Uganda)	Yellow-orange
13	Nyarambe	Western (Kenya)	Cream
14	Nyakagwa	Western (Kenya)	Cream
15	Naspot x New Kawogo 3	NaCRRI (Uganda)	Yellow-orange
16	Ejumula x New Kawogo 2	NaCRRI (Uganda)	Cream
17	Nangili	Western (Kenya)	Yellow-orange
18	Kenspot 2	Eastern (Kenya)	White
19	SPK 013	Western (Kenya)	White
20	Mugande x New Kawogo 4	NaCRRI (Uganda)	Yellow-orange
21	Alupe-or	Western (Kenya)	Orange
22	12 Marooko	Western (Kenya)	Cream
23	Kenspot 5	Eastern (Kenya)	Orange
24	36 Kalamb Nyerere	Western (Kenya)	Cream-yellow
25	K/KA/2004/215	Western (Kenya)	Yellow
26	Ejumula x New Kawogo 3	NaCRRI (Uganda)	Yellow
27	292-H-12	Western (Kenya)	Yellow-cream
28	Mogesi Gikenja	Western (Kenya)	White
29	Lungabure	Western (Kenya)	Cream-white
30	Kenspot 4	Eastern (Kenya)	Orange
31	Vitaa	Western (Kenya)	Cream
32	9 Nduma	Western (Kenya)	Purple-cream
33	24 Kampala	Western (Kenya)	Yellow-orange
34	Obugi	Western (Kenya)	Yellow-orange
35	56682-03	Western (Kenya)	Cream
36	Nyawo Nyathiodiewo	Western (Kenya)	Orange
37	Gachaka	Western (Kenya)	Yellow-orange
38	Mugande	Western (Kenya)	White

39	Amina	Western (Kenya)	Orange
40	Fumbara jikoni	Western (Kenya)	Cream
41	Ejumula	Western (Kenya)	Orange
42	Karunde	Western (Kenya)	Cream
43	SPK 004	Western (Kenya)	Orange
44	Kuny kibuonjo	Western (Kenya)	Cream-white
45	K/KA/2002/12	Western (Kenya)	White
46	55 Nganyomba	Western (Kenya)	Cream
47	1 Ujili	Western (Kenya)	Yellow
48	Santo Amaro	Western (Kenya)	Cream
49	Mugande x New kawogo 2	NaCRRI (Uganda)	Cream
50	Wera	Western (Kenya)	Yellow
51	Kemb 10	Western (Kenya)	Yellow
52	Mbita	Western (Kenya)	Yellow
53	Naspot x New Kawogo 1	NaCRRI (Uganda)	Cream
54	Kibuonjo	Western (Kenya)	Cream-white
55	29 Kuny kibuonjo	Western (Kenya)	Yellow
56	62 Odhiogo	Western (Kenya)	Yellow
57	52 Nyakisumu	Western (Kenya)	Yellow-orange
58	Ejumula x New kawogo 1	NaCRRI (Uganda)	Cream
59	Bungoma	Western (Kenya)	Cream
60	K117	Western (Kenya)	White
61	Fundukhusia	Western (Kenya)	Yellow-orange
62	SPK 031	Western (Kenya)	Orange
63	Mugande x New kawogo 1	NaCRRI (Uganda)	Yellow
64	Mwavuli	Western (Kenya)	Cream
65	Polo yiengo	Western (Kenya)	Yellow
66	Mugande x New kawogo 3	NaCRRI (Uganda)	Cream
67	Sinia	Western (Kenya)	Yellow
68	Tainung	Eastern (Kenya)	Orange

*All the crosses in this study are F1 hybrids from a polycross obtained from National Crops Resources Research Institute (NaCRRI), Uganda.

4.2.2 Description of the trial sites

The experiment was done on-station at Miyare Agriculture Training College (ATC) farm situated in the Migori County and at the border of Homabay County and Kenya Agricultural and Livestock Research Organization (KALRO) situated in Embu County. The sites were separated to enable the investigation of environmental effects on agro-morphological and nutrition characters. KALRO Embu is characterized by an altitude of

1497 m asl, an average annual rainfall of 1252 mm, an average annual temperature of 19.5 ^{o}C and humic nitisols (KALRO, 2013). On the other hand, ATC - Miyare is characterized by an altitude of 1300-1620 m asl, an average annual rainfall of 1600-1800 mm, an average annual temperature of 16-17 ^{o}C and humic acrisols (GOK, 2013). The chemical assessment of top soils of the experimental sites is shown in Table 4.2.

Table 4.2: Chemical composition of soils at KALRO- Embu and ATC - Miyare

		KALRO- Embu	**ATC -Miyare**
Parameter	**Guide (optimum range for sweet potato production)**		
Phosphorus	20.0-100 ppm	57.3 ppm	30.3 ppm
Potassium	181-906 ppm	637 ppm	283 ppm
Calcium	2230-3250 ppm	2470 ppm	1170 ppm
Magnesium	278-502 ppm	448 ppm	251 ppm
Sodium	<267 ppm	26.8 ppm	23.6 ppm
Organic matter	3.00 - 8.00 %	4.98 %	5.03 %
Nitrogen	0.20 - 0.50 %	0.32 %	0.34 %

Source: Analysis was done by Crop Nutrition Laboratory Services, 2014
Key: ppm means parts per million

4.2.3 Experimental design and plant establishment

The sixty-eight (68) sweet potato genotypes were planted in a Randomized Complete Block Design (RCBD) on 27th March, 2014 and 28th April, 2014 for ATC Miyare and KALRO –Embu respectively. Blocking was done for heterogeneity of soils. Soils are known to have heterogenous physical, chemical and biological properties. The arrangement of the genotypes within the blocks is shown in figure 4.1. Each plot size was 1.5 m x 3.75 m while the plant spacing was 30 cm x 75 cm giving 25 plants per plot. Sweet potato cuttings measuring 30 cm long (9-node numbers per cutting) from each genotype were planted in five rows. No pesticides were applied during the course of the experiment. Weeding was done at both sites six weeks after planting. The eperimental fields were rain fed at both sites. The crop at both sites was harvested 160 days after planting. Sweet potato root samples in each plot were washed, packed and

transported to KALRO (Njoro) biochemical laboratory for dry matter and nutrition (namely protein, total carotenoids, total starch and sucrose) tests.

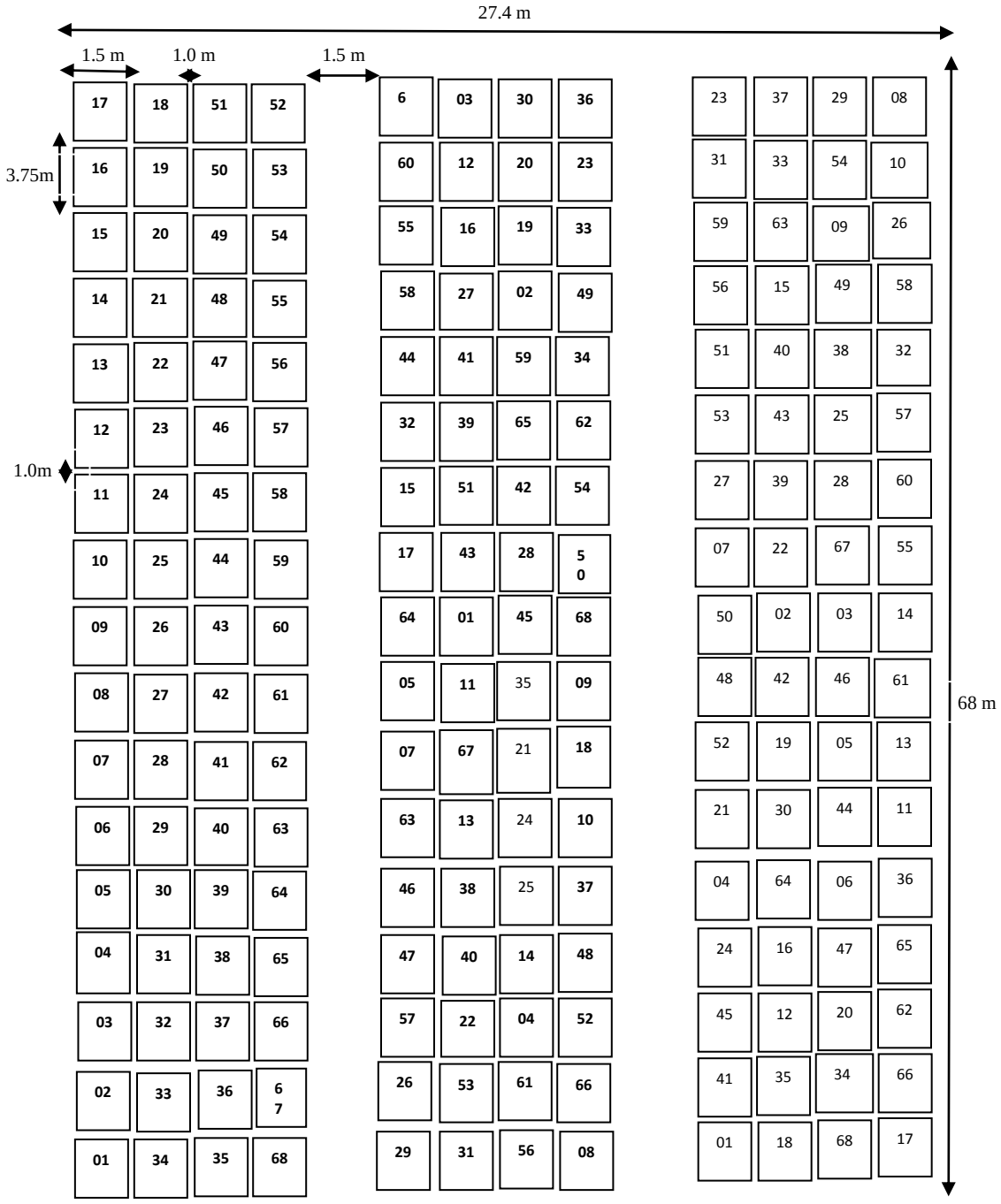

Figure 4.1: Field experimental layout in a RCBD for ATC -Miyare and KALRO -Embu sites

Key: 01 -Nyautenge, **02** -SPK 013, **03**-Ejumula x New kawogo 1, **04** -Naspot 1, **05** -Fundukusia, **06** -24 Kampala, **07** -Ejumula x New kawogo 2, **08** -Naspot x New kawogo 3, **09** -Saly boro, **10** -Lungabure, **11** -Nyarambe, **12** -Sinia, **13** -Mugande x New kawogo 1, **14** -Gachaka, **15** -Karunde, **16** -Odinga, **17** -292-H-12, **18** -Oduogo Jodongo, **19** -Alupe or, **20** -Mugande x New kawogo 4, **21** -K117, **22** -Santo Amaro, **23** -Naspot x New kawogo 2, **24** -Kenspot 3, **25** -55 Nganyomba, **26** -Mbita, **27** -Kenspot 5, **28** -12 Marooko, **29** -Kenspot 1, **30** -Nangili, **31** -Nyamuguta, **32** -Tainung, **33** -36 Kalmb Nyerere, **34** -Mugande x New kawogo 3, **35** -Kibuonjo, **36** -K/KA/2004/215, **37** -1-Ujili, **38** -Ejumula x New kawogo 4, **39** -Kuny kibuonjo, **40** -Nyakagwa, **41** -Mwavuli, **42** -5 Nyandere, **43** -K/KA/2002/12, **44** -62 Odhiogo, **45** -Naspot x New kawogo 1, **46** -Kenspot 4, **47** -Kenspot 2, **48** -Amina, **49** -91/2187, **50** -Polo yiengo, **51** -Nyawo Nyathiodiewo, **52** -Kemb 10, **53** -SPK 004, **54** -Obugi, **55** -9 Nduma, **56** -Mogesi Gikenja, **57** -Mugande, **58** -Ejumula, **59** -Fumbara jikoni, **60** -SPK 031, **61** -Mugande x New kawogo 2, **62** -Ejumula x New kawogo 3, **63** -56682-03, **64** -Wera, **65** -Vitaa, **66** -52 Nyakisumu, **67** -29 Kuny kibuonjo, **68** -Bungoma

4.2.4 Evaluation of agro-morphological characters

Agro-morphological characterization of the above and below ground parts was conducted using Internertional Potato Center (CIP) guide (Huaman, 1992) at 100 and 160 days after planting, respectively. The evaluation was done on nine (9) plants of each genotypye excluding the border plants of each plot. Table 4.3 shows key agro-morphological characters that were used in the agro-morphological evaluation of the sweet potato genotypes.

Table 4.3: List of descriptors used to characterize sweet potato genotypes

Storage root characters	
Storage root shape	Described as the storage root outline shown in a longitudinal section: 1 Round (an almost circular outline with a length to breadth [L/B] ratio of about 1:1), 2 Round elliptic (a slightly circular outline with acute ends. The L/B ratio not more than 2:1), 3 Elliptic (an outline with about the same breadth at equal distance from both ends which are slightly acute. The L/B ratio should not be more than 3:1), 4 Ovate (an outline resembling the longitudinal section of an egg. The broadest part is in the distal end), 5 Obovate (an outline which is inversely ovate. The broadest part is in the proximal end), 6 Oblong (an almost rectangular outline with sides nearly parallel and corners rounded. The L/B ratio about 2:1), 7 Long oblong (an oblong outline with a L/B ratio of at least 3:1), 8 Long elliptic (an elliptic outline with a L/B ratio of at least 3:1), 9 (Long irregular or curved)
Storage root size variability	3 (Uniform), 5 (Slightly variable), 7 (Moderately variable), 9 (Highly variable
Storage root stalk	Description of the length of the stalk joining the storage roots to the stems: 0 Sessile or absent, 1 Very short (<2 cm), 3 Short (2-5 cm), 5 Intermediate (6-8 cm), 7 Long (9-12 cm), 9 Very long (> 12 cm)
Storage root length	Storage root dimensions recorded on the most predominant size of storage roots produced by nine plants. Average length of ten storage roots in cm
Storage root diameter	Average of largest diameter of ten storage roots in centimeters
Oxidation of roots	Description of the relative amount of oxidation observed about 5 minutes after the cross section is made in medium sized storage roots: 0 (None), 1 (Very little), 3 (Little), 5 (Some), 7 (Abundant), 9 (Very abundant)
Latex production in storage roots	Description of the relative amount of latex observed about 5 seconds after the cross section is made in medium sized storage roots: 0 (None), 1 (Very little), 3 (Little), 5 (Some), 7 (Abundant), 9 (Very abundant)
Storage root cortex thickness	1 Very thin (<1 mm), 3 Thin (2mm), 5 Intermediate (2.1-2.9 mm), 7 Thick (3-4 mm), 9 Very thick (> 4 mm)
Weight of largest root	Weight of largest root in kilograms
Vine characters	
Vine growth rate	Description of the relative speed of growth of the main vines based on the average length reached at about 60 days from planting: 3 Slow (<50 cm), 5 Intermediate (50-100 cm), 7 Fast (>100 cm)
Vine internode length	1 Very short (<3 cm), 3 Short (3-5 cm), 5 Intermediate (6-9 cm), 7 long (10-12 cm), 9 Very long (>12 cm)
Vine inernode diameter	1 Very thin (<3 mm), 3 Thin (4-6 mm), 5 Intermediate (6-9 mm), 7 Thick (10-12 mm), 9 Very Thick (>12 mm)
Foliage characters	
Mature leaf size	Measured vertically from the apex. 3 Small (<8 cm), 5 Medium (8-15 cm), 7 Large (> 15 cm)
Abaxial leaf vein pigmentation	Description of the distribution of anthocyanin pigmentation shown in the veins of the lower surface of leaves. The most frequent expression should be recorded: 1 (Yellow), 2 (Green), 3 (Pigmented spot in the base of main rib), 4 (Pigmented spots in several veins), 5 (Main rib partially pigmented), 6 (Main rib mostly or totally pigmented), 7 (All veins partially pigmented), 8 (All veins totally pigmented), 9 (lower surface and veins totally pigmented)
Petiole length	The average petiole length of leaves located between the 8th and 10th node from the apical shoots: 1 Very short (<10 cm), 3 Short (10-15 cm), 5 Intermediate (16-20 cm), 7 Long (21-25 cm), 9 Very long (>25 cm)
Type of lobbing	0 (No lateral lobes/entire), 1 (very slight teeth), 5 (Moderate), 7 (Deep), 9 (Very deep)
Type of lobbing	0 (No lateral lobes/entire), 1 (very slight teeth), 5 (Moderate), 7 (Deep), 9 (Very deep)
Shape of central lobe	0 (Absent), 1(Teeth), 2 (Triangular), 3 (Semi-circular), 4 (Semi-elliptic), 5 Elliptic, 6 (Lanceolate), 7(Oblanceolate), 8 (Linear –broad), 9 (Linear –narrow)
Others	
Plant type	Description of the growth habit at about 90 days from planting: 3 (Compact), 5 (Semi-compact), 7 (Spreading), 9 (Extremely spreading)

Source: CIP guide (Huaman, 1992)

4.2.5 Molecular characterization

4.2.5.1 DNA extraction

DNA was extracted from fresh leaves of each genotype using the cetyl trimethyl ammonium bromide (CTAB) protocol modified from the Doyle and Doyle (1990) method. The modification involved omission of the ammonium acetate step and a longer DNA precipitation time of 12 hrs. The quality and quantity of the extracted DNA was checked by running it on a 1% agarose gel and using a nanodrop spectrophotometer. The DNA was then diluted to a working concentration of 30ng/µl.

4.2.5.2 Microsatellite (SSR) markers amplification

Polymerase Chain Reaction (PCR) amplification was done in an Applied Biosystem 2720 Thermo Cycler (Life technologies) using 13 microsatellite primer pairs (Table 4.4) obtained from Inqaba Biotechnical Industries Ltd. The amplification was performed in a 10 µl reaction containing Gotaq Green Master Mix (Thermo scientific), 25 mM $MgCl_2$ (Promega), 10 µM of each primer (Inqaba Biotec), 25 ng DNA working concentration and ddH_20. The pre-amplification conditions were 45 cycles which included (i) initial denaturation at 94 ^oC for 5 min., (ii) denaturation at 94 ^oC for 30 sec., (iii) annealing for 30 sec., (iv) extension at 72 ^oC for 2 min., and (v) final extension 72 ^oC for 10 min. After amplification, 10 ul of each of the amplicons was loaded on a 2% agarose gel (Bioline). Gel electrophoresis was done at a voltage of 80 V and a current of 400 mA for 1 hour in Tris Borate EDTA buffer. The amplicons were visualised as fluorescent bands under UV light on an Ebox VX5 Transilluminator (Wilber Lourmat). The size of the amplified markers was determined by using O'gene ruler green ready to use 100 bp or 1 Kb molecular ladder (Thermo Scientific). For each sample, the presence of a band (allele) was recorded as either present or absent.

Table 4.4: List of microsatellite markers and primer pairs used in the study

Primer	Sequence	Repeat Mortif	At (ºC)	Reference
IBR03	F GTAGAGTTGAAGAGCGAGCA R CCATAGACCCATTGATGAAG	(GCG)5	53	Benavides (unp.)
IBR12	F GATCGAGGAGAAGCTCCACA R GCCGGCAAATTAAGTCCATC	(CAG)5A	55	Benavides (unp.)
IB242	F GCGGAACGGACGAGAAAA R ATGGCAGAGTGAAAATGGAACA	(CT)3CA(CT)11	54	Buteler *et al*.,1999
IB275	F AGTTCCAAAGAGAAGAGTGGAG R AAGCCTACCCGAGAGATAACC	(CT)27	56	Buteler *et al*.,1999
J175	F ATCTATGAAATCCATCACTCTCG R ACTCAATTGTAAGCCAACCCTC	(AATC)4	54	Solis *et al*., (unp.)
IB316	F CAAACGCACAACGCTGTC R CGCGTCCCGCTTATTTAAC	(CT)3C(CT)8	55	Buteler *et al*.,1999
IB324	F TTTGGCATGGGCCTGTATT R GTTCTTCTGCACTGCCTGATTC	*	53	Tseng *et al*., 2002
IBCIP	F CCCACCCTTCATTCCATTACT RAACAACAACAAAAGGTAGAGCAG	(ACC)7A	56	Yanez, 2002
IBJ522	F ACCCGCATAGACACTCACCT R TGACCGAAGTGTATCTAGTGG	(CAC)6-7	56	Solis *et al*., (unp.)
IBS07	F GCTTGCTTGTGGTTCGAT R CAAGTGAAGTGATGGCGTTT	(TGTC)7	53	Benavides (unp.)
J67	F CACCCATTTGATCATCTCAACC R GGCTCTGAGCTTCCATTGTTAG	(GAA)5	56	Solis *et al*., (unp.)
JB1809	F CTTCTCTTGCTCGCCTGTTC R GATAGTCGGAGGCATCTCCA	(CCT)6(CCG)6	57	Solis *et al*., (unp.)
IB297	F GCAATTTCACACACAAACACG R CCCTTCTTCCACCACTTTCA	(CT)13	54	Buteler *et al*.,1999

*__At__ : Annealing temperature

4.2.6 Nutritional characterization

4.2.6.1 Determination of the dry matter content

Determination of dry matter content was conducted following the method reported by Asare (2004). Petri-dishes were washed in distilled water, labelled and dried in oven at 80 ^{o}C. The petri-dishes were then sterilized by dry heat in the oven at 105 ^{o}C for 30 minutes and placed in the dessicator for 30 minutes. Fresh root samples of sweet potato were chopped into small pieces of 1 cm^3. A sample of 100 g of chopped and grated fresh roots (from each genotype) were dried in an oven at 105 °C for 48 h. Dry matter was expressed as the percentage using equation one.

Calculation:

$$dm\% = 100\% - \left[\frac{w_1 - w_2}{w_1} \times 100\%\right]$$ ……Equation one

Where: *dm* is dry matter

(W_1) is the initial weight of the sample on fresh weight basis.

(W_2) is the weight of dried samples after the dishes were placed in a dessicator for 30 minutes to cool.

4.2.6.2 Nutritional analysis

(i) Protein determination

Protein analysis was done using the Association of American Cereal Chemists (AACC, 2010) guidelines. One-gram catalyst (made up of 1000 g Potassium sulphate, 5 g Selenium and 25 g Copper sulphate mixed together thoroughly) was weighed and put in numbered digestion tubes. One gram of sample was put in a digestion tube and 7.5 mls concentrated Sulphuric acid (Nitrogen free) added to it. This was digested in a digester (Tecator, Sweden) for 30 minutes at 398 ^{o}C or until the mixture cleared. It was then removed from the digestion block and left to cool for 20-30 minutes. After cooling, 25 mls of distilled water was added to the mixture then followed by addition of 25 mls NaOH which was added slowly to avoid the vigorous reaction of the acid and base. Distillation followed after addition of a base, into a conical flask with 0.1 N boric acid for 4 minutes which contained bromophenol blue dye. Blue colour in boric acid changed to green upon receiving nitrogen in form of ammonia. This was then back-titrated using 0.1 N hydrochloric acid which changed colour of the mixture in the conical flask from green to blue. The titre volume was recorded and was used in the following formula (equation two) for calculation of average percent protein;

$$\text{Average protein \%} = \frac{(T-B) \times N \times 14.007 \times 100 \times 6.25}{W}$$ .....Equation two

Where: T= Titre volume in sample (ml)

B= Titre volume for control (ml)

N= Normality of Acid to 4 decimal points

W= Sample weight in (mg)

6.25= Conversion Factor for Nitrogen specific for sweet potato plant sample (AOAC, 1992).

The whole process was replicated three times with a control consisting of all the above reagents and conditions except the experimental samples.

(ii) Sucrose and starch determination

Analysis of sucrose (free sugar) and starch were conducted following the method reported by (Smith *et al.*, 1964). About 0.05 g of flour was weighed into centrifuge tubes. The powder was wetted with 1.0 ml 95% ethanol. Afterwards, 2.0 ml of distilled water was added and contents mixed. Then 10.0 ml of hot 95% ethanol was added and votexed. The products were centrifuged with bench centrifuge for 10 minutes. The supernatant was decanted into 100 ml volumetric flask and made up to the mark. An aliquot of 1.0 ml of the extract was transferred to a clean test tube then 0.5 ml 5% phenol added and mixed. Afterwards 2.5 ml of concentrated H_2SO_4 (98%) was added and votexed. After cooling of the mixture had taken place, the absorbance at 490 nm was read and recorded. At 490 nm is the wavelength at which the sucrose absorbs the highest amount of light. The absorbance of the blank (distilled water) was also read and recorded. A standard curve was made using 0-100 µg/ml using Standard sucrose (Figure 4.2). Sugars (sucrose) obtained after hydrolysis of the residue was converted to starch by multiplying it by 0.9.

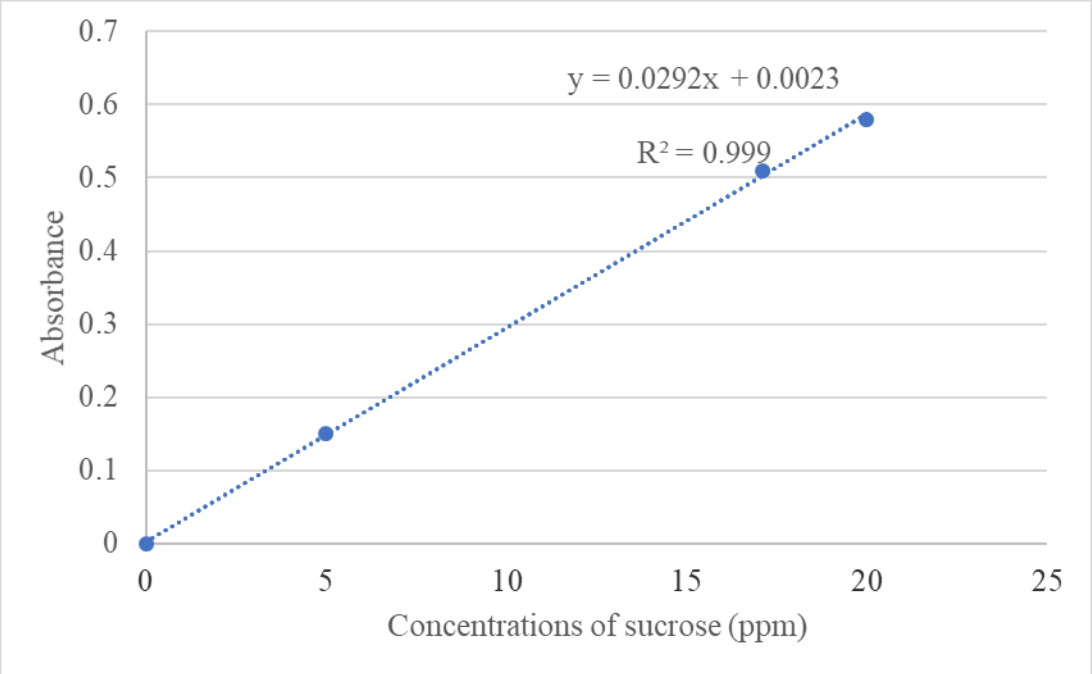

Figure 4.2: Standard curve of sucrose

Calculation:

Total starch = Total sucrose x 0.9 (Smith *et al.*, 1964) ……Equation three

(iii) Total Carotenoids determination

Carotenoids were extracted following the methods suggested by improved method of Wellburn, (1994). About 0.24 g of sweet potato fresh tuber samples was weighed and cut into small pieces. These pieces were transferred to a clean test tube that has a lid (cap). Diethyl ether (3 ml) was pipetted and added to the test tube so as to help in dissolving the solutes in the sweet potato. The test tube was wrapped with aluminium foil (to prevent exposure of diethyl to light to prevent oxidation). The caps of the tubes were then wrapped with parafilm to prevent pouring of the liquid. The liquid was taken to a shaker that revolves at 75 revolutions per minute (rpm) to aid in mixing of the contents. The products were then centrifuged for 20 min at 3500 rpm. The supernatant

was then transferred to a new glass tube (without disturbing the pellet). The UV/visible spectrophotometer was blanked with 1 ml diethyl ethyl at wavelengths 641.8 (642), 660 and 470. The readings of each sample were recorded at different wavelengths (i.e. 470 nm, 642 nm and 660 nm) and carrotenoids concentration calculated according to the equation given by Lichtenthaler (1987) as follows:

$$\text{Total carrotenoids} = \left[\frac{(1000\ A_{470} - 1.30\ C_a - 33.12\ C_b)}{213}\right] \quad \text{.....Equation four}$$

Where: A = Absorbance

C_a (Chlorophyll a) = $9.93\ A_{660} - 0.75\ A_{642}$

C_b (Chlorophyll b) = $16.23\ A_{642} - 2.42\ A_{660}$

4.2.7 Data analysis

4.2.7.1 Agro-morphological analysis

Analysis of variance of the quantitative agro-morphological data was done using Statistical Analysis System programme (SAS Institute Inc, 1997). Data were classified according to genotypes, locations and blocks or replications. Variation between combined sites data was done using Statistical Analysis System programme (SAS Institute Inc, 1997). Also, variation within single sites was determined by analysis of variances (ANOVA) using the same statistical programme and means were separated using LSD at p=0.05. Analysis of the qualitative agro-morphological data was done using frequency tables and data presented in pie charts. Cluster analysis was done on standardized agro-morphological data based on the Euclidian distance co-efficient and Un-weighted Pair Group Method with Arithmetic means (UPGMA) using NCSS -pc version 11 (Jerry, 2000). Hierarchical programme in Number cruncher statistical systems (NCSS) was used to generate dendrograms. Data points with the smaller distances between them were grouped together. The correlation matrix was done using DARwin version 6 software (Perrier and Jacquemoud-Collet, 2006). Correlations among traits were carried out by the optional statement PEARSON.

4.2.7.2 Molecular (SSR) analysis

PCR bands (alleles) were scored for all the markers. The data was entered on an excel sheet in a binary form with '0' indicating absence of an allele while '1' its presence. However, for analysis on Popgene the scoring was '2' for presence of an allele and '1' for absence. Any extra amplification on any marker was scored as a separate allele. The data was then analysed using DARwin version 6 software (Perrier and Jacquemoud-Collet, 2006) for Un-weighted Pair Group Method with Arithmetic means (UPGMA) tree while Powermarker version 3 software (Liu and Muse, 2005) was used to compute markers summary statistics. Hierarchical programme in Number cruncher statistical systems (NCSS) was used to generate a dendrogram. Cluster analysis was done on SSR data based on Jaccard coefficient. The number of effective alleles was computed using Popgene software (Yeh *et al*., 1997).

4.2.7.3 Nutritional analysis

Analysis of variance of the nutritional charaters was done using SAS (SAS Institute Inc, 1997). Data were classified relative to genotypes, locations and blocks or replications. Variation between combined sites data was done using Statistical Analysis System programme (SAS Institute Inc, 1997). In Analysis of Variance (ANOVA), each trait (namely protein, total carotenoids, total starch, sucrose and dry matter) was analyzed from each experimental site separately to determine experimental means and coefficient of variation. Variation within sites was determined by ANOVA using the same statistical programme and means were separated using LSD at $p=0.05$. Cluster analysis was done on standardized nutrition data based on the Euclidian distance co-efficient and UPGMA using NCSS -pc version 11 (Jerry, 2000). Hierarchical programme in Number cruncher statistical systems (NCSS) was used to generate dendrograms. Data points with the smaller distances between them were grouped together.

4.2.7.4 Comparative analysis of agro-morphological, molecular and nutritional data

The data was analysed using DARwin version 6 software (Perrier and Jacquemoud-Collet, 2006) for UPGMA tree for agro-morphological, nutrition and molecular data. The correlation between the data was computed using the quartet tree distance and consensus tree. The quartet tree distance and consensus dendrogram were computed using the same software (Perrier and Jacquemoud-Collet, 2006).

4.3 Results

4.3.1 Agro-morphological characterization

4.3.1.1 Quantitative characters

The 68 evaluated sweet potato genotypes exhibited agro-morphological diversity in aerial (vine and foliage) and storage root characters. Analysis of variance for pooled data showed that site significantly ($p \leq 0.05$) affected the expression of agro-morphological characters (Table 4.5; Appendix 2). Therefore, quantitative descriptors were calculated for each site (Table 4.6). Analysis of variance for individual sites showed significant ($p \leq 0.05$) differences of the evaluated quantitative agro-morphological characters (Table 4.6; Appendix 2).

Table 4.5: F Probability values of agro-morphological characters for combined sites (ATC - Miyare and KALRO -Embu)

Source of variation Variables	P values		
	Genotype	Site	Genotype × Site
Vine growth rate	<0.0001	<0.0001	<0.0001
Vine internode length	<0.0001	0.002	0.004
Vine internode diameter	<0.0001	<0.0001	<0.0001
Storage root cortex thickness	<0.0001	<0.0001	0.003
Storage root stalk	<0.0001	0.001	0.005
Mature leaf size	<0.0001	0.002	0.002
Storage root length	<0.0001	<0.0001	0.0005
Largest storage root diameter	<0.0001	0.04	0.05
Petiole length	<0.0001	0.03	0.04
Weight of largest storage root	<0.0001	<0.0001	<0.0001
Root yield	<0.0001	<0.0001	<0.0001

Table 4.6: F Probability values of agro-morphological characters for individual sites (ATC -Miyare and KALRO -Embu

Source of variation Variables	P values	
	ATC -Miyare	KALRO-Embu
Vine growth rate	0.047	0.045
Vine internode length	0.048	0.046
Vine internode diameter	0.044	0.039
Storage root cortex thickness	0.001	0.001
Storage root stalk	0.01	0.001
Mature leaf size	0.049	0.05
Storage root length	0.047	0.045
Largest storage root diameter	0.05	0.05
Petiole length	0.001	0.001
Weight of largest storage root	0.05	0.05
Root yield	0.001	0.001

4.3.1.1.1 Vine growth rate (VGR)

There were significant differences ($p \leq 0.05$) on the VGR at ATC -Miyare (Table 4.7). VGR of all genotypes in this site ranged from slow to fast. Genotypes that had the least (about 50 cm) VGR included Alupe or, Nyawo Nyathiodiewo, SPK 004 and Naspot x

New Kawogo 3. They were regarded as having a slow VGR as guided by Huaman (1992). Genotype Wera had the fastest (> 100 cm) VGR.

Analysis of variance indicated significant differences ($p \leq 0.05$) on VGR at KALRO - Embu (Table 4.7). VGR ranged from slow (<50 cm) to intermediate (50-100 cm). Genotypes that had the least VGR in this site were Ejumula x New Kawogo 4, Ejumula x New Kawogo 2 and Kenspot 2 among others. All the above-mentioned genotypes had measured <50 cm hence regarded as having a slow VGR. Genotypes that had the highest VGR measured between 50-100 cm and included Kenspot 3, Kenspot 5 and Ejumula among others.

4.3.1.1.2 Vine internode length (VIL)

There were significant differences ($p \leq 0.05$) on VIL at ATC -Miyare (Table 4.7). VIL of all genotypes in this site ranged from very short to short. There were no genotypes that exhibited intermediate, long or very long VIL in this site. Genotypes that had the lowest (<3 cm) VIL included Naspot x New Kawogo 3, 24 Kampala and Mugande. Genotypes Nangili, Amina, Ejumula x New Kawogo 1 and Mwavuli had VIL of 3-5 cm in ATC - Miyare and were rated as having short VIL.

Analysis of variance indicated significant differences ($p \leq 0.05$) on VIL at KALRO - Embu (Table 4.7). VIL ranged from very short to short. There were no genotypes that exhibited intermediate, long or very long VIL at this site. Genotypes that had the lowest (<3 cm) VIL in this site were Saly boro, Odinga and Ejumula x New Kawogo 4 among others. Genotypes that had short (3-5 cm) VIL included Kenspot 5, Fundukhusia and Mwavuli.

4.3.1.1.3 Vine internode diameter (VID)

There were significant differences ($p \leq 0.05$) on VID at ATC -Miyare (Table 4.7). VID of all genotypes in this site ranged from very thin to thin. There were no genotypes that

exhibited intermediate, long or very long VID in this site. Genotypes that had the least (<3 cm) VID included Nyamuguta, Nyautenge and Nyarambe among others. Genotype 36 Kalamb Nyerere had a thin (4-6 cm) VID.

The results of this study revealed significant differences ($p \leq 0.05$) on VID at KALRO - Embu (Table 4.7). VID ranged from very thin to thin VID. There were no genotypes that exhibited intermediate, long or very long VID in this site. Genotype Nangili had the least (1.00 mm) VID On the other hand, genotype Ejumula x New Kawogo 1 had a thin (3.67 mm) VID.

4.3.1.1.4 Storage root cortex thickness (SRCT)

Analysis of variance indicated significant differences ($p \leq 0.001$) on SRCT at ATC - Miyare (Table 4.7). SRCT of all genotypes in this site ranged from thin to intermediate SRCT. There were no genotypes that exhibited very thin, thick or very thick SRCT in this site. Genotypes that had the largest (2.1-2.9 mm) SRCT included Saly boro, Nyakagwa and Kuny kibuonjo among others and were regarded as having intermediate SRCT. The rest of the genotypes had SRCT of 2 mm and hence were rated as having thin SRCT.

There were significant differences ($p \leq 0.001$) on SRCT at KALRO -Embu (Table 4.7). SRCT of all genotypes in this site ranged from thin to intermediate SRCT. There were no genotypes that exhibited very thin, thick or very thick SRCT in this site. Genotypes that had the largest (2.1-2.9 mm) SRCT at ATC Miyare included Kuny kibuonjo, Nyakagwa and SPK 013 among others and were regarded as having intermediate SRCT. The rest of the genotypes at this site had SRCT of 2 mm and hence were rated as having thin SRCT.

Table 4.7: Means for vine and root character(s) recorded on the 68 sweet potato genotypes at ATC -Miyare and KALRO Embu sites grown during the long rains in 2014

	GENOTYPE	Vine growth rate (cm)		Vine internode length (cm)		Vine internode diameter (mm)		Storage root cortex thickness (mm)	
		ATC Miyare	KALRO Embu	ATC Miyare	KALRO Embu	ATC Miyare	KALRO Embu	ATC Miyare	KALRO Embu
1	Kenspot 1	6.33 ab	5.00 ab	3.00 ab	2.33 abc	3.00 bc	2.33 abc	5.00 abc	4.33 bcd
2	Saly boro	5.00 bc	3.67 bc	1.67 bc	1.00 c	3.00 bc	3.00 ab	6.33 a	3.00 d
3	91/2187	5.67 abc	5.00 ab	3.00 ab	2.33 abc	3.00 bc	3.00 ab	3.00 d	3.00 d
4	Oduogo jodongo	5.00 bc	3.67 bc	1.67 bc	1.67 bc	3.67 ab	2.33 abc	5.67 ab	3.00 d
5	5 Nyandere	5.67 abc	3.67 bc	2.33 abc	1.67 bc	3.00 bc	3.00 ab	3.67 cd	3.67 cd
6	Odinga	5.00 bc	4.33 abc	2.33 abc	1.00 c	3.00 bc	2.33 abc	3.67 cd	3.00 d
7	Naspot 1	5.67 abc	3.67 bc	3.00 ab	2.33 abc	3.00 bc	3.00 ab	3.67 cd	3.67 cd
8	Kenspot 3	5.67 abc	5.67 a	2.33 abc	3.00 ab	3.00 bc	3.00 ab	3.67 cd	3.67 cd
9	Naspot x New Kawogo 2	5.67 abc	4.33 abc	2.33 abc	2.33 abc	3.00 bc	3.00 ab	3.00 d	3.00 d
10	Nyamuguta	5.67 abc	3.67 bc	3.67 a	1.67 bc	2.33 c	3.00 ab	5.67 ab	3.67 cd
11	Nyautenge	6.33 ab	5.00 ab	3.00 ab	2.33 abc	2.33 c	2.33 abc	4.33 bcd	4.33 bcd
12	Ejumula x New Kawogo 4	5.00 bc	3.00 c	1.67 bc	1.00 c	3.67 ab	2.33 abc	4.33 bcd	3.67 cd
13	Nyarambe	5.67 abc	3.67 bc	3.00 ab	1.00 c	2.33 c	2.33 abc	4.33 bcd	3.00 d
14	Nyakagwa	5.67 abc	3.67 bc	1.67 bc	2.33 abc	3.00 bc	2.33 abc	6.33 a	5.67 ab
15	Naspot x New Kawogo 3	4.33 c	3.67 bc	1.00 c	1.67 bc	3.00 bc	2.33 abc	3.00 d	3.00 d
16	Ejumula x New Kawogo 2	5.67 abc	3.00 c	1.67 bc	1.00 c	3.00 bc	2.33 abc	3.67 cd	3.00 d
17	Nangili	5.67 abc	3.67 bc	3.67 a	1.67 bc	3.67 ab	1.00 c	3.00 d	3.00 d
18	Kenspot 2	5.00 bc	3.00 c	1.67 bc	1.00 c	3.00 bc	2.33 abc	4.33 bcd	3.00 d
19	SPK 013	5.67 abc	5.00 ab	2.33 abc	3.00 ab	3.00 bc	3.00 ab	5.00 abc	5.67 ab
20	Mugande x New Kawogo 4	5.00 bc	3.67 bc	2.33 abc	2.33 abc	3.00 bc	2.33 abc	5.67 ab	3.67 cd
21	Alupe or	4.33 c	3.00 c	3.00 ab	1.67 bc	3.00 bc	3.00 ab	6.33 a	3.67 cd
22	12 Marooko	5.67 abc	4.33 abc	1.67 bc	1.67 bc	3.00 bc	3.00 ab	3.00 d	3.00 d
23	Kenspot 5	5.67 abc	5.67 a	2.33 abc	3.67 a	3.00 bc	2.33 abc	3.00 d	6.33 a
24	36 Kalamb Nyerere	6.33 ab	4.33 abc	3.00 ab	2.33 abc	4.33 a	2.33 abc	3.67 cd	4.33 bcd
25	K/KA/2004/215	5.00 bc	3.67 bc	2.33 abc	2.33 abc	3.00 bc	3.00 ab	5.67 ab	3.00 d
26	Ejumula x New Kawogo 3	5.67 abc	3.67 bc	3.00 ab	1.67 bc	3.00 bc	3.00 ab	3.67 cd	3.00 d
27	292-H-12	5.67 abc	3.67 bc	3.67 a	1.67 bc	3.00 bc	3.00 ab	3.67 cd	5.00 abc
28	Mogesi Gikenja	5.67 abc	4.33 abc	2.33 abc	1.67 bc	3.67 ab	3.00 ab	3.00 d	3.67 cd
29	Lungabure	5.00 bc	3.00 c	2.33 abc	1.00 c	3.67 ab	2.33 abc	3.00 d	3.00 d
30	Kenspot 4	5.67 abc	4.33 abc	3.67 a	1.67 bc	3.00 bc	2.33 abc	5.67 ab	3.67 cd
31	Vitaa	5.67 abc	4.33 abc	2.33 abc	2.33 abc	3.00 bc	3.00 ab	3.67 cd	3.67 cd
32	9 Nduma	5.00 bc	3.67 bc	2.33 abc	2.33 abc	2.33 c	2.33 abc	5.67 ab	3.67 cd
33	24 Kampala	5.00 bc	3.00 c	1.00 c	1.00 c	3.00 bc	2.33 abc	3.67 cd	3.00 d
34	Obugi	5.67 abc	4.33 abc	2.33 abc	1.67 bc	3.00 bc	2.33 abc	5.00 abc	4.33 bcd
35	56682-03	5.00 bc	5.00 ab	3.00 ab	3.00 ab	3.00 bc	3.00 ab	3.00 d	3.00 d
36	Nyawo Nyathiodiewo	4.33 c	3.67 bc	2.33 abc	1.67 bc	3.00 bc	3.00 ab	4.33 bcd	3.00 d
37	Gachaka	6.33 ab	4.33 abc	2.33 abc	1.00 c	3.00 bc	3.00 ab	3.00 d	4.33 bcd
38	Mugande	5.00 bc	3.00 c	1.00 c	1.00 c	3.00 bc	2.33 abc	4.33 bcd	3.00 d

39	Amina	5.00 bc	3.67 bc	3.67 a	1.67 bc	3.00 bc	2.33 abc	4.33 bcd	5.67 ab
40	Fumbara jikoni	5.67 abc	3.67 bc	2.33 abc	1.67 bc	3.00 bc	2.33 abc	4.33 bcd	3.00 d
41	Ejumula	5.67 abc	5.67 a	2.33 abc	1.67 bc	3.00 bc	2.33 abc	3.67 cd	3.67 cd
42	Karunde	6.33 ab	3.67 bc	2.33 abc	1.00 c	3.00 bc	2.33 abc	3.67 cd	3.00 d
43	SPK 004	4.33 c	5.67 a	2.33 abc	2.33 abc	3.00 bc	1.67 bc	4.33 bcd	4.33 bcd
44	Kuny kibuonjo	5.67 abc	4.33 abc	1.67 bc	1.67 bc	3.00 bc	3.00 ab	6.33 a	6.33 a
45	K/KA/2002/12	5.00 bc	4.33 abc	2.33 abc	1.67 bc	3.00 bc	3.00 ab	5.00 abc	4.33 bcd
46	55 Nganyomba	5.67 abc	3.67 bc	1.67 bc	1.00 c	3.00 bc	2.33 abc	4.33 bcd	3.67 cd
47	1-Ujili	5.00 bc	3.67 bc	1.67 bc	1.00 c	2.33 c	2.33 abc	3.67 cd	3.67 cd
48	Santo Amaro	5.67 abc	5.00 ab	2.33 abc	3.00 ab	3.00 bc	2.33 abc	5.67 ab	3.00 d
49	Mugande x New Kawogo 2	5.00 bc	4.33 abc	1.67 bc	1.00 c	3.00 bc	2.33 abc	4.33 bcd	4.33 bcd
50	Wera	7.00 a	3.67 bc	2.33 abc	1.67 bc	3.00 bc	3.00 ab	4.33 bcd	3.00 d
51	Kemb 10	5.00 bc	3.67 bc	2.33 abc	2.33 abc	3.00 bc	3.00 ab	3.67 cd	4.33 bcd
52	Mbita	5.67 abc	4.33 abc	3.00 ab	2.33 abc	3.00 bc	3.00 ab	5.00 abc	5.00 abc
53	Naspot x New Kawogo 1	5.00 bc	4.33 abc	2.33 abc	1.67 bc	3.00 bc	2.33 abc	5.00 abc	3.00 d
54	Kibuonjo	5.67 abc	3.67 bc	2.33 abc	1.00 c	3.00 bc	3.00 ab	4.33 bcd	3.67 cd
55	29 Kuny kibuonjo	5.67 abc	4.33 abc	1.67 bc	2.33 abc	3.00 bc	3.00 ab	3.00 d	3.00 d
56	62 Odhiogo	5.67 abc	4.33 abc	2.33 abc	2.33 abc	3.00 bc	2.33 abc	5.67 ab	3.00 d
57	52 Nyakisumu	5.67 abc	4.33 abc	2.33 abc	2.33 abc	3.67 ab	1.67 bc	4.33 bcd	3.00 d
58	Ejumula x New Kawogo 1	5.67 abc	3.67 bc	3.67 a	1.67 bc	3.00 bc	3.67 a	3.00 d	3.67 cd
59	Bungoma	5.00 bc	3.00 c	1.67 bc	1.67 bc	3.00 bc	3.00 ab	3.00 d	3.00 d
60	K 117	5.00 bc	3.67 bc	2.33 abc	1.67 bc	3.00 bc	3.00 ab	3.67 cd	3.67 cd
61	Fundukhusia	5.67 abc	5.67 a	2.33 abc	3.67 a	2.33 c	1.67 bc	5.67 ab	5.67 ab
62	SPK 031	5.67 abc	4.33 abc	1.67 bc	1.67 bc	2.33 c	1.67 bc	3.67 cd	3.00 d
63	Mugande x New Kawogo 1	5.67 abc	3.00 c	3.00 ab	1.00 c	2.33 c	2.33 abc	4.33 bcd	3.00 d
64	Mwavuli	5.67 abc	5.67 a	3.67 a	3.67 a	3.67 ab	2.33 abc	5.00 abc	3.00 d
65	Polo yiengo	5.67 abc	4.33 abc	2.33 abc	1.67 bc	3.67 ab	3.00 ab	5.00 abc	3.00 d
66	Mugande x New Kawogo 3	5.00 bc	3.67 bc	2.33 abc	1.67 bc	3.00 bc	2.33 abc	3.67 cd	3.67 cd
67	Sinia	5.67 abc	4.33 abc	3.00 ab	2.33 abc	3.67 ab	2.33 abc	4.33 bcd	3.00 d
68	Tainung	5.00 bc	4.33 abc	2.33 abc	1.67 bc	2.33 c	2.33 abc	4.33 bcd	3.00 d
	Site mean	5.44	4.08	2.39	1.85	3.02	2.57	4.28	3.67
	LSD Value	0.41	0.07	0.40	0.85	0.02	0.56	0.29	0.67
	CV	17.87	25.57	23.78	25.55	21.42	17.52	27.1	27.6
	P value	0.047	0.045	0.048	0.046	0.044	0.039	0.001	0.001

Means with the same letters along a column are not significantly different according to LSD test *($p \leq 0.05$).*

Scale as guided by Huaman (1992):

1. Vine growth rate (VGR): 3 = slow (<50 cm); 5 = intermediate (50-100 cm); while 7 = fast (>100 cm).
2. Vine internode length (VIL): 1 = very short (<3 cm); 3 = short (3-5 cm); 5 = intermediate (6-9 cm); 7 = long (10-12 cm); while 9 = very long (>12 cm).
3. Vine internode diameter (VID): 1 mm = very thin (<3 mm); 3 = thin (4-6 mm); 5 = intermediate (6-9 mm); 7 = thick (10-12 mm); while 9 = very thick (>12 mm).
4. Storage root cortex thickness (SRCT): 1 = very thin (<1 mm); 3 = thin (2 mm); 5 = intermediate (2.1-2.9 mm); 7 = thick (3-4 mm); while 9 = very thick (>4 mm).

4.3.1.1.5 Storage root stalk (SRS)

Storage root stalk of the evaluated genotypes at ATC -Miyare showed significant differences ($p \leq 0.01$) as shown in Table 4.8. SRS of all genotypes in this site ranged from short to very long SRC. There were no genotypes that exhibited very short SRS in this site. Genotypes that had the shortest (2-5 cm) SRS included Kibuonjo, Gachaka and Fumbara jikoni among others and were regarded as having short SRS. On the other hand, genotypes Naspot 1, 9 Nduma and 24 Kampala had very long (> 12 cm) SRS.

Analysis of variance indicated significant differences ($p \leq 0.001$) on SRS at KALRO -Embu (Table 4.8). Among the 68 genotypes evaluated at KALRO –Embu, SRS ranged from very short to intermediate SRS. There were no genotypes that exhibited long and very long SRS in this site. Genotypes that had the shortest (<2 cm) SRS at this site were Naspot 1, 12 Marooko and Nangili among others and were regarded as having very short SRS. Genotypes that had the longest (5-8 cm) SRS included Kenspot 5, SPK 013 and Mogesi Gikenja and were regarded as having an intermediate SRS.

4.3.1.1.6 Mature leaf size (MLS)

There were significant differences ($p \leq 0.05$) on MLS at ATC -Miyare (Table 4.8). MLS of all genotypes in this site ranged from very small to medium. There were no genotypes that exhibited large MLS in this site. Genotypes that had the smallest (<8 cm) MLS at ATC Miyare included Naspot x New Kawogo 3, 9 Nduma, 1-Ujili and Mugande x New Kawogo 2 and were regarded as having small MLS. Otherwise genotype 55 Nganyomba had the largest MLS. Further, Analysis of variance indicated significant differences ($p \leq 0.05$) on MLS at KALRO -Embu (Table 4.8). However, all the 68 genotypes evaluated at KALRO –Embu, had MLS ranging from 8-15 cm.

4.3.1.1.7 Storage root length (SRL)

The results of this study showed significant differences ($p \leq 0.05$) on storage root length (SRL) at ATC -Miyare (Table 4.8). SRL of all genotypes in this site ranged from 4.60

cm to 16.05 cm. Genotypes that recorded the shortest SRL included Mugande x New Kawogo (4.6 cm), Naspot x New Kawogo 2 (6.62 cm) and Nyarambe (7.10 cm) among others. Genotypes that recorded the longest SRL were Gachaka (16.05 cm), Mugande (14.92 cm) and Nyamuguta (14.53 cm) among others.

There were significant differences ($p \leq 0.05$) on storage root length (SRL) at KALRO - Embu (Table 4.8). SRL of all genotypes in this site ranged from 9.83 cm to 20.83 cm. Genotypes that recorded the shortest SRL included Nyawo Nyathiodiewo (9.83 cm), Polo yiengo (12.90 cm) and Nangili (13.03 cm) among others. Genotypes that recorded the longest SRL were Nyautenge (20.83 cm), Amina (18.50 cm) and Gachaka (15.03 cm) among others.

4.3.1.1.8 Largest storage root diameter (SRD)

Analysis of variance indicated significant differences ($p \leq 0.05$) on storage root diameter (SRD) at ATC -Miyare (Table 4.8). SRD of all genotypes in this site ranged from 2.33 cm to 13.33 cm. Genotypes that recorded the shortest SRD included Mugande x New Kawogo 2 (2.33 cm), 56682-03 (3.10 cm), and Ejumula x New Kawogo 1 (3.33 cm). Genotypes that recorded the longest SRD were Kenspot 3 (13.33 cm), Kibuonjo (12.67 cm) and 36 Kalamb Nyerere (12.00 cm) among others.

This study showed significant differences ($p \leq 0.05$) on storage root diameter (SRD) at KALRO -Embu (Table 4.8). SRD of all genotypes in this site ranged from 4.73 cm to 10.61 cm. Genotypes that recorded the shortest SRD included 20 Kuny kibuonjo (4.73 cm), Nyawo Nyathiodiewo (4.83 cm) and Ejumula x New Kawogo 2 (5.73 cm). Genotypes that recorded the longest SRD at ATC Miyare were Kenspot 5 (10.60 cm), 5 Nyandere (9.38 cm) and Kenspot 1 (9.33 cm) among others.

Table 4.8: Means for root and foliage characters recorded on 68 sweet potato genotypes at ATC -Miyare and KALRO Embu sites grown during the long rains in 2014

	GENOTYPE	Storage root stalk (cm)		Mature leaf size (cm)		Storage root length (cm)		Largest storage root diameter (cm)	
		ATC Miyare	KALRO Embu	ATC Miyare	KALRO Embu	ATC Miyare	KALRO Embu	ATC Miyare	KALRO Embu
1	Kenspot 1	5.67 cde	4.33 bcd	5.00 b	5.67 a	11.09 abcdefghi	15.50 bcdefg	6.70 cdefghijk	9.33 abc
2	Saly boro	5.67 cde	3.00 def	5.00 b	5.67 a	13.22 abcdef	17.17 abcdef	6.33 defghijk	6.23 bcdefg
3	91/2187	6.33 bcde	3.67 cde	5.00 b	5.67 a	10.20 bcdefghi	14.40 bcdefgh	7.20 bcdefghijk	7.10 bcdefg
4	Oduogo jodongo	5.67 cde	3.00 def	5.00 b	5.67 a	11.94 abcdefghi	19.03 abc	7.00 cdefghijk	7.03 bcdefg
5	5 Nyandere	5.67 cde	3.67 cde	5.00 b	5.67 a	9.09 defghij	17.10 abcdef	7.17 cdefghijk	9.38 abc
6	Odinga	7.00 abcd	3.00 def	5.00 b	5.67 a	10.13 bcdefghi	14.07 bcdefgh	6.33 defghijk	6.07 bcdefg
7	Naspot 1	9.00 a	1.00 g	5.00 b	5.00 a	10.41 bcdefghi	16.10 abcdef	5.67 defghijk	6.07 bcdefg
8	Kenspot 3	5.67 cde	3.00 def	5.00 b	5.67 a	8.81 efghij	15.73 abcdef	13.33 a	6.80 bcdefg
9	Naspot x New Kawogo 2	5.67 cde	3.00 def	5.00 b	5.67 a	6.62 ij	16.20 abcdef	7.23 bcdefghijk	7.17 abcdefg
10	Nyamuguta	6.33 bcde	4.33 bcd	5.00 b	5.67 a	14.53 abc	15.10 bcdefgh	6.60 cdefghijk	8.07 abcdefg
11	Nyautenge	5.67 cde	3.00 def	5.00 b	5.67 a	14.20 abcde	20.83 a	5.87 defghijk	8.90 abcd
12	Ejumula x New Kawogo 4	7.67 abc	4.33 bcd	5.00 b	5.67 a	12.75 abcdefg	14.17 bcdefgh	5.67 defghijk	7.13 abcdefg
13	Nyarambe	6.33 bcde	3.00 def	5.00 b	5.00 a	7.10 hij	12.77 fgh	4.73 fghijk	6.47 bcdefg
14	Nyakagwa	5.67 cde	3.00 def	5.00 b	5.67 a	12.16 abcdefgh	16.20 abcdef	4.27 ghijk	8.00 abcdefg
15	Naspot x New Kawogo 3	5.67 cde	3.67 cde	4.33 c	5.67 a	8.72 fghij	16.47 abcdef	7.13 cdefghijk	7.23 abcdefg
16	Ejumula x New Kawogo 2	7.67 abc	3.00 def	5.00 b	5.00 a	12.73 abcdefg	13.57 defgh	6.43 defghijk	5.73 defg
17	Nangili	6.33 bcde	1.67 fg	5.00 b	5.67 a	13.27 abcdef	13.03 fgh	6.73 cdefghijk	7.43 abcdefg
18	Kenspot 2	5.67 cde	4.33 bcd	5.00 b	5.67 a	12.10 abcdefgh	15.80 abcdef	3.67 ijk	7.03 bcdefg
19	SPK 013	6.33 bcde	5.67 ab	5.00 b	5.67 a	10.20 bcdefghi	19.30 ab	9.23 abcdefgh	9.07 abcd
20	Mugande x New Kawogo 4	6.33 bcde	3.00 def	5.00 b	5.00 a	10.95 abcdefghi	14.83 bcdefgh	4.27 ghijk	7.60 abcdefg
21	Alupe or	5.67 cde	3.00 def	5.00 b	5.00 a	8.10 defghij	15.50 bcdefg	4.70 fghijk	6.30 bcdefg
22	12 Marooko	7.00 abcd	1.00 g	5.00 b	5.67 a	12.37 abcdefgh	14.73 bcdefgh	5.67 defghijk	8.53 abcdef
23	Kenspot 5	7.67 abc	6.33 a	5.00 b	5.00 a	9.72 bcdefghij	10.40 gh	4.83 fghijk	10.60 a
24	36 Kalamb Nyerere	7.67 abc	3.00 def	5.00 b	5.00 a	10.51 bcdefghi	18.40 abcde	12.00 abc	7.90 abcdefg
25	K/KA/2004/215	7.00 abcd	3.67 cde	5.00 b	5.67 a	13.14 abcdef	14.50 bcdefgh	4.00 hijk	6.83 bcdefg
26	Ejumula x New Kawogo 3	6.33 bcde	3.00 def	5.00 b	5.67 a	10.54 bcdefghi	14.10 bcdefgh	4.80 fghijk	8.00 abcdefg
27	292-H-12	6.33 bcde	3.67 cde	5.00 b	5.00 a	11.93 abcdefghi	15.80 abcdef	6.00 defghijk	6.90 bcdefg
28	Mogesi Gikenja	8.33 ab	5.00 abc	5.00 b	5.67 a	10.28 bcdefghi	14.93 bcdefgh	10.03 abcdef	7.77 abcdefg
29	Lungabure	5.67 cde	4.33 bcd	5.00 b	5.00 a	13.43 abcdef	15.90 abcdef	6.57 cdefghijk	6.57 bcdefg
30	Kenspot 4	4.33 ef	3.00 def	5.00 b	5.67 a	7.52 ghij	14.93 bcdefgh	6.50 defghijk	6.90 bcdefg
31	Vitaa	6.33 bcde	3.67 cde	5.00 b	5.00 a	11.96 abcdefghi	15.27 bcdefg	5.67 defghijk	8.57 abcdef
32	9 Nduma	9.00 a	3.67 cde	4.33 c	5.67 a	9.33 cdefghij	16.07 abcdef	4.33 ghijk	7.27 abcdefg
33	24 Kampala	9.00 a	3.67 cde	5.00 b	5.00 a	12.42 abcdefgh	14.17 bcdefgh	5.33 efghijk	5.77 defg
34	Obugi	5.67 cde	3.00 def	5.00 b	5.67 a	11.86 abcdefghi	18.57 abcd	7.53 bcdefghijk	7.37 abcdefg
35	56682-03	7.00 abcd	4.33 bcd	5.00 b	5.00 a	9.03 defghij	14.93 bcdefgh	3.10 jk	9.55 ab
36	Nyawo Nyathiodiewo	5.00 def	4.33 bcd	5.00 b	5.67 a	8.60 fghij	9.83 h	5.40 efghijk	4.83 g
37	Gachaka	4.33 ef	3.00 def	5.00 b	5.67 a	16.05 a	15.03 bcdefgh	4.67 fghijk	6.40 bcdefg
38	Mugande	6.33 bcde	4.33 bcd	5.00 b	5.00 a	14.92 ab	15.70 abcdef	5.00 efghijk	6.47 bcdefg

39	Amina	5.67 cde	4.33 bcd	5.00 b	5.00 a	10.50 bcdefghi	18.50 abcd	6.00 defghijk	7.47 abcdefg
40	Fumbara jikoni	4.33 ef	3.00 def	5.00 b	5.67 a	8.75 fghij	15.97 abcdef	7.00 cdefghijk	7.73 abcdefg
41	Ejumula	5.67 cde	2.33 efg	5.00 b	5.67 a	11.39 abcdefghi	17.43 abcdef	10.33 abcde	7.87 abcdefg
42	Karunde	6.33 bcde	4.33 bcd	5.00 b	5.67 a	12.07 abcdefgh	15.67 abcdefg	6.67 cdefghijk	6.87 bcdefg
43	SPK 004	6.33 bcde	4.33 bcd	5.00 b	5.67 a	10.40 bcdefghi	13.30 defgh	4.93 efghijk	5.20 fg
44	Kuny kibuonjo	5.67 cde	4.33 bcd	5.00 b	5.00 a	11.13 abcdefghi	15.90 abcdef	6.80 cdefghijk	6.23 bcdefg
45	K/KA/2002/12	6.33 bcde	3.00 def	5.00 b	5.67 a	10.60 bcdefghi	16.93 abcdef	7.17 cdefghijk	6.27 bcdefg
46	55 Nganyomba	5.67 cde	3.67 cde	5.67 a	5.67 a	10.71 abcdefghi	15.67 abcdefg	4.80 fghijk	8.90 abcd
47	1-Ujili	6.33 bcde	3.67 cde	4.33 c	5.67 a	13.14 abcdef	16.63 abcdef	4.53 ghijk	7.00 bcdefg
48	Santo Amaro	6.33 bcde	2.33 efg	5.00 b	5.67 a	10.31 bcdefghi	15.83 abcdef	5.03 efghijk	7.73 abcdefg
49	Mugande x New Kawogo 2	7.67 abc	3.00 def	4.33 c	5.67 a	4.60 j	16.30 abcdef	2.33 k	6.87 bcdefg
50	Wera	7.00 abcd	4.33 bcd	5.00 b	5.67 a	11.37 abcdefghi	15.30 bcdefg	7.00 cdefghijk	7.45 abcdefg
51	Kemb 10	6.33 bcde	5.00 abc	5.00 b	5.00 a	9.98 bcdefghij	15.83 abcdef	8.00 abcdefghij	7.60 abcdefg
52	Mbita	4.33 ef	2.33 efg	5.00 b	5.00 a	12.19 abcdefgh	16.07 abcdef	7.33 bcdefghijk	6.15 bcdefg
53	Naspot x New Kawogo 1	7.67 abc	3.67 cde	5.00 b	5.67 a	10.10 abcdefghi	13.20 efgh	5.80 defghijk	6.93 bcdefg
54	Kibuonjo	3.00 f	2.33 efg	5.00 b	5.67 a	9.77 bcdefghij	13.90 cdefgh	12.67 ab	7.30 abcdefg
55	29 Kuny kibuonjo	5.00 def	3.00 def	5.00 b	5.67 a	14.23 abcd	14.40 bcdefgh	5.33 efghijk	4.73 g
56	62 Odhiogo	7.67 abc	3.00 def	5.00 b	5.67 a	8.60 fghij	15.90 abcdef	7.00 cdefghijk	9.45 ab
57	52 Nyakisumu	6.33 bcde	3.67 cde	5.00 b	5.67 a	8.41 fghij	17.53 abcdef	11.00 abcd	6.30 bcdefg
58	Ejumula x New Kawogo 1	6.33 bcde	3.00 def	5.00 b	5.00 a	10.29 bcdefghi	13.73 defgh	3.33 ijk	9.33 abc
59	Bungoma	6.33 bcde	3.00 def	5.00 b	5.67 a	9.88 bcdefghij	15.30 bcdefg	7.17 cdefghijk	7.50 abcdefg
60	K 117	7.67 abc	4.33 bcd	5.00 b	5.67 a	9.92 bcdefghij	16.13 abcdef	8.20 abcdefghij	5.37 efg
61	Fundukhusia	5.00 def	3.00 def	5.00 b	5.00 a	7.62 ghij	17.97 abcdef	8.60 abcdefghi	8.57 abcdef
62	SPK 031	4.33 ef	4.33 bcd	5.00 b	5.67 a	9.09 defghij	13.20 efgh	5.00 efghijk	8.80 abcde
63	Mugande x New Kawogo 1	6.33 bcde	3.00 def	5.00 b	5.00 a	8.74 fghij	16.07 abcdef	8.25 abcdefghij	8.60 abcdef
64	Mwavuli	7.67 abc	2.33 efg	5.00 b	5.00 a	11.10 abcdefghi	15.40 bcdefg	5.43 efghijk	8.45 abcdef
65	Polo yiengo	5.67 cde	3.00 def	5.00 b	5.67 a	10.17 bcdefghi	12.90 fgh	9.57 abcdefg	7.85 abcdefg
66	Mugande x New Kawogo 3	6.33 bcde	2.33 efg	5.00 b	5.67 a	10.78 abcdefghi	15.57 abcdefg	4.03 hijk	7.70 abcdefg
67	Sinia	7.67 abc	3.00 def	5.00 b	5.67 a	14.68 abc	16.37 abcdef	9.23 abcdefgh	7.90 abcdefg
68	Tainung	5.67 cde	3.00 def	5.00 b	5.67 a	11.78 abcdefghi	15.00 bcdefgh	5.17 efghijk	5.95 cdefg
	Site mean	6.28	3.42	4.97	5.46	10.84	15.52	6.47	7.32
	LSD Value	0.22	0.22	0.91	0.46	0.84	0.57	0.47	0.32
	CV	23.83	29.79	6.26	9.84	10.26	20.69	21.90	28.37
	P value	0.01	0.001	0.049	0.05	0.047	0.045	0.05	0.05

Means with the same letters along a column are not significantly different according to LSD test *($p \leq 0.05$)*.

Scale as guided by Huaman (1992):

1. Storage root stalk (SRS): 0 = sessile or absent; 1 = very short (<2 cm); 3 = short (2-5 cm); 5 = intermediate (6-8 cm); 7 = long (9-12 cm); while 9 = very long (>12 cm).
2. Mature leaf size (MLS) data shown in Table 4.8 as follows: 3 = small (<8 cm); 5 = medium (8-15 cm); 7 = large (>15 cm).

4.3.1.1.9 Petiole length

There were significant differences ($p \leq 0.001$) on petiole length at ATC -Miyare (Table 4.9). Petiole length of all genotypes in this site ranged from very short to intermediate. There were no genotypes that exhibited long or very long petiole length in this site. Genotypes that had the shortest (<10 cm) petiole length included Mugande x New Kawogo 2, Fundukhusia and Tainung and were regarded as very short. Genotypes Ejumula x New Kawogo 2, Karunde and Wera had petiole lengths of 16-20 cm and were rated as intermediate.

Petiole length at KALRO -Embu indicated significant differences ($p \leq 0.001$) as shown in Table 4.9. Among the 68 genotypes evaluated at KALRO –Embu, petiole length ranged from very short to intermediate. There were no genotypes that exhibited long or very long petiole length in this site. Genotypes that had the shortest (<10 cm) petiole length at this site were Kenspot 1, 292-H-12 and 24 Kampala among others and were regarded as very short. Only one genotype (Kuny kibuonjo) recorded a petiole length of 16-20 cm.

4.3.1.1.10 Weight of largest storage root

Analysis of variance indicated significant differences ($p \leq 0.05$) on weight of largest storage root (WLSR) at ATC -Miyare (Table 4.9). WLSR of all genotypes in this site ranged from 0.20 kg to 1.07 kg. Genotypes that recorded the least weights at ATC -Miyare were 1-Ujili (0.20 kg) and Mugande x New Kawogo 3 (0.20 kg). On the other hand, genotype Mbita recorded the highest weight of 1.07 kg at ATC Miyare. This was followed by genotypes Naspot 1 (0.83 kg), Polo yiengo (0.83 kg) and Wera (0.80 kg).

There were significant differences ($p \leq 0.05$) in relation to weight of largest storage root (WLSR) at KALRO -Embu (Table 4.9). WLSR of all genotypes in this site ranged from 0.23 kg to 0.77 kg. Genotype Ejumula x New Kawogo 2 recorded the least weight of

0.23 kg while Kenspot 1 recorded the highest weight of 0.77 kg. Genotype Kenspot 1 was followed by genotypes Amina (0.70 kg) and Kenspot 5 (0.70 kg).

4.3.1.1.11 Commercial root yield

Storage root yield at ATC -Miyare indicated significant differences ($p \leq 0.001$) as shown in Table 4.9. Root yield of all genotypes in this site ranged from 0.84 t/ha to 16.82 t/ha. Genotypes that recorded the lowest root yield at ATC -Miyare were 56682-03 (0.84 t/ha), 52 Nyakisumu (1.17 t/ha) and Tainung (1.44 t/ha) among others. Genotypes Nyautenge (16.82 t/ha), Gachaka (10.62 t/ha) and Sinia (10.08 t/ha) recorded the highest yield.

Analysis of variance indicated significant differences ($p \leq 0.001$) on the storage root yield at KALRO -Embu (Table 4.9). Root yield of all genotypes in this site ranged from 1.07 t/ha to 17.04 t/ha. Genotypes that recorded the lowest root yield at KALRO -Embu were K/KA/2004/215 (1.07 t/ha), Kuny kibuonjo (2.38 t/ha) and Naspot x New Kawogo 1 (2.74 t/ha) among others. Genotypes Kemb 10 (17.04 t/ha), Nyautenge (15.23 t/ha), Amina (14.53 t/ha), and Alupe or (14.18 t/ha) recorded the highest yield among others.

Table 4.9: Means for leaf and agronomical characters recorded on the 68 sweet potato genotypes at ATC -Miyare and KALRO -Embu sites grown during the long rains in 2014

	GENOTYPE	Petiole length (cm)		Weight of largest root (kg)		Root yield (t/ha)	
		ATC Miyare	KALRO Embu	ATC Miyare	KALRO Embu	ATC Miyare	KALRO Embu
1	Kenspot 1	3.67 cde	2.33 d	0.47 bcdefgh	0.77 a	7.17 efgh	9.07 hijkl
2	Saly boro	3.00 def	3.00 cd	0.43 bcdefgh	0.37 cdef	4.80 lmnopqrstu	8.74 hijklmno
3	91/2187	3.00 def	3.00 cd	0.47 bcdefgh	0.37 cdef	4.87 lmnopqrst	2.86 BCDE
4	Oduogo jodongo	4.33 bcd	4.33 abc	0.57 bcdefgh	0.43 abcdef	7.10 fghi	11.04 efgh
5	5 Nyandere	4.33 bcd	3.00 cd	0.33 defgh	0.63 abcd	4.08 opqrstuvwx	12.37 cdef
6	Odinga	4.33 bcd	3.00 cd	0.27 efgh	0.47 abcdef	6.34 ghijkl	8.97 hijklm
7	Naspot 1	3.00 def	4.33 abc	0.83 ab	0.43 abcdef	6.00 hijklmn	12.04 def
8	Kenspot 3	3.67 cde	4.33 abc	0.60 bcdefg	0.47 abcdef	7.17 efgh	5.63 qrstuvwxyz
9	Naspot x New Kawogo 2	3.00 def	3.00 cd	0.50 bcdefgh	0.50 abcdef	5.35 ijklmnopq	8.85 hijklmn
10	Nyamuguta	3.00 def	3.00 cd	0.47 bcdefgh	0.50 abcdef	4.61 lmnopqrstuv	6.98 lmnopqrstuv
11	Nyautenge	4.33 bcd	3.67 bcd	0.53 bcdefgh	0.67 abc	16.82 a	15.23 ab
12	Ejumula x New Kawogo 4	3.67 cde	4.33 abc	0.37 cdefgh	0.40 cdef	2.72 wxyzABCDE	2.83 BCDE
13	Nyarambe	3.67 cde	4.33 abc	0.27 efgh	0.37 cdef	3.33 stuvwxyzABC	6.48 opqrstuvwx
14	Nyakagwa	3.00 def	3.67 bcd	0.17 gh	0.50 abcdef	3.01 vwxyzABCD	12.54 cde
15	Naspot x New Kawogo 3	3.67 cde	3.67 bcd	0.43 bcdefgh	0.47 abcdef	3.71 qrstuvwxyzA	6.48 opqrstuvwx
16	Ejumula x New Kawogo 2	6.33 a	3.00 cd	0.13 h	0.23 f	2.17 yzABCDEF	3.02 ABCDE
17	Nangili	3.00 def	3.00 cd	0.40 bcdefgh	0.33 cdef	4.91 lmnopqrs	8.79 hijklmno
18	Kenspot 2	3.00 def	3.67 bcd	0.37 cdefgh	0.53 abcdef	3.16 stuvwxyzABCD	8.65 ijklmno
19	SPK 013	3.67 cde	3.67 bcd	0.40 bcdefgh	0.63 abcd	8.89 bcde	7.91 jklmnopq
20	Mugande x New Kawogo 4	4.33 bcd	2.33 d	0.20 fgh	0.60 abcde	2.11 zABCDEF	9.42 ghijk
21	Alupe or	3.00 def	2.33 d	0.50 bcdefgh	0.33 cdef	5.49 hijklmnop	14.18 bc
22	12 Marooko	3.00 def	3.00 cd	0.63 abcdef	0.57 abcdef	3.37 stuvwxyzABC	6.11 pqrstuvwx
23	Kenspot 5	3.67 cde	4.33 abc	0.53 bcdefgh	0.70 ab	3.51 rstuvwxyzAB	8.33 ijklmnop
24	36 Kalamb Nyerere	4.33 bcd	3.00 cd	0.57 bcdefgh	0.67 abc	5.17 jklmnopqr	8.80 hijklmno
25	K/KA/2004/215	3.00 def	3.67 bcd	0.30 efgh	0.33 cdef	4.28 nopqrstuvwx	1.07 E
26	Ejumula x New Kawogo 3	3.67 cde	3.00 cd	0.30 efgh	0.55 abcdef	4.53 mnopqrstuv	6.57 nopqrstuvw
27	292-H-12	4.33 bcd	2.33 d	0.43 bcdefgh	0.37 cdef	2.57 xyzABCDEF	6.63 mnopqrstuv
28	Mogesi Gikenja	4.33 bcd	3.00 cd	0.50 bcdefgh	0.60 abcde	4.00 opqrstuvwx	7.92 jklmnopq
29	Lungabure	4.33 bcd	3.67 bcd	0.77 abcd	0.47 abcdef	6.88 fghijk	5.82 qrstuvwxyz
30	Kenspot 4	3.67 cde	3.67 bcd	0.40 bcdefgh	0.40 cdef	5.14 jklmnopqr	7.48 klmnopqrs
31	Vitaa	3.00 def	3.67 bcd	0.53 bcdefgh	0.50 abcdef	4.51 mnopqrstuv	3.59 zABCD
32	9 Nduma	3.00 def	3.00 cd	0.27 efgh	0.50 abcdef	5.60 hijklmno	5.96 qrstuvwxyz
33	24 Kampala	3.00 def	2.33 d	0.63 abcdef	0.30 def	1.90 BCDEF	3.23 ABCDE
34	Obugi	4.33 bcd	3.67 bcd	0.70 abcde	0.63 abcd	9.21 bcd	9.55 ghijk
35	56682-03	3.00 def	3.00 cd	0.40 bcdefgh	0.63 abcd	0.84 F	5.02 uvwxyzABC
36	Nyawo Nyathiodiewo	4.33 bcd	3.67 bcd	0.40 bcdefgh	0.30 def	9.44 bcd	8.64 ijklmno
37	Gachaka	3.67 cde	3.67 bcd	0.47 bcdefgh	0.50 abcdef	10.62 b	5.20 stuvwxyzAB
38	Mugande	4.33 bcd	4.33 abc	0.40 bcdefgh	0.53 abcdef	8.07 defg	6.99 lmnopqrstuv

39	Amina	4.33 bcd	3.67 bcd	0.43 bcdefgh	0.70 ab	6.90 fghij	14.53 bc
40	Fumbara jikoni	4.33 bcd	3.67 bcd	0.63 abcdef	0.53 abcdef	3.43 rstuvwxyzABC	4.80 vwxyzABC
41	Ejumula	3.00 def	4.33 abc	0.33 defgh	0.60 abcde	5.13 klmnopqr	8.85 hijklmn
42	Karunde	5.67 ab	3.00 cd	0.37 cdefgh	0.37 cdef	3.12 tuvwxyzABCD	5.09 tuvwxyzABC
43	SPK 004	3.00 def	3.00 cd	0.27 efgh	0.27 ef	3.90 opqrstuvwxy	4.23 wxyzABCD
44	Kuny kibuonjo	3.00 def	5.67 a	0.30 efgh	0.33 cdef	2.04 ABCDEF	2.38 DE
45	K/KA/2002/12	3.67 cde	3.67 bcd	0.47 bcdefgh	0.40 cdef	4.56 mnopqrstuv	8.67 ijklmno
46	55 Nganyomba	3.67 cde	3.00 cd	0.47 bcdefgh	0.57 abcdef	3.28 stuvwxyzABC	9.00 hijklm
47	1-Ujili	3.00 def	3.00 cd	0.20 fgh	0.33 cdef	1.69 CDEF	4.26 wxyzABCD
48	Santo Amaro	3.67 cde	3.67 bcd	0.37 cdefgh	0.40 cdef	3.04 uvwxyzABCD	11.49 efg
49	Mugande x New Kawogo 2	1.67 f	3.00 cd	0.27 efgh	0.43 abcdef	1.73 CDEF	5.39 rstuvwxyzA
50	Wera	5.00 abc	3.67 bcd	0.80 abc	0.55 abcdef	4.82 lmnopqrst	9.22 ghijkl
51	Kemb 10	3.67 cde	3.67 bcd	0.55 bcdefgh	0.60 abcde	9.21 bcd	17.04 a
52	Mbita	3.00 def	3.00 cd	1.07 a	0.55 abcdef	8.57 cdef	6.49 nopqrstuvwx
53	Naspot x New Kawogo 1	3.67 cde	3.00 cd	0.40 bcdefgh	0.47 abcdef	3.00 vwxyzABCD	2.74 CDE
54	Kibuonjo	3.67 cde	3.00 cd	0.40 bcdefgh	0.47 abcdef	4.11 opqrstuvwx	7.46 klmnopqrst
55	29 Kuny kibuonjo	4.33 bcd	3.67 bcd	0.47 bcdefgh	0.33 cdef	3.81 pqrstuvwxyz	7.70 klmnopqr
56	62 Odhiogo	4.33 bcd	3.00 cd	0.37 cdefgh	0.55 abcdef	4.79 lmnopqrstu	10.43 efghi
57	52 Nyakisumu	3.67 cde	2.33 d	0.50 bcdefgh	0.47 abcdef	1.17 EF	6.06 pqrstuvwxy
58	Ejumula x New Kawogo 1	3.00 def	3.00 cd	0.27 efgh	0.47 abcdef	4.15 opqrstuvwx	8.63 ijklmno
59	Bungoma	4.33 bcd	3.67 bcd	0.60 bcdefg	0.43 abcdef	6.04 hijklm	6.21 pqrstuvwx
60	K 117	3.67 cde	3.00 cd	0.17 gh	0.63 abcd	8.20 def	10.14 fghij
61	Fundukhusia	1.67 f	3.67 bcd	0.40 bcdefgh	0.63 abcd	8.20 def	10.14 fghij
62	SPK 031	3.67 cde	3.00 cd	0.30 efgh	0.40 cdef	5.62 hijklmno	4.19 xyzABCD
63	Mugande x New Kawogo 1	3.67 cde	3.67 bcd	0.40 bcdefgh	0.47 abcdef	9.26 bcd	8.84 hijklmno
64	Mwavuli	3.00 def	5.00 ab	0.47 bcdefgh	0.55 abcdef	2.85 vwxyzABCDE	7.33 klmnopqrstu
65	Polo yiengo	4.33 bcd	3.67 bcd	0.83 ab	0.37 cdef	4.40 mnopqrstuvw	3.61 zABCD
66	Mugande x New Kawogo 3	4.33 bcd	3.00 cd	0.20 fgh	0.50 abcdef	3.00 vwxyzABCD	3.69 yzABCD
67	Sinia	4.33 bcd	2.33 d	0.70 abcde	0.33 cdef	10.08 bc	7.35 klmnopqrstu
68	Tainung	2.33 ef	3.00 cd	0.47 bcdefgh	0.45 abcdef	1.44 DEF	5.70 qrstuvwxyz
	Site mean	3.66	3.38	0.45	0.48	5.07	7.51
	LSD Value	0.65	0.35	0.05	0.05	0.17	0.54
	CV	30.82	29.82	30.65	23.71	21.00	20.00
	p value	0.05	0.046	0.05	0.05	0.001	0.001

Means with the same letters along a column are not significantly different according to LSD test *($p \leq 0.05$)*.

Scale on petiole length as guided by Huaman (1992):

1 = very short (<10 cm);
3 = short (10-15 cm);
5 = intermediate (16-20 cm);
7 = long (21-25 cm); while
9 = very long (>25 cm).

4.3.1.2 Qualitative characters

4.3.1.2.1 Plant type

Plant type data is shown in Table 4.10. The genotypes exhibited two major different plant forms. At both sites, plant types ranged from from spreading and 'extrmely spreading'.

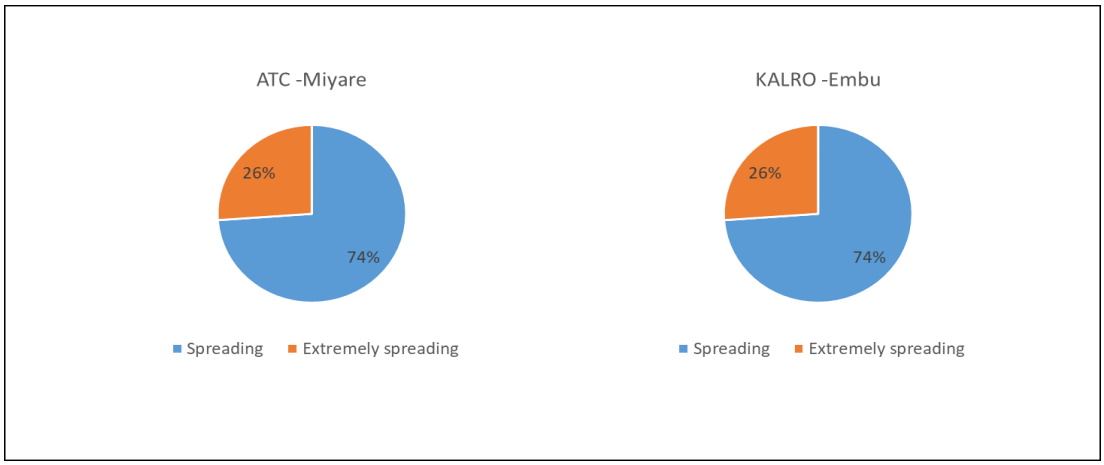

Figure 4.3: Plant type forms exhibited by sweet potato genotypes at ATC -Miyare and KALRO-Embu

Out of the two plant type forms, the most common was the spreading (Figure 4.3). At both sites (ATC –Miyare and KALRO –Embu), 74% of the genotypes exhibited the 'spreading form' while 26% of the genotypes at both sites exhibited the 'extremely spreading form' (Figure 4.3). None of the genotypes recorded compact or semi-compact growth habit.

4.3.1.2.2 Abaxial leaf vine pigmentation

Abaxial leaf vine pigmentation (ALVP) data is shown in Table 4.10.

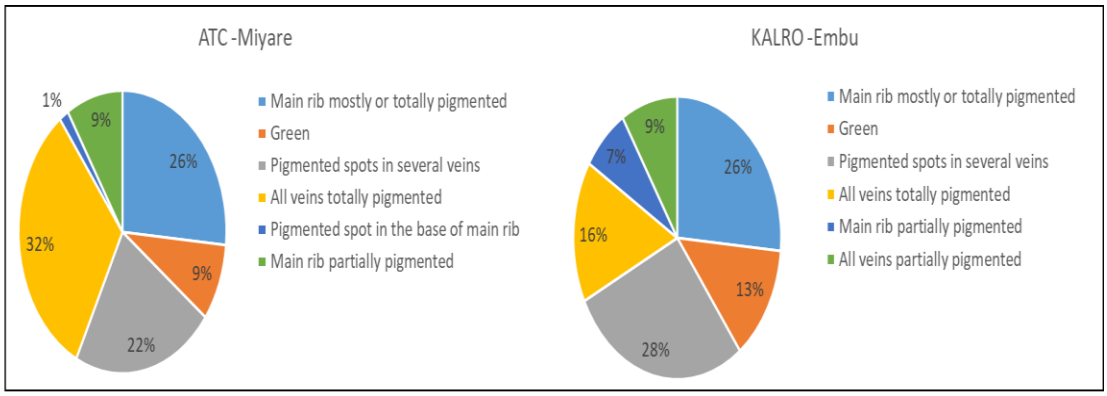

Figure 4.4: Abaxial leaf vine pigmentation as exhibited by sweet potato genotypes at ATC -Miyare and KALRO -Embu

At ATC –Miyare majority (32%) of the genotypes had all veins totally pigmented with anthocyanin, 26% of the genotypes had the main rib mostly or totally pigmented with anthocyanin, 22% of the genotypes had pigminted spots of anthocyanin in several veins, 9% of the genotypes had the main rib partially pigmented or green and only 1% of the genotypes had pigmented spots of anthocyanin in the base of main mid rib (Figure 4.4). None of the genotypes had all veins partially pigmented with anthocyanin.

At KALRO –Embu, the genotypes exhibited pigmented spots with anthocyanin in several veins (28%), main rib mostly or totally pigmented with anthocyanin (26%), all veins totally pigmented with anthocyanin (16%), green (13%), all veins partially pigmented with anthocyanin (9%), and main rib partially pigmented with anthocyanin (7%) while none of the genotypes had pigmented spots in the base of main mid rib (Figure 4.4).

Table 4.10: Plant and leaf characters recorded on the 68 sweet potato genotypes at ATC -Miyare and KALRO Embu sites grown during the long rains in 2014

	GENOTYPE	Plant type		Abaxial leaf vein pigmentation	
		ATC Miyare	KALRO Embu	ATC Miyare	KALRO Embu
1	Kenspot 1	Extremely spreading	Extremely spreading	Main rib mostly or totally pigmented	Main rib mostly or totally pigmented
2	Saly boro	Spreading	Spreading	Pigmented spots in several veins	Main rib mostly or totally pigmented
3	91/2187	Spreading	Extremely spreading	Main rib mostly or totally pigmented	Main rib mostly or totally pigmented
4	Oduogo jodongo	Spreading	Spreading	Main rib mostly or totally pigmented	Pigmented spots in several veins
5	5 Nyandere	Spreading	Spreading	Main rib mostly or totally pigmented	Green
6	Odinga	Spreading	Spreading	All veins totally pigmented	All veins totally pigmented
7	Naspot 1	Spreading	Extremely spreading	Green	Green
8	Kenspot 3	Extremely spreading	Extremely spreading	Main rib mostly or totally pigmented	Pigmented spots in several veins
9	Naspot x New Kawogo 2	Spreading	Extremely spreading	Main rib mostly or totally pigmented	Main rib mostly or totally pigmented
10	Nyamuguta	Spreading	Spreading	All veins totally pigmented	All veins partially pigmented
11	Nyautenge	Extremely spreading	Spreading	Green	Pigmented spots in several veins
12	Ejumula x New Kawogo 4	Extremely spreading	Spreading	Pigmented spots in several veins	Main rib mostly or totally pigmented
13	Nyarambe	Spreading	Spreading	All veins totally pigmented	All veins totally pigmented
14	Nyakagwa	Spreading	Spreading	Main rib mostly or totally pigmented	All veins totally pigmented
15	Naspot x New Kawogo 3	Spreading	Spreading	All veins totally pigmented	All veins partially pigmented
16	Ejumula x New Kawogo 2	Spreading	Spreading	Main rib partially pigmented	Pigmented spots in several veins
17	Nangili	Spreading	Spreading	All veins totally pigmented	All veins partially pigmented
18	Kenspot 2	Spreading	Spreading	Pigmented spot in the base of main rib	Main rib partially pigmented
19	SPK 013	Spreading	Spreading	Pigmented spots in several veins	Pigmented spots in several veins
20	Mugande x New Kawogo 4	Spreading	Spreading	Main rib mostly or totally pigmented	Pigmented spots in several veins
21	Alupe or	Spreading	Spreading	Main rib mostly or totally pigmented	Main rib mostly or totally pigmented
22	12 Marooko	Spreading	Spreading	Main rib partially pigmented	Main rib partially pigmented
23	Kenspot 5	Extremely spreading	Spreading	All veins totally pigmented	Pigmented spots in several veins
24	36 Kalamb Nyerere	Spreading	Extremely spreading	All veins totally pigmented	All veins totally pigmented
25	K/KA/2004/215	Spreading	Spreading	All veins totally pigmented	Main rib mostly or totally pigmented
26	Ejumula x New Kawogo 3	Spreading	Spreading	All veins totally pigmented	Green
27	292-H-12	Spreading	Spreading	All veins totally pigmented	All veins totally pigmented
28	Mogesi Gikenja	Spreading	Extremely spreading	All veins totally pigmented	All veins totally pigmented
29	Lungabure	Spreading	Spreading	Pigmented spots in several veins	Pigmented spots in several veins
30	Kenspot 4	Extremely spreading	Spreading	All veins totally pigmented	All veins partially pigmented
31	Vitaa	Spreading	Spreading	Pigmented spots in several veins	Green
32	9 Nduma	Spreading	Spreading	All veins totally pigmented	Main rib mostly or totally pigmented
33	24 Kampala	Extremely spreading	Spreading	Main rib partially pigmented	Main rib partially pigmented
34	Obugi	Spreading	Spreading	Pigmented spots in several veins	Pigmented spots in several veins
35	56682-03	Spreading	Extremely spreading	All veins totally pigmented	All veins totally pigmented
36	Nyawo Nyathiodiewo	Spreading	Spreading	All veins totally pigmented	All veins partially pigmented
37	Gachaka	Spreading	Spreading	Pigmented spots in several veins	Pigmented spots in several veins
38	Mugande	Spreading	Spreading	Main rib partially pigmented	Pigmented spots in several veins
39	Amina	Spreading	Spreading	Main rib mostly or totally pigmented	All veins totally pigmented

40	Fumbara jikoni	Spreading	Spreading	All veins totally pigmented	Pigmented spots in several veins
41	Ejumula	Extremely spreading	Extremely spreading	Pigmented spots in several veins	Green
42	Karunde	Spreading	Spreading	Main rib mostly or totally pigmented	Main rib mostly or totally pigmented
43	SPK 004	Spreading	Extremely spreading	Green	Green
44	Kuny kibuonjo	Spreading	Extremely spreading	Pigmented spots in several veins	Pigmented spots in several veins
45	K/KA/2002/12	Spreading	Spreading	Pigmented spots in several veins	Pigmented spots in several veins
46	55 Nganyomba	Extremely spreading	Spreading	Main rib mostly or totally pigmented	Pigmented spots in several veins
47	1-Ujili	Spreading	Extremely spreading	All veins totally pigmented	Main rib mostly or totally pigmented
48	Santo Amaro	Extremely spreading	Spreading	Pigmented spots in several veins	Pigmented spots in several veins
49	Mugande x New Kawogo 2	Spreading	Spreading	Main rib partially pigmented	Main rib partially pigmented
50	Wera	Spreading	Spreading	Main rib partially pigmented	Main rib partially pigmented
51	Kemb 10	Extremely spreading	Spreading	Pigmented spots in several veins	Pigmented spots in several veins
52	Mbita	Extremely spreading	Extremely spreading	All veins totally pigmented	All veins totally pigmented
53	Naspot x New Kawogo 1	Spreading	Spreading	Pigmented spots in several veins	Pigmented spots in several veins
54	Kibuonjo	Spreading	Spreading	Main rib mostly or totally pigmented	Main rib mostly or totally pigmented
55	29 Kuny kibuonjo	Spreading	Extremely spreading	Pigmented spots in several veins	Pigmented spots in several veins
56	62 Odhiogo	Extremely spreading	Extremely spreading	Green	Green
57	52 Nyakisumu	Spreading	Spreading	All veins totally pigmented	Main rib mostly or totally pigmented
58	Ejumula x New Kawogo 1	Spreading	Spreading	Green	Green
59	Bungoma	Spreading	Spreading	Main rib mostly or totally pigmented	Main rib mostly or totally pigmented
60	K 117	Extremely spreading	Spreading	Main rib mostly or totally pigmented	Main rib mostly or totally pigmented
61	Fundukhusia	Extremely spreading	Extremely spreading	Green	Green
62	SPK 031	Spreading	Spreading	All veins totally pigmented	All veins partially pigmented
63	Mugande x New Kawogo 1	Extremely spreading	Extremely spreading	Pigmented spots in several veins	Main rib mostly or totally pigmented
64	Mwavuli	Extremely spreading	Spreading	Main rib mostly or totally pigmented	Main rib mostly or totally pigmented
65	Polo yiengo	Spreading	Extremely spreading	Main rib mostly or totally pigmented	Main rib mostly or totally pigmented
66	Mugande x New Kawogo 3	Spreading	Spreading	All veins totally pigmented	Main rib mostly or totally pigmented
67	Sinia	Spreading	Spreading	Main rib mostly or totally pigmented	All veins totally pigmented
68	Tainung	Extremely spreading	Spreading	All veins totally pigmented	All veins totally pigmented

4.3.1.2.3 Latex production in the roots

There was no single genotype whose roots did not produce latex after making a cross section cut at ATC -Miyare (Table 4.11). Genotypes that recorded very little latex included Ejumula x New Kawogo 3, K/KA/2002/12, Kemb 10, 29 Kuny kibuonjo, Kenspot 1, Ejumula x New Kawogo 2, 292-H-12, Mugande x New Kawogo 2 and Wera. Genotypes that recorded the highest amounts of latex at ATC -Miyare were 9 Nduma, Fumbara jikoni, Nyautenge, Nangili and Gachaka.

Similarly, sweet potato roots of all genotypes at KALRO -Embu produced latex after cross section cuts was made on them (Table 4.11). Genotypes that recorded very little latex included Odinga, Ejumula x New Kawogo 4, Mugande x New Kawogo 4 and Wera. Genotypes that recorded the highest amounts of latex at KALRO -Embu were 9 Nduma, K117, Polo yiengo Naspot 1, Kenspot 3, Nyarambe, Nangili, SPK 013 and Sinia.

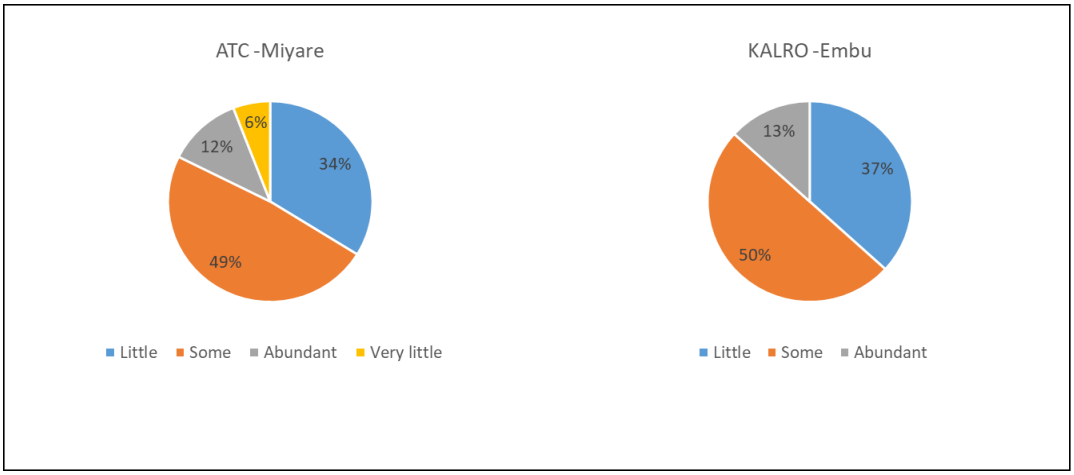

Figure 4.5: Latex production as exhibited by sweet potato genotypes at ATC -Miyare and KALRO -Embu

Most of the genotypes (49% at ATC –Miyare and 50% at KALRO –Embu) produced some amount of latex while 34% and 37% of the genotypes at ATC –Miyare and

KALRO –Embu respectively produced little latex (Figure 4.5). Only 12% and 13% of the genotypes at ATC –Miyare and KALRO –Embu respectively produced abundant latex (Figure 4.5). At ATC –Miyare 6% of the genotpes produced very little latex (Figure 4.5).

4.3.1.2.4 Oxidation of roots

It was observed that majority of the genotypes that produced little latex underwent minimal oxidation while those that produced high amounts of latex recorded abundant oxidation.

There was no single genotype whose roots were not oxidised after making a cross section cut at ATC –Miyare (Table 4.11). Genotypes that recorded very little oxidation in this site included K/KA/2002/12, Mugande x New Kawogo 2, 29 Kuny kibuonjo, Kenspot 1, Ejumula x New Kawogo 2, Ejumula x New Kawogo 3, Vitaa, obugi and SPK 004. Genotypes that recorded the abundant oxidation were Nyautenge, Fumbara jikoni, K117, Nangili, SPK 013, 12 Marooko, K/KA/2004/215, 9 Nduma, Mugande, Mugande x New Kawogo 3 and Sinia.

In the same way, sweet potato roots of all genotypes at KALRO -Embu underwent oxidation after cross section cuts was made on them (Table 4.11). Genotypes that recorded very little oxidation in this site included 62 Odhiogo, 1 -Ujili, Kenspot 1, Oduogo jodongo, Mugande x New Kawogo 4 and Vitaa. Genotypes that recorded the abundant oxidation were Nyarambe, Ejumula, K117 and Polo yiengo.

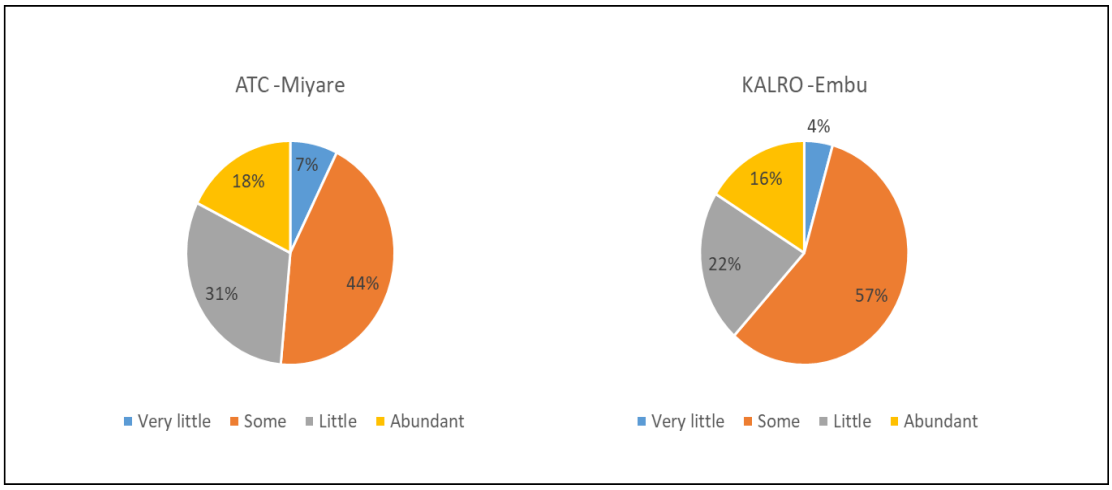

Figure 4.6: Root oxidation as exhibited by sweet potato genotypes at ATC -Miyare and KALRO -Embu

Many of the genotypes (44% at ATC –Miyare and 57% at KALRO –Embu) exhibited some oxidation while 31% and 22% of the genotypes at ATC –Miyare and KALRO –Embu respectively exhibited little oxidation (Figure 4.6). Further, 18% and 16% of the genotypes at ATC –Miyare and KALRO –Embu respectively exhibited abundant oxidation (Figure 4.6). Only 7% and 4% of the genotypes had very little oxidation, at ATC –Miyare and KALRO –Embu, respectively (Figure 4.6).

4.3.1.2.5 Storage root size variability

Storage root size variability data is shown in Table 4.11.

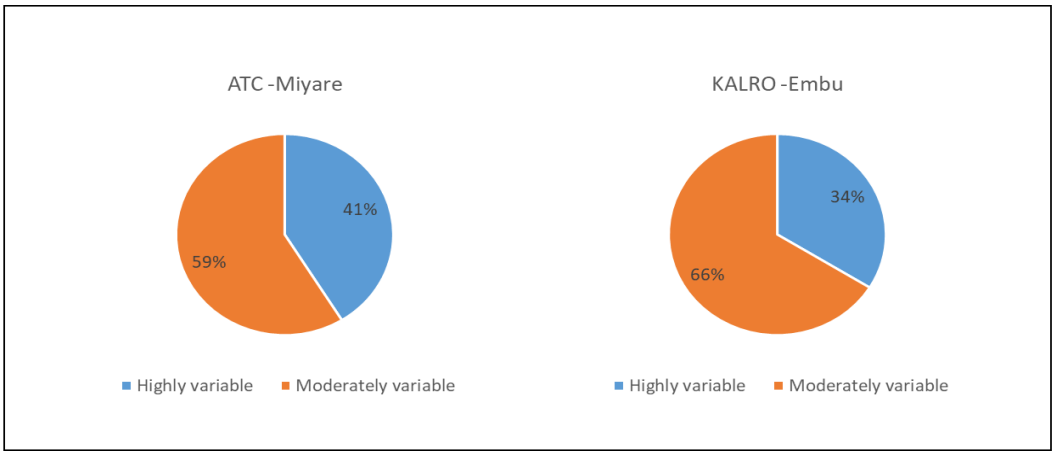

Figure 4.7: Storage root size variability as exhibited by sweet potato genotypes at ATC -Miyare and KALRO -Embu

Majority of the root genotypes (59% at ATC –Miyare and 66% at KALRO –Embu) were moderately variable in sizes while 41% and 34% of the genotypes at ATC – Miyare and KALRO respectively had their roots highly variable sizes (Figure 4.7).

4.3.1.2.6 Storage root shape

Storage root shape data is shown in Table 4.11.

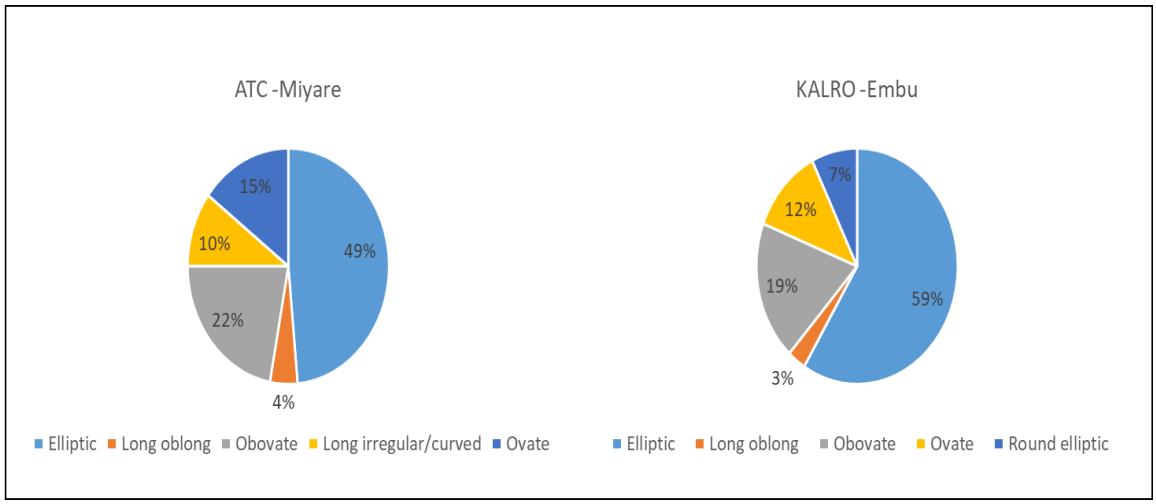

Figure 4.8: Storage root shape as exhibited by sweet potato genotypes at ATC -Miyare and KALRO -Embu

Genotypes were recorded as elliptic (49%), obovate (22%), ovate (15%), long irregular/curved (10%) or long oblong (4%) at ATC –Miyare (Figure 4.8). At this site, there were no genotypes whose roots were found to be round, oblong, round elliptic or long elliptic in shape.

At KALRO –Embu genotypes were recorded as elliptic (59%), obovate (19%), ovate (12%), round elliptic (7%) and long oblong (3%) as shown in Figure 4.8. At the same site, there were no genotypes whose roots were found to be either round, oblong, long elliptic or long irregular/curved in shape (Figure 4.8).

Table 4.11: Root characters recorded on the 68 sweet potato genotypes at ATC – Miyare and KALRO –Embu sites grown during the long rains in 2014

	GENOTYPE	Latex production		Oxidation of roots		Storage root variability		Storage root shape	
		ATC Miyare	KALRO Embu	ATC Miyare	KALRO Embu	ATC Miyare	KALRO Embu	ATC Miyare	KALRO Embu
1	Kenspot 1	Little	Little	Very little	Little	Highly variable	Highly variable	Elliptic	Ovate
2	Saly boro	Some	Some	Some	Some	Moderately variable	Moderately variable	Elliptic	Obovate
3	91/2187	Some	Some	Some	Some	Highly variable	Moderately variable	Long oblong	Elliptic
4	Oduogo jodongo	Little	Little	Little	Little	Moderately variable	Moderately variable	Obovate	Obovate
5	5 Nyandere	Some	Some	Some	Some	Moderately variable	Moderately variable	Elliptic	Elliptic
6	Odinga	Some	Little	Some	Some	Moderately variable	Moderately variable	Elliptic	Elliptic
7	Naspot 1	Little	Abundant	Little	Abundant	Highly variable	Moderately variable	Long irregular/curved	Obovate
8	Kenspot 3	Little	Abundant	Some	Some	Highly variable	Moderately variable	Elliptic	Elliptic
9	Naspot x New Kawogo 2	Little	Little	Little	Some	Moderately variable	Highly variable	Ovate	Round elliptic
10	Nyamuguta	Little	Little	Little	Some	Highly variable	Moderately variable	Long irregular/curved	Obovate
11	Nyautenge	Abundant	Some	Abundant	Some	Highly variable	Highly variable	Elliptic	Elliptic
12	Ejumula x New Kawogo 4	Little	Little	Little	Some	Moderately variable	Moderately variable	Obovate	Elliptic
13	Nyarambe	Some	Abundant	Some	Abundant	Moderately variable	Moderately variable	Elliptic	Obovate
14	Nyakagwa	Some	Some	Some	Some	Moderately variable	Moderately variable	Obovate	Elliptic
15	Naspot x New Kawogo 3	Little	Some	Some	Some	Highly variable	Highly variable	Elliptic	Elliptic
16	Ejumula x New Kawogo 2	Little	Little	Little	Little	Highly variable	Moderately variable	Long oblong	Elliptic
17	Nangili	Abundant	Abundant	Abundant	Some	Moderately variable	Moderately variable	Elliptic	Elliptic
18	Kenspot 2	Some	Some	Some	Abundant	Moderately variable	Moderately variable	Elliptic	Elliptic
19	SPK 013	Abundant	Abundant	Abundant	Abundant	Highly variable	Highly variable	Obovate	Elliptic
20	Mugande x New Kawogo 4	Abundant	Little	Some	Very little	Moderately variable	Moderately variable	Long elliptic	Round elliptic
21	Alupe or	Some	Some	Some	Some	Moderately variable	Moderately variable	Long irregular/curved	Obovate
22	12 Marooko	Little	Little	Abundant	Little	Highly variable	Moderately variable	Elliptic	Elliptic
23	Kenspot 5	Little	Some	Little	Little	Moderately variable	Moderately variable	Obovate	Elliptic
24	36 Kalamb Nyerere	Some	Some	Some	Some	Highly variable	Highly variable	Elliptic	Elliptic
25	K/KA/2004/215	Some	Little	Abundant	Some	Moderately variable	Highly variable	Long oblong	Elliptic
26	Ejumula x New Kawogo 3	Very little	Little	Very little	Some	Moderately variable	Moderately variable	Obovate	Ovate
27	292-H-12	Little	Little	Little	Little	Highly variable	Moderately variable	Elliptic	Obovate
28	Mogesi Gikenja	Some	Some	Some	Some	Highly variable	Moderately variable	Long oblong	Elliptic
29	Lungabure	Some	Some	Some	Some	Highly variable	Highly variable	Obovate	Obovate
30	Kenspot 4	Little	Some	Little	Abundant	Moderately variable	Moderately variable	Elliptic	Elliptic
31	Vitaa	Little	Little	Little	Little	Moderately variable	Highly variable	Obovate	Elliptic
32	9 Nduma	Abundant	Abundant	Abundant	Abundant	Moderately variable	Moderately variable	Obovate	Obovate
33	24 Kampala	Some	Some	Some	Some	Highly variable	Highly variable	Long irregular/curved	Long oblong
34	Obugi	Little	Some	Little	Some	Highly variable	Moderately variable	Ovate	Long oblong
35	56682-03	Some	Little	Some	Some	Slightly variable	Moderately variable	Obovate	Elliptic
36	Nyawo Nyathiodiewo	Little	Little	Little	Some	Moderately variable	Highly variable	Elliptic	Elliptic

37	Gachaka	Abundant	Some	Some	Abundant	Highly variable	Highly variable	Obovate	Obovate
38	Mugande	Some	Some	Abundant	Some	Highly variable	Moderately variable	Ovate	Ovate
39	Amina	Some	Some	Little	Some	Moderately variable	Moderately variable	Elliptic	Ovate
40	Fumbara jikoni	Abundant	Some	Abundant	Some	Moderately variable	Moderately variable	Elliptic	Elliptic
41	Ejumula	Little	Some	Some	Abundant	Moderately variable	Moderately variable	Obovate	Elliptic
42	Karunde	Some	Little	Some	Some	Moderately variable	Moderately variable	Ovate	Obovate
43	SPK 004	Little	Some	Little	Little	Moderately variable	Highly variable	Obovate	Elliptic
44	Kuny kibuonjo	Some	Some	Some	Some	Moderately variable	Moderately variable	Long irregular/curved	Ovate
45	K/KA/2002/12	Very little	Some	Very little	Some	Highly variable	Highly variable	Long irregular/curved	Elliptic
46	55 Nganyomba	Some	Some	Some	Some	Highly variable	Highly variable	Ovate	Elliptic
47	1-Ujili	Some	Little	Some	Very little	Moderately variable	Moderately variable	Elliptic	Elliptic
48	Santo Amaro	Some	Some	Little	Some	Moderately variable	Moderately variable	Elliptic	Round elliptic
49	Mugande x New Kawogo 2	Little	Little	Very little	Little	Moderately variable	Highly variable	Elliptic	Elliptic
50	Wera	Little	Little	Little	Some	Moderately variable	Highly variable	Elliptic	Elliptic
51	Kemb 10	Very little	Some	Little	Little	Highly variable	Highly variable	Elliptic	Elliptic
52	Mbita	Some	Little	Some	Little	Moderately variable	Moderately variable	Elliptic	Ovate
53	Naspot x New Kawogo 1	Little	Some	Little	Some	Moderately variable	Moderately variable	Long irregular/curved	Round elliptic
54	Kibuonjo	Some	Some	Some	Some	Moderately variable	Highly variable	Ovate	Elliptic
55	29 Kuny kibuonjo	Very little	Little	Very little	Little	Moderately variable	Highly variable	Elliptic	Elliptic
56	62 Odhiogo	Some	Little	Little	Very little	Moderately variable	Highly variable	Elliptic	Obovate
57	52 Nyakisumu	Some	Little	Some	Some	Highly variable	Moderately variable	Elliptic	Elliptic
58	Ejumula x New Kawogo 1	Some	Some	Some	Some	Modertaely variable	Moderately variable	Ovate	Elliptic
59	Bungoma	Little	Little	Little	Little	Moderately variable	Moderately variable	Obovate	Elliptic
60	K 117	Abundant	Abundant	Abundant	Abundant	Highly variable	Moderately variable	Elliptic	Elliptic
61	Fundukhusia	Some	Some	Some	Some	Highly variable	Highly variable	Elliptic	Round elliptic
62	SPK 031	Some	Some	Some	Some	Highly variable	Moderately variable	Ovate	Elliptic
63	Mugande x New Kawogo 1	Little	Some	Little	Little	Highly variable	Highly variable	Elliptic	Ovate
64	Mwavuli	Some	Little	Some	Little	Moderately variable	Moderately variable	Ovate	Elliptic
65	Polo yiengo	Some	Abundant	Some	Abundant	Highly variable	Moderately variable	Obovate	Elliptic
66	Mugande x New Kawogo 3	Some	Some	Abundant	Some	Moderately variable	Moderately variable	Elliptic	Elliptic
67	Sinia	Some	Abundant	Abundant	Abundant	Highly variable	Highly variable	Ovate	Ovate
68	Tainung	Some	Some	Little	Some	Moderately variable	Moderately variable	Elliptic	Obovate

4.3.2 Dendrogram based on qualitative agro-morphological characters

The qualitative morphological characters used to generate the dendrogram (Figure 4.9) were type of leaf lobbing, number of lobes, shape of central lobe, plant type and abaxial leaf pigmentation. The above-mentioned morphological characters showed a high polymorphism of 2.6 among the 68 sweet potato genotypes (Figure 4.9).

The dendrogram (Figure 4.9) separated the genotypes into two major clusters (A and B) at about 1.4 Euclidean distance. Cluster A contained 11 genotypes and consisted of 2 sub-clusters. The genotypes Ejumula x New Kawogo 2, Kenspot 2, Naspot x New Kawogo 1 and Tainung did not fall into any sub-group (Figure 4.9). Cluster B contained 57 genotypes and formed 3 major sub-clusters (Figure 4.9). All genotypes in cluster B had five leaf lobes while those in cluster A did not show any distinguishable relationship or pattern. Ejumula x New Kawogo 2 and Kenspot 2 are the only genotypes that had seven leaf lobes. Further, 3 genotypes (Kenspot 4, Santo Amaro and Bungoma) were the only ones having three leaf lobes. Out of the 68 genotypes evaluated, only Naspot x New Kawogo 1 had a "linear type" shape of the central lobe. Most of the genotypes that shared a common name did not cluster together since they showed some differences in the qualitative phenotypic characters. For instance, Kenspot 1 was grouped in cluster 5, Kenspot 2 and Kenspot 4 were grouped in cluster 1, while Kenspot 3 and 5 were grouped in cluster 4 (Figure 4.9).

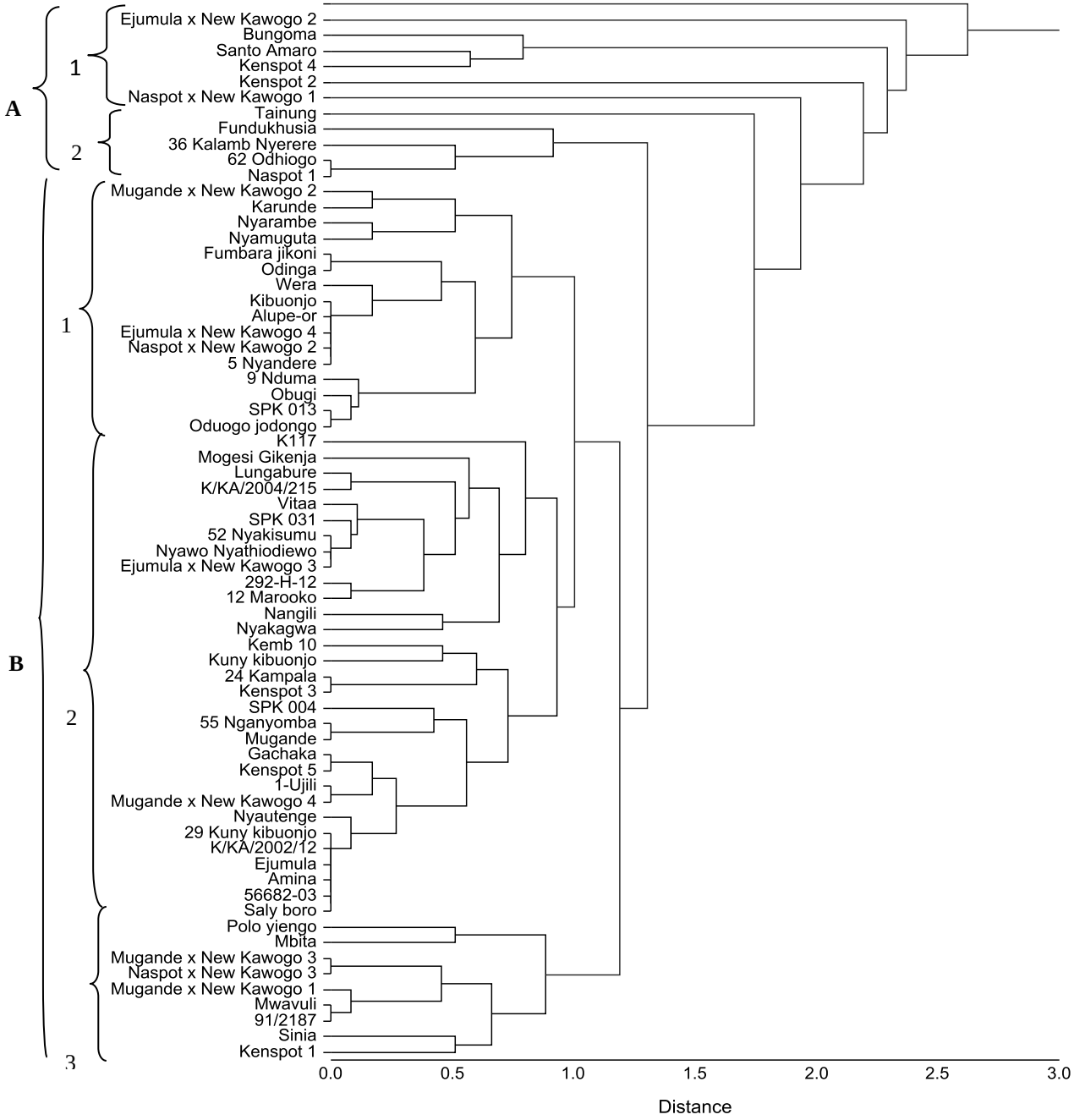

Figure 4.9: Dendrogram (based on Euclidean distance coefficient) of 68 genotypes generated from qualitative agro-morphological characters

4.3.3 Dendrogram based on quantitative agro-morphological characters

Quantitative characters that were used to generate the dendrograms (Figure 4.10 and 4.11) were vine growth rate, vine internode length, vine internode diameter, storage root cortex thickness, storage root stalk, mature leaf size, storage root length, storage root diameter, petiole length, weight of largest tuber and yield.

From the hierarchical cluster analysis, quantitative characters showed a high polymorphism of about 2.5 among the 68 sweet potato genotypes at ATC –Miyare (Figure 4.10). The tree obtained separated the genotypes into two major clusters (A and B) at about 2.5 Euclidean distance. Cluster A contained 36 genotypes and consisted of 2 sub-clusters. Cluster B contained 32 genotypes and formed 3 sub-clusters (Figure 4.10). Both cluster A and B did not show any distinguishable relationship or pattern.

From the hierarchical cluster analysis, quantitative characters showed a high polymorphism of about 2.8 among the 68 sweet potato genotypes at KALRO –Embu (Figure 4.11). The tree obtained separated the genotypes into two major clusters (A and B) at about 2.7 Euclidean distance. Cluster A contained 22 genotypes and consisted of 2 sub-clusters. Cluster B contained 46 genotypes and formed 3 sub-clusters (Figure 4.11). Both cluster A and B did not show any distinguishable relationship or pattern.

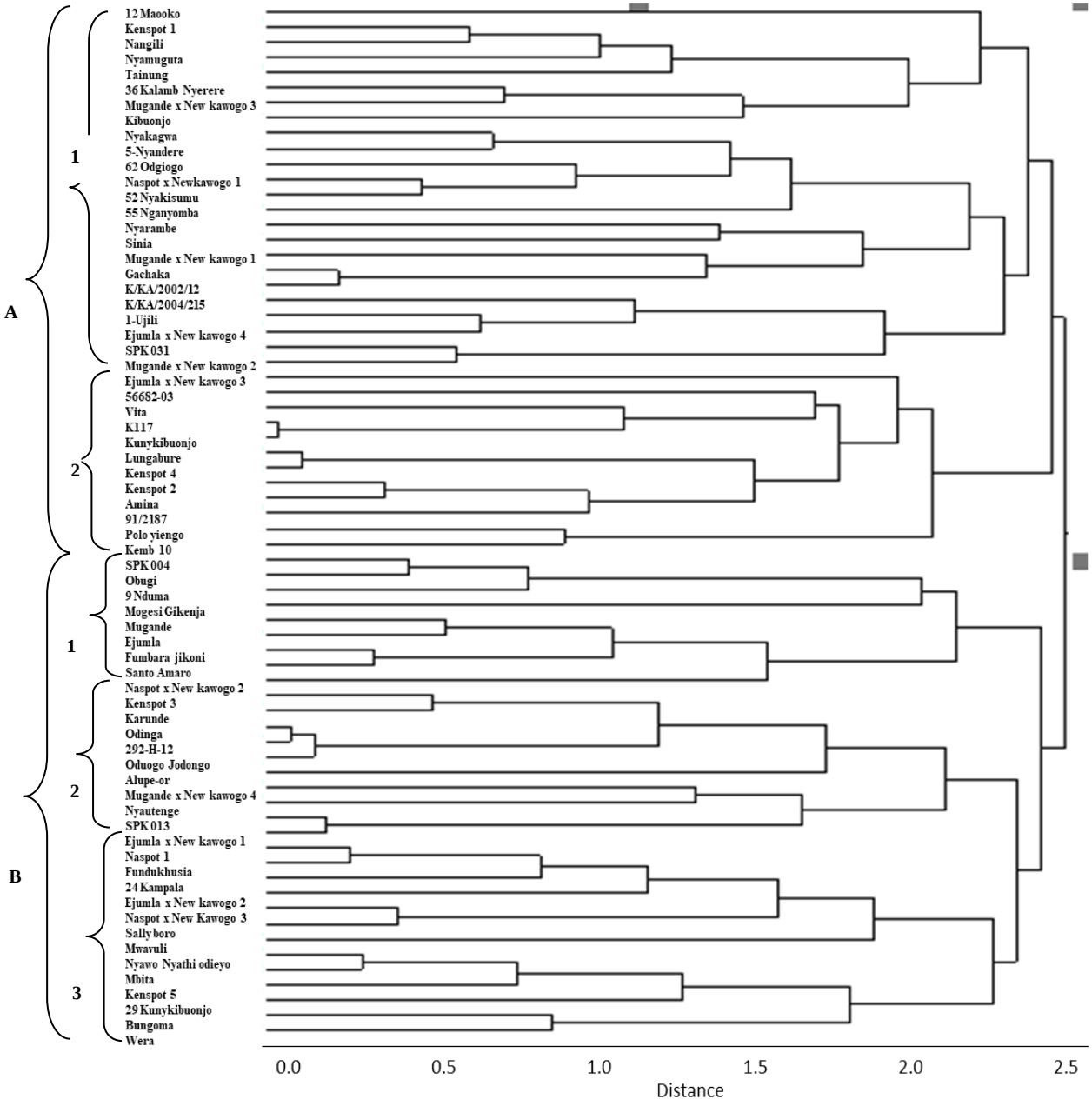

Figure 4.10: Dendrogram (based on Euclidean distance coefficient) of 68 genotypes generated from quantitative data at ATC -Miyare

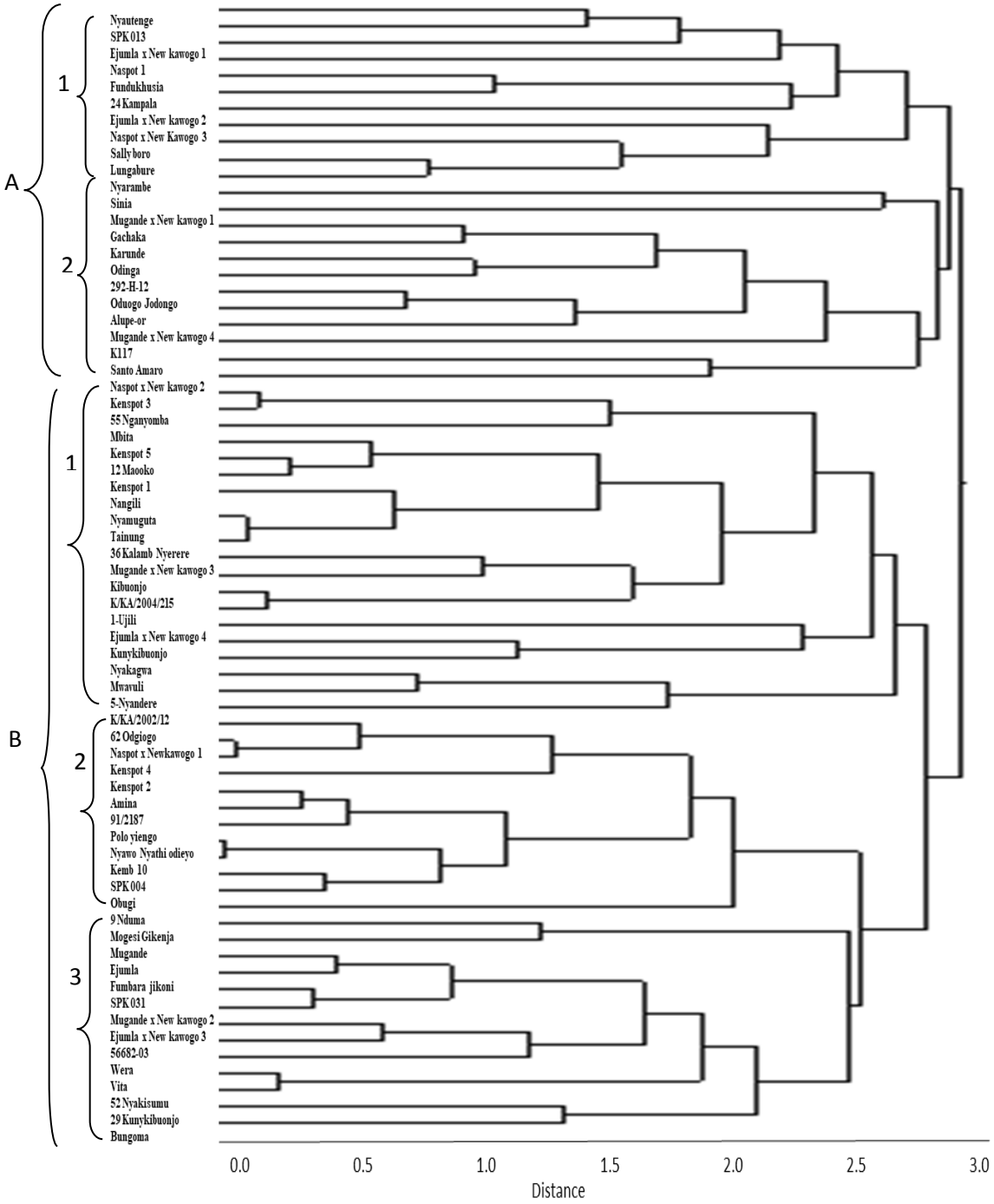

Figure 4.11: Dendrogram (based on Euclidean distance coefficient) of 68 genotypes generated from quantitative data at KALRO -Embu

4.3.4 Correlation among quantitative agro-morphological characters

Significant correlations ($p \leq 0.05$) were recorded among quantitative agro-morphological characters of the 68 sweet potato genotypes in ATC- Miyare (Table 4.12). Positive significant correlations were recorded between vine growth rate and vine internode length ($p = 0.0001$, $r = 0.6$), vine growth rate and mature leaf size ($p < 0.0001$, $r = 0.7$), storage root stalk and root yield ($p < 0.0001$, $r = 0.5$), and root yield and largest storage root diameter ($p < 0.0001$, $r = 0.5$).

Similarly, significant correlations ($p \leq 0.05$) were recorded among the quantitative agro-morphological characters of the 68 sweet potato genotypes in KALRO- Embu (Table 4.13). Positive significant correlations were recorded between vine growth rate and vine internode length ($p = 0.0001$, $r = 0.7$), largest storage root diameter and weight of largest root ($p < 0.0001$, $r = 0.6$), storage root length and weight of largest root ($p < 0.0001$, $r = 0.6$). Root yield had significant positive correlation with weight of largest root ($p < 0.0001$, $r = 0.5$).

Table 4.12: Correlations among quantitative agro-morphological traits recorded on the 68 sweet potato genotypes at ATC – Miyare

Variables	Vine growth rate	Vine internode length	Vine internode diameter	Storage root cortex thickness	Storage root stalk	Mature leaf size	Storage root length	Largest storage root diameter	Petiole length	Weight of largest root	Root yield
Vine growth rate	1.0										
Vine internode length	r = 0.6*	1.0									
Vine internode diameter	r = 0.1	r = 0.0	1.0								
Storage root cortex thickness	r = -0.1	r = 0.0	r = -0.1	1.0							
Storage root stalk	r = -0.1	r = 0.0	r = 0.2	r = -0.1	1.0						
Mature leaf size	r = 0.7*	r = 0.2	r = 0.2	r = 0.0	r = -0.2	1.0					
Storage root length	r = 0.2	r = -0.1	r = 0.1	r = 0.0	r = 0.0	r = 0.2	1.0				
Largest storage root diameter	r = 0.3	r = 0.1	r = 0.3	r = -0.1	r = -0.2	r = 0.2	r = -0.1	1.0			
Petiole length	r = 0.2	r = -0.1	r = 0.3	r = -0.2	r = 0.0	r = 0.2	r = 0.2	r = 0.2	1.0		
Weight of largest root	r = 0.3	r = 0.1	r = 0.3	r = -0.1	r = -0.1	r = 0.2	r = 0.2	r = 0.3	r = 0.1	1.0	
Root yield	r = 0.2	r = 0.2	r =-0.1	r = 0.0	r = -0.2*	r = 0.1	r = 0.1	r = 0.5*	r = 0.2	r = 0.3	1.0

*Significant at $p \leq 0.05$

Table 4.13: Correlations among quantitative agro-morphological traits recorded on the 68 sweet potato genotypes at KALRO –Embu

Variables	Vine growth rate	Vine internode length	Vine internode diameter	Storage root cortex thickness	Storage root stalk	Mature leaf size	Storage root length	Largest storage root diameter	Petiole length	Weight of largest root	Root yield
Vine growth rate	1.0										
Vine internode length	r = 0.7*	1.0									
Vine internode diameter	r = -0.1	r = -0.0	1.0								
Storage root cortex thickness	r = 0.3	r = 0.3	r = 0.0	1.00							
Storage root stalk	r = 0.0	r = 0.1	r = 0.0	r = 0.3	1.0						
Mature leaf size	r = 0.1	r = -0.1	r = -0.1	r = -0.3	r = -0.1	1.0					
Storage root length	r = 0.1	r = 0.1	r = -0.1	r = 0.3	r = -0.1	r = 0.1	1.0				
Largest storage root diameter	r = 0.3	r = 0.4	r = -0.0	r = 0.2	r = 0.1	r = -0.1	r = 0.1	1.0			
Petiole length	r = 0.2	r = 0.2	r = 0.1	r = 0.2	r = 0.1	r = -0.2	r = 0.1	r = -0.0	1.0		
Weight of largest root	r = 0.3	r = 0.4	r = 0.0	r = 0.4	r = 0.2	r = -0.1	r = 0.6*	r = 0.6*	r = 0.0	1.0	
Root yield	r = 0.0	r = 0.2	r = 0.0	r = 0.2	r = -0.1	r = -0.1	r = 0.4	r = 0.2	r = 0.0	r = 0.5*	1.0

*Significant at $p \leq 0.05$

4.3.5 Molecular characterization

The molecular bands of the 13 primers obtained in this study are presented in Appendix 7.

4.3.5.1 Major allele frequency

The major allele frequency value ranged from 0.5882 to 0.9412 with a mean of 0.7563. Marker JB1809a had the lowest major allele frequency while marker J67b and J67c had the highest major allele frequency (Table 4.14). These values were quite high with all the values above 0.5. The total number of alleles amplified was 21.

4.3.5.2 Gene diversity

The gene diversity values ranged from 0.1107 to 0.4844 with a mean value of 0.3384. Markers J67b and J67c had the lowest values while marker JB1809a had the highest value (Table 4.14).

4.3.5.3 Polymorphic information content

The PIC values ranged from 0.1046 to 0.3671 with a mean value of 0.2723. Markers J67b and J67c had the lowest values while marker J1809a had the highest value (Table 4.14).

4.3.5.4 Effective number of alleles

The number of effective alleles values ranged from 1.0921 to 1.9396 with a mean value of 1.5513. Markers J67b and J67c had the lowest values while marker J1809a had the highest value (Table 4.14).

Table 4.14: Table of summary statistics of the 21 alleles amplified in the sweet potato genotypes

Marker	Major Allele Frquency	SampleSize	Allele No.	Availability	ne*	Gene Diversity	PIC
IBR03	0.6176	68.0000	2.0000	1.0000	1.8951	0.4723	0.3608
IBR12	0.7794	68.0000	2.0000	1.0000	1.5241	0.3439	0.2847
IB242	0.6471	68.0000	2.0000	1.0000	1.8408	0.4567	0.3524
IB275	0.6765	68.0000	2.0000	1.0000	1.7785	0.4377	0.3419
J175	0.6765	68.0000	2.0000	1.0000	1.7785	0.4377	0.3419
J175b	0.8971	68.0000	2.0000	1.0000	1.1918	0.1847	0.1676
IB297	0.7794	68.0000	2.0000	1.0000	1.4859	0.3439	0.2847
IB316	0.7647	68.0000	2.0000	1.0000	1.5241	0.3599	0.2951
IB324	0.7059	68.0000	2.0000	1.0000	1.7101	0.4152	0.3290
IBCIP	0.6029	68.0000	2.0000	1.0000	1.9187	0.4788	0.3642
IBCIPb	0.8382	68.0000	2.0000	1.0000	1.3349	0.2712	0.2344
IBCIPc	0.7794	68.0000	2.0000	1.0000	1.4859	0.3439	0.2847
IBJ522	0.6029	68.0000	2.0000	1.0000	1.9187	0.4788	0.3642
IBJ522b	0.8971	68.0000	2.0000	1.0000	1.1918	0.1847	0.1676
IBS07	0.7059	68.0000	2.0000	1.0000	1.6741	0.4152	0.3290
J67a	0.6029	68.0000	2.0000	1.0000	1.9187	0.4788	0.3642
J67b	0.9412	68.0000	2.0000	1.0000	1.0921	0.1107	0.1046
J67c	0.9412	68.0000	2.0000	1.0000	1.0921	0.1107	0.1046
JB1809a	0.5882	68.0000	2.0000	1.0000	1.9396	0.4844	0.3671
JB1809b	0.9265	68.0000	2.0000	1.0000	1.1245	0.1362	0.1270
JB1809c	0.9118	68.0000	2.0000	1.0000	1.1577	0.1609	0.1480
Mean	0.7563	68.0000	2.0000	1.0000	1.5513	0.3384	0.2723

ne* = effective number of alleles

4.3.5.5 Cluster analysis based on SSR markers

A dedrogram was constructed based on dissimilarity matrix computed using Jaccard's coefficient. The dissimilarity matrix was computed using 1000 bootstraps. The tree (Figure 4.12) revealed two major clusters (A and B). At about 1.2 distance, cluster A had 48 genotypes with two sub-clusters 1 and 2 (Figure 4.12). The two sub clusters (1 and 2) had 3 and 45 genotypes respectively. Genotype Fundukhusia was an outlier since it did not fall in any of the two sub-clusters (Figure 4.12). At about 1.2 distance, cluster B contained 20 genotypes with two sub-clusters 3 and 4 (Figure 4.12). The two sub-clusters had 5 and 14 genotypes respectively (Figure 4.12). Saly boro was an outlier because it was not grouped in the two sub-clusters (Figure 4.12).

The genotypes did not form specific groups according to geographic regions (Figure 4.12). Furthermore, many genotypes that shared a common name did not show genetic similarities (Figure 4.12). For instance, Kenspot 2 and Kenspot 5 were grouped in sub-cluster 1 while Kenspot 3 and Kenspot 4 nested together in sub-cluster 2 (Figure 4.12). Similarly, genotype Kibuonjo was grouped in sub-cluster 4 while genotypes 29 Kuny Kibuonjo and Kuny kibuonjo were grouped in sub-cluster 2 (Figure 4.12). Most of the F_1 clones were nested in different clusters. For instance, Naspot x New Kawogo 1, Naspot x New Kawogo 2 and Naspot x New Kawogo 3 were grouped in sub-clusters 2, 2 and 4 respectively (Figure 4.12).

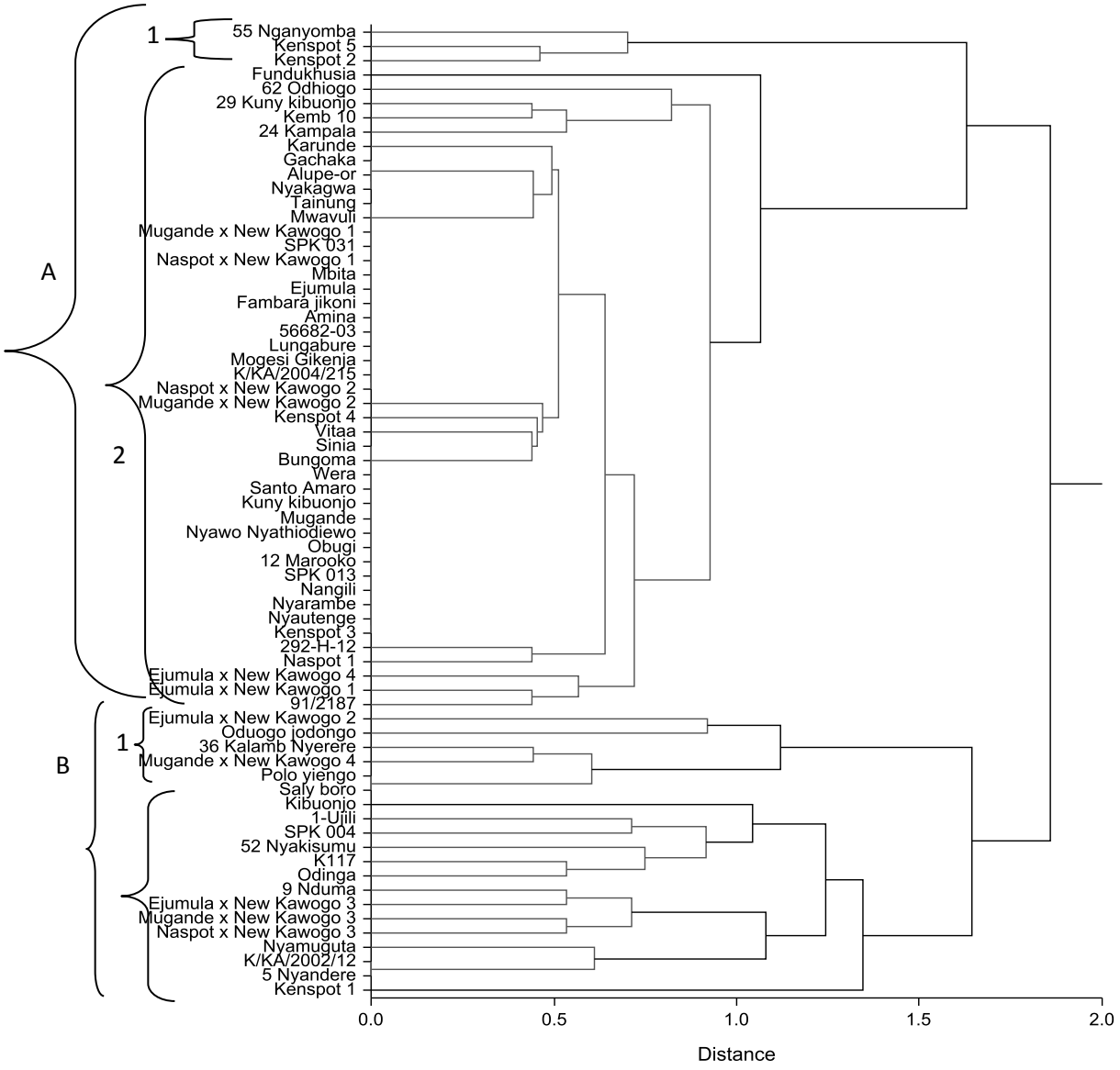

Figure 4.12: Dendrogram based on Jaccard's coefficient of dissimilarity

4.3.6 Nutritional characterization

There were significant ($p \leq 0.001$) interactions between genotypes and environment in relation to nutrition characters (Table 4.15; Appendix 2) therefore, sites were analyzed separately. The analysis of variance (ANOVA) showed that genotypes at both KARLO

–Embu site and ATC –Miyare site were significantly ($p \leq 0.0001$) different in mean values for root dry matter, root protein, root carotenoids, root sucrose and root starch (Table 4.16).

Table 4.15: F Probability values of nutrition characters for combined sites (ATC - Miyare and KARLO -Embu)

Source of variation / Variables	P values		
	Site	Genotype	Site × Genotype
Dry matter	<0.0001	<0.0001	<0.0001
Protein	<0.0001	<0.0001	<0.0001
Total carotenoids	<0.0001	<0.0001	<0.0001
Sucrose	<0.0001	<0.0001	<0.0001
Starch	<0.0001	<0.0001	<0.0001

Table 4.16: F Probability values of nutrition charaters for individual sites (ATC - Miyare and KARLO -Embu)

Source of variation / Variables	P values	
	ATC -Miyare	KALRO -Embu
Dry matter	<0.0001	<0.0001
Protein	<0.0001	<0.0001
Total carotenoids	<0.0001	<0.0001
Sucrose	<0.0001	<0.0001
Starch	<0.0001	<0.0001

4.3.6.1 Root dry matter

Analysis of variance indicated significant differences ($p \leq 0.0001$) on root dry matter content at ATC -Miyare (Table 4.17). Root dry matter content of all genotypes at this site ranged from 21.40 % to 42.59 %. Five genotypes that recorded the highest dry matter content at ATC -Miyare were Kenspot 1 (42.9 %), Saly boro (41.42 %), 91/2187 (41.27 %), Mugande x New Kawogo 1 (41.17 %) and 5 Nyandere (40.46 %). Five genotypes that recorded the lowest dry matter content at ATC Miyare were Tainung (21.40 %), Sinia (24.07 %), Ejumula x New Kawogo 1 (21.15 %), Polo yiengo (25.58 %) and Mwavuli (27.04 %).

There were significant differences ($p \leq 0.0001$) on root dry matter content at KALRO - Embu (Table 4.17). Dry matter content of all genotypes at this site ranged from 24.39 % to 46.44 %. Five genotypes that recorded the highest dry matter content at KALRO - Embu were 9 Nduma (46.44 %), Kenspot 3 (41.20%), Kenspot 2 (41.17 %), Obugi (38.50%) and Nyamuguta (37.93 %). Five genotypes that recorded the lowest dry matter content were Tainung (24.39 %), 62 Odhiogo (26.57 %), K/KA/2004/215 (27.21 %), Naspot x New Kawogo 1 (27.34 %), Ejumula x New Kawogo 1 (28.02 %).

4.3.6.2 Root protein

Root protein content at ATC -Miyare showed significant differences ($p \leq 0.0001$) as shown in Table 4.17. Protein content of all genotypes at this site ranged from 3.38 % to 21.62 %. Five genotypes that recorded the highest protein content at ATC -Miyare were Nyamuguta (21.62 %), Odinga (20.52 %), Mbita (20.09 %, Kenspot 1 (19.30 %) and Santo Amaro (19.08 %). Five genotypes that recorded the lowest protein content at ATC Miyare were 36 Kalamb Nyerere (3.38 %), 52 Nyakisumu (6.26 %), Kemb 10 (6.28 %), Bungoma (6.30 %) and Kenspot 5 (6.41 %).

Analysis of variance indicated significant differences ($p \leq 0.0001$) on protein content at KALRO -Embu (Table 4.17). Protein content of all genotypes at this site ranged from 2.21 % to 11.27 %. Five genotypes that recorded the highest protein content at KALRO -Embu were Wera (11.27 %), Naspot 1 (9.42 %), Fundukhusia (8.52 %), Santo Amaro (8.51 %) and SPK 013 (8.48 %). Five genotypes that recorded the lowest protein content were Kenspot 2 (2.21 %), K117 (2.62 %), Tainung (3.08 %), K/KA/2002/12 (3.30 %) and 292-H-12 (3.34 %).

4.3.6.3 Root total carotenoids

Significant differences ($p \leq 0.0001$) were obtained on total carotenoids content at ATC - Miyare (Table 4.17). Total carotenoids content of all genotypes at this site ranged from 27.55 µg/g to 43.62 µg/g. Five genotypes that recorded the highest total carotenoids

content at ATC -Miyare were Kenspot 2 (43.62 µg/g), Mugande x New Kawogo 1 (43.31 µg/g), SPK 031 (39.37 µg/g), Kenspot 4 (36.03 µg/g) and Tainung (27.55 µg/g). Five genotypes that recorded the lowest total carotenoids content at ATC Miyare were 5 Nyandere (5.42), Ejumula x New Kawogo 2 (5.45 µg/g), 9 Nduma (5.58 µg/g), Naspot x New Kawogo 1 (5.60 µg/g) and Vitaa (5.67 µg/g).

There were significant differences ($p \leq 0.0001$) on total carotenoids content at KALRO -Embu (Table 4.17). Total carotenoids content of all genotypes in this site ranged from 5.25 µg/g to 45.42 µg/g. Five genotypes that recorded the highest total carotenoids content at KALRO -Embu were Ejumula x New Kawogo 2 (45.42 µg/g), Alupe or (34.55 µg/g), Kenspot 5 (32.22 µg/g), Tainung (30.57 µg/g) and 12 Marooko (26.06 µg/g). Five genotypes that recorded the lowest total carotenoids content were 55 Nganyomba (5.25 µg/g), 24 Kampala (5.38 µg/g), Kibuonjo (5.49 µg/g), Lungabure (5.55 µg/g) and Mugande x New Kawogo 3 (5.98 µg/g),

4.3.6.4 Root sucrose

Analysis of variance indicated significant differences ($p \leq 0.0001$) on sucrose content at ATC -Miyare (Table 4.17). Sucrose matter content of all genotypes in this site ranged from 9.2 ppm to 123.67 ppm. Five genotypes that recorded the highest sucrose content at -ATC Miyare were Odinga (123.67 ppm), Mwavuli (107.60 ppm), Ejumula x New Kawogo 1 (105.40 ppm), Kenspot 5 (103.70 ppm) and Sinia (102.40 ppm). Five genotypes that recorded the lowest sucrose content at ATC Miyare were Polo yiengo (9.20 ppm), Fundukhusia (14.07 ppm), Kenspot 1 (14.30 ppm), Kenspot 2 (15.30 ppm) and Mugande x New Kawogo 1 (15.63 ppm)

Similarly, significant differences ($p \leq 0.0001$) were obtained on sucrose content at KALRO -Embu (Table 4.17). Sucrose content of all genotypes in this site ranged from 1.57 ppm to 175.50 ppm. Five genotypes that recorded the highest sucrose content at KALRO -Embu were Naspot x New Kawogo 3 (175 ppm), Naspot 1 (123.43 ppm),

Kuny kibuonjo (101.43 ppm), Kenspot 1 (93.50 ppm), Amina (88.23 ppm). Five genotypes that recorded the lowest sucrose content were 292-H-12 (1.57 ppm), 5 Nyandere (15.63 ppm), K/KA/2002/12 (16.77 PPM), Ejumula x New Kawogo 3 (22.47 ppm) and Ejumula x New Kawogo 4 (22.57 ppm).

4.3.6.5 Root starch

Those varieties that had high values in sucrose showed high values in starch at both sites. There were significant differences ($p \leq 0.0001$) on starch content at ATC -Miyare (Table 4.17). Starch matter content of all genotypes in this site ranged from 8.30 ppm to 111.30 ppm. Five genotypes that recorded the highest starch content at ATC Miyare were Odinga (111.30 ppm), Kenspot 5 (96.73 ppm), Ejumula x New Kawogo 1 (94.90 ppm), 24 Kampala 92.33 ppm) and Sinia (92.17 ppm). Five genotypes that recorded the lowest starch content at ATC -Miyare were Polo yiengo (8.30 ppm), Fundukhusia (14.33 ppm), Kenspot 1 (12.87 ppm), Kenspot 2 (13.77 ppm) and Mugande x New Kawogo 1 (13.03 ppm)

Analysis of variance showed significant differences ($p \leq 0.0001$) on starch content at KALRO -Embu (Table 4.17). Starch content of all genotypes in this site ranged from 1.40 ppm to 157.93ppm. Five genotypes that recorded the highest starch content at KALRO -Embu were Naspot x New Kawogo 3 (157.93 ppm), Naspot 1 (111.07 ppm), Kuny kibuonjo (91.30 ppm), Kenspot 1 (84.13 ppm), Amina (79.43 ppm). Five genotypes that recorded the lowest starch content were 292-H-12 (1.40 ppm), 5 Nyandere (14.07 ppm), K/KA/2002/12 (15.07 ppm), Ejumula x New Kawogo 3 (20.23 ppm) and Ejumula x New Kawogo 4 (20.33 ppm).

Table 4.17: Means for root dry matter, protein, total carotenoids, sucrose and total starch of the 68 sweet potato genotypes at ATC – Miyare and KALRO -Embu grown during the long rains in 2014

	Sweet potato genotypes	Dry matter (%)		Root Protein (%)		Root total Carotenoids (µg/g)		Root Sucrose (ppm)		Root total starch (ppm)	
		Miyare (ATC)	KALRO (Embu)	ATC - Miyare	KALRO (Embu)	ATC - Miyare	KALRO (Embu)	ATC - Miyare	KALRO (Embu)	ATC - Miyare	KALRO (Embu)
1	Kenspot 1	42.59a	30.33 pq	19.30d	4.26 opqrstu	19.10k	7.36 xyz	14.30N	93.50 d	12.87I	84.13 d
2	Saly boro	41.42ab	32.07lmn	11.63pq	7.24 ef	14.24op	6.58 C	47.87pq	41.23 xw	43.08mn	37.13 xy
3	91/2187	41.27b	32.52 kl	14.43jk	4.08 pqrstuv	12.56q	8.58 s	44.43st	25.50 E	41.47no	22.97 G
4	Mugande x New kawogo 1	41.17b	33.28 i	20.16bc	5.54 hijklmn	42.31b	10.39 o	15.63MN	41.70 xw	13.03I	37.50 xy
5	5 Nyandere	40.46bc	34.54 h	15.54h	5.07 lmnopqr	5.42I	12.66 k	16.27M	15.63 G	14.63HI	14.07 J
6	Odinga	40.42bc	36.13 f	20.52b	6.29 fghijk	8.97A	7.05 zAB	123.67a	55.43 opq	111.30a	49.90 opq
7	Naspot 1	40.30bc	34.11 h	12.83n	9.42 b	7.59D	7.07 zAB	53.47m	123.43 b	48.13jk	111.07 b
8	Kenspot 3	40.23bcd	41.20 b	12.15o	3.85 ustv	10.24u	9.08 r	42.80tu	56.90 o	39.97op	51.20 o
9	Ejumula x New kawogo 4	40.15bcd	33.51 i	11.42pq	6.50 fghi	7.59D	11.15 nm	35.47wx	22.57 F	31.93st	20.33 I
10	Nyamuguta	40.15bcd	37.93 d	21.62a	6.52 fgh	6.13H	6.06 EF	74.57g	55.77 op	67.10f	50.17 op
11	Nyautenge	40.15bcd	32.26 klm	13.46m	5.34 jklmno	8.53B	7.55 xy	34.10xyz	23.13 F	30.70stuv	20.83 HI
12	Naspot x New kawogo 3	39.42cde	34.43 h	6.51x	8.26 ced	12.32qr	7.05 zAB	41.50u	175.50 a	37.33qr	157.93 a
13	Nyarambe	39.22cdef	35.61 g	14.03kl	6.03 ghijkl	12.28qr	6.99 B	51.37n	62.33 m	46.20kl	56.13 m
14	Nyakagwa	39.02def	30.36 pq	11.39pq	4.05 qrstuv	11.08t	7.80 vw	55.63l	48.47 u	52.03i	43.60 u
15	Ejumula x New kawogo 3	38.60efg	37.49 de	16.46f	5.20 klmnop	11.47s	45.42 a	44.73rs	22.47 F	40.27op	20.23 I
16	Oduogo jodongo	38.55efg	32.15 lm	14.56j	5.56 hijklmn	10.19uv	6.60 C	57.57k	62.23 m	51.87i	56.00 m
17	Nangili	38.24efgh	35.51 g	14.02kl	5.57 hijklmn	26.41f	6.60 C	23.67GH	60.53 nm	21.30CD	54.50 mn
18	Kenspot 2	38.17efghi	41.17 b	9.62t	2.21 w	43.62a	22.61 g	15.30MN	56.60 opq	13.77I	50.07 opq
19	SPK 013	38.11fghi	29.98 q	11.22q	8.48 bcd	11.59s	6.37 CDE	34.70wxy	71.63 j	31.23stuv	64.47 j
20	K/KA/2004/215	38.08fghi	27.21 w	11.65p	5.56 hijklmn	14.54no	12.26 l	49.77no	76.40 h	44.80lm	68.77 h
21	Alupe or	38.08fghi	30.30 pq	14.41jkl	5.15 klmnopq	9.22yza	34.55 b	43.07stu	52.40 srt	38.73pq	47.17 rst
22	12 Marooko	38.03fghi	36.39 f	11.51pq	4.47 nopqrst	8.07C	26.06 e	32.37AB	76.43 h	29.13vwx	68.80 h
23	Kenspot 5	38.02fghi	28.06 v	6.41x	4.06 pqrstuv	7.04E	32.22 c	103.70d	59.30 n	96.73b	53.37 n
24	36 Kalamb Nyerere	37.37ghij	34.45 h	3.38y	4.97 lmnopqrs	9.31xyza	8.05 uv	29.77CDE	82.60 g	26.80zy	74.33 g
25	Mugande x New kawogo 4	37.37ghij	28.48 uv	17.32e	4.61 mnopqrs	8.54B	9.46 q	57.80k	47.50 u	52.00i	42.77 u
26	Mugande x New kawogo 3	37.37ghij	33.44 i	13.09mn	4.06 pqrstuv	9.34xyz	5.98 F	46.27qr	40.33 xwy	41.67no	36.30 yz
27	292-H-12	37.10hijk	34.40 h	11.25pq	3.34 tuvw	6.62FG	6.60 C	20.37JK	1.57 H	18.30EFG	1.40 K
28	Mogesi Gikenja	37.02hijk	37.08 e	16.22fg	4.07 pqrstuv	6.79EF	6.55 C	34.80wxy	35.63 ABC	31.33stu	32.07 CD
29	Lungabure	37.01hijk	31.18 o	6.56x	8.49 cbd	25.48g	5.55 GH	30.83BCD	27.47 E	27.73xyz	25.70 F
30	Kenspot 4	36.97ijk	30.57 p	17.16e	5.60 hijklmn	36.03d	25.03 f	19.70KL	25.47 E	17.70FG	22.93 GH
31	Vitaa	36.59jkl	32.35 klm	15.14hi	4.47 nopqrst	5.67I	8.40 st	66.37h	34.53 C	59.73g	38.53 wx
32	9 Nduma	36.38jklm	46.44 a	7.19w	5.31 klmno	5.58I	7.01 AB	32.43zAB	81.10 g	29.20uvwx	75.93 fg
33	24 Kampala	36.37jklm	35.25 g	12.39o	6.97 fg	10.13uv	5.38 GH	102.63d	67.33 kl	92.33c	60.60 kl
34	Obugi	36.37jklm	38.50 c	16.26fg	4.01 qrstuv	15.35l	7.40 xy	80.60f	42.27 w	72.53e	49.03 pqr
35	56682-03	36.31jklmn	31.45 o	16.01g	5.54 hijklmn	7.57D	7.32 xyzA	29.57DE	68.57 k	26.60zy	61.70 k
36	Nyawo Nyathiodiewo	36.30jklmn	31.60 no	14.01l	7.01 fg	21.12i	11.37 m	15.73MN	68.83 k	13.90I	61.97 k
37	Gachaka	36.30jklmn	32.10 lm	17.38e	6.46 fghij	6.11H	5.60 G	18.57L	34 .83 BC	16.70GH	31.33 D

38	Mugande	36.01klmn	35.53 g	13.30m	4.07 pqrstuv	8.42BC	6.13 DEF	26.77F	51.60 st	24.07AB	46.43 st
39	Amina	35.60imno	36.57 f	6.56x	4.63 mnopqrs	6.30GH	9.20 rq	55.70l	88.23 e	50.13ij	79.43 e
40	Fumbara jikoni	35.35lmnop	32.50 klm	10.11s	6.06 ghijkl	9.47xy	7.40 xy	31.27BC	74.67 ih	28.17wxy	67.20 hi
41	Ejumula	35.33imnopq	34.43 h	7.59w	6.08 ghijkl	9.05zA	6.39 CD	36.23w	39.77 xy	32.60s	35.80 yzA
42	Karunde	35.26mnopq	34.31 h	9.60tu	6.51 fgh	11.63s	21.12 h	21.43IJ	44.67 v	19.30DEF	40.20 vw
43	SPK 004	35.09nopq	33.21 i	17.27e	4.27 opqrstu	19.56j	12.32 l	49.37op	65.60 l	46.03kl	59.07 l
44	Kuny kibuonjo	34.59opqr	32.02 mn	14.62j	7.24 ef	7.59D	10.02 p	56.33kl	101.43 c	50.67i	91.30 c
45	K/KA/2002/12	34.43opqr	34.36 h	8.53v	3.30 uvw	9.62wx	7.53 wx	85.33e	16.77 G	76.80d	15.07 J
46	55 Nganyomba	34.20pqrs	29.48 r	13.16mn	5.45 hijklmn	10.06uv	5.25 H	46.73q	47.63 u	42.07no	42.90 u
47	1-Ujili	34.14pqrs	33.61 i	19.02d	5.09 lmnopq	9.85vw	7.43 x	24.43G	51.20 t	21.98BC	46.07 t
48	Santo Amaro	34.07qrs	34.17 h	19.08d	8.51 cd	9.12yzA	8.23 tu	60.27j	47.00 u	54.27h	42.27 vu
49	Naspot x New kawogo 1	33.52rst	27.34 w	18.90d	5.43hijklmn	5.60I	7.00 AB	22.43HI	30.67 D	20.20CDE	27.60 FE
50	Wera	33.34 rst	33.34 i	11.46pq	11.27 a	9.35xyz	7.50 wx	16.63M	38.53 yz	14.93HI	34.67 zAB
51	Kemb 10	33.15st	32.51 klm	6.28x	5.60 hijklmn	14.60n	11.04 n	39.17v	41.77 wx	35.27r	37.60 xw
52	Mbita	33.15st	29.52 rs	20.09c	6.28 fghijk	22.44h	13.58 j	31.33C	31.40 D	28.17wxy	28.27 E
53	Ejumula x New kawogo 2	32.57tu	30.35 pq	10.59r	3.94 rstuv	5.45I	8.61 s	24.77G	53.37 rs	22.30BC	48.03 qrst
54	Kibuonjo	32.54tu	33.33 i	8.51v	5.33 jklmno	7.62D	5.49 GH	19.63KL	31.40 D	17.67FG	28.27 E
55	29 Kuny kibuonjo	32.49tu	32.71 jk	8.52v	5.36 ijklmno	14.99m	7.58 wx	32.30AB	54.40 pqr	30.17tuvw	48.97 pqr
56	62 Odhiogo	32.29tu	26.57 x	9.19u	4.48 nopqrst	12.00r	8.18 tu	33.53zyA	36.63 zAB	30.20tuvw	32.97 BCD
57	52 Nyakisumu	31.51uv	33.11 ij	6.26x	4.49 nopqrs	9.05zA	15.12 i	31.60B	55.60 opq	28.43wxy	50.07 opq
58	Naspot x New kawogo 2	30.52vw	35.40 g	16.14fg	6.07 ghijkl	6.04H	6.12 DEF	62.47i	40.23 xy	56.23h	36.20 yz
59	Bungoma	30.19wx	35.60 g	6.30x	5.31 klmno	14.47no	7.43 xy	62.13i	34.57 C	55.93h	32.30 CD
60	K 117	30.11wx	32.02 mn	17.31e	2.62 w	6.57FG	9.21 qr	19.17KL	73.63 ij	17.27FG	66.27 ij
61	Fundukhusia	30.06wx	29.01 rst	13.29m	8.52 cd	8.32BC	5.52 GH	14.07N	72.33 j	14.33I	65.10 ij
62	SPK 031	29.08xy	28.90 stu	11.45pq	10.92 a	39.37c	13.55 j	28.50E	84.73 f	25.67zA	76.27 fg
63	Mugande x New kawogo 2	28.14yz	28.58 tu	17.32e	4.48 nopqrst	6.50FG	6.55 C	46.27qr	37.43 zA	41.63no	33.70 ABC
64	Mwavuli	27.04z	32.18 lm	9.62t	5.64 hijklm	8.20BC	6.55 C	107.60b	53.67 qr	96.80b	48.30 pqrs
65	Polo yiengo	25.58A	29.20 rs	12.37o	7.35 def	14.10p	7.09yzAB	9.20O	37.53 zA	8.30J	33.77 ABC
66	Ejumula x New kawogo 1	25.15AB	28.02 v	11.22q	7.24 ef	8.14C	6.18 DEF	105.40c	48.37 u	94.90b	43.53 u
67	Sinia	24.07B	30.30 pq	11.64p	7.01 fg	8.26BC	6.56 C	102.40d	85.77 f	92.17c	77.20 f
68	Tainung	21.40C	24.39 y	15.12i	3.08 vw	27.55e	30.57 d	44.53s	65.53 l	40.07ll	59.00 l
	Site mean	35.36	32.88	12.92	5.67	12.55	10.52	43.95	54.01	39.73	48.95
	LSD (0.05)	1.33	2.81	2.94	0.67	1.51	1.54	3.95	4.01	2.73	4.95
	CV	2.22	0.94	1.97	12.53	1.76	1.89	2.36	2.33	3.35	2.69
	***p* value**	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001

Means with the same letters (in the same case) along a column are not significantly different according to LSD test *(p≤0.05)*.

4.3.7 Cluster analyses based on nutrition characters of 68 genotypes

Using the means of nutrition characters recorded at the two sites (ATC –Miyare and KARLO –Embu), two dendrograms were derived (Figure 4.13 and 4.14) based on Euclidean distance coefficient.

The dendrogram obtained using nutrition characters at ATC -Miyare site, separated the genotypes into two major clusters (A and B) within an Euclidean distance ranging from 0.0 to 1.9 (Figure 4.13). Cluster A contained 8 genotypes and consisted of 3 sub-clusters (Figure 4.13). Cluster A genotypes had high contents of sucrose and starch. Cluster B contained 60 genotypes and formed three sub-clusters (Figure 4.13). Genotypes in cluster B had less sucrose and starch contents as compared to those in cluster A. The genotype Tainung fell into a sub-group on its own (Figure 4.13) probably due to the fact that it rated very low in all other nutrition aspects with an exception of total carotenoids content.

The dendrogram obtained using nutrition characters at KALRO -Embu site, separated the genotypes into four clusters (Figure 4.14) within an Euclidean distance ranging from 0.0 to 2.6 (Figure 4.14). Cluster A contained 3 genotypes; cluster B contained 5 genotypes; cluster C contained 7 genotypes; while cluster D contained 53 genotypes (Figure 4.14). Cluster A constituted of genotypes that had high sucrose, starch and dry matter content. Cluster B constituted of genotypes that had high total carotenoids content and moderately high contents of sucrose and starch. Cluster C and D did not show any distinguishable relationship or pattern.

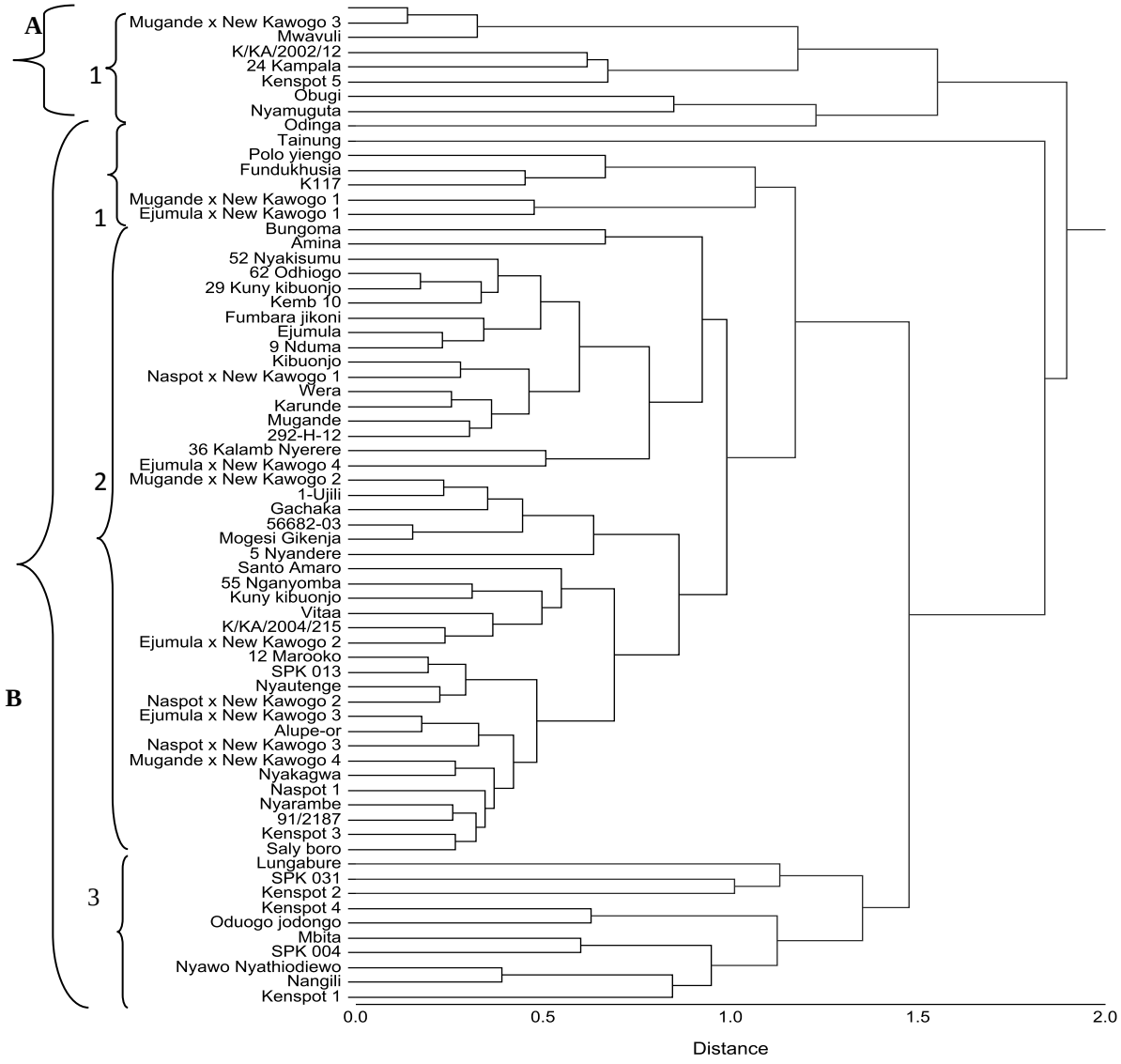

Figure 4.12: Dendrogram (based on Euclidean distance coefficient) of 68 genotypes generated from nutrition data (ATC –Miyare)

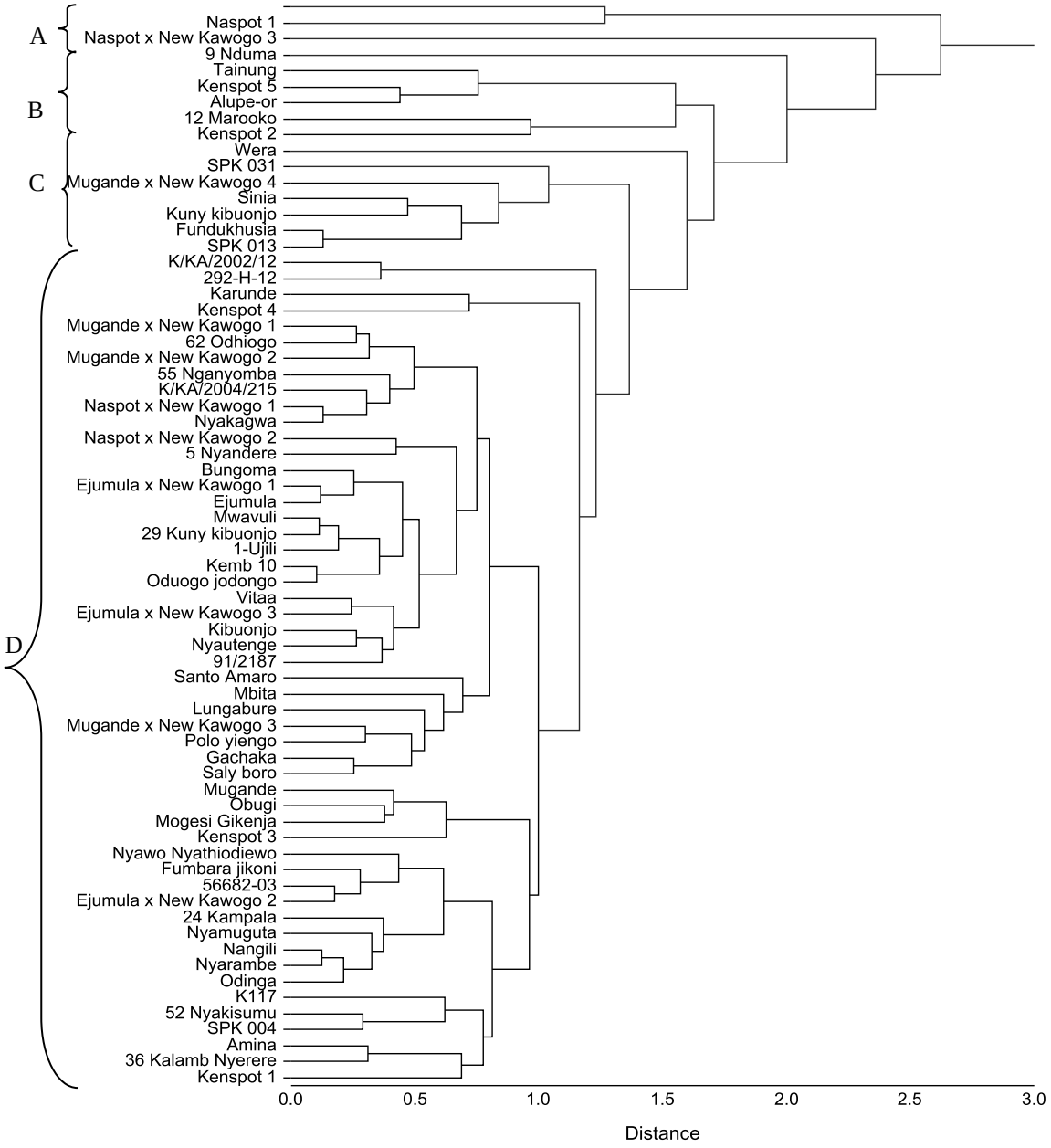

Figure 4.13: Dendrogram (based on Euclidean distance coefficient) of 68 genotypes generated from nutrition data (KALRO –Embu)

4.3.8 Comparison between SSR data and other (agro-morphological or nutrition) data

4.3.8.1 Comparison between SSR data and agro-morphological data

Using qualitative agro-morphological characters, the 68 genotypes were grouped into five clusters with dissimilarity indices ranging from 0 to 3 suggesting a very high genetic diversity among the genotypes. Conversely, using the SSR –based analysis, 4 clusters were obtained. The dissimilarity indices ranged from 0 to 1 showing a relatively moderate diversity among the 68 genotypes. There was an observation of some genotypes clustering together both in the agro-morphological and SSR dendrograms. For instance, the genotypes K/KA/2002/12, Ejumula, 29 Kuny Kibuonyo, Amina, 56682-03 and Saly boro identified together as a group based on qualitative agro-morphological descriptors (Figure 4.9) were closely related (nested on the dendogram) using the SSR markers (Figure 4.9).

The consensus between qualitative agro-morphological and the molecular based dendrograms was performed by using the strict rule consensus method consisting of simple counts of the frequency of occurrence of clusters in the set of trees (Perrier and Jacquemoud-Collet, 2006). It was observed that between the two trees, 3.9% of the clusters agreed (Table 4.18). This weak consensus between the two dendrograms suggested that there was no correlation between the agro-morphological and molecular data. The Quartet tree distance estimate used as a measure of dissilimirality between the two dendrograms was 0.71 (Table 4.18) demonstrating the absence of correlation between the two approaches used in the genetic diversity estimation.

4.3.8.2 Comparison between SSR data and nutritional data

It was observed that between the SSR dendrogram and nutrition dendrogram (drawn from either KALRO –Embu or ATC –Miyare) 3.9% of the clusterd agreed (Table 4.18). This weak consensus between either of the two dendrograms suggested that there was no correlation between the molecular and the nutrition data. The Quartet tree distance

estimate used as a measure of dissilimirality between the two dedrograms (SSR tree and either of the nutrition trees) was more than 0.5 (Table 4.18) demonstrating the absence of correlation between the molecular and the nutrition data in the estimation of genetic diversity.

Table 4.18: Comparisons between SSR data and other data (agro-morphological and nutritional data)

Parameter	**Quartet dendrogram distance**	**Consensus dendrogram**
Comparison between SSR data and agro-morphological data (qualitative traits)	0.748324	2.1%
Comparison between SSR data and nutrition data (ATC –Miyare)	0.712425	3.9%
Comparison between SSR data and Nutrition data (KALRO –Embu)	0.692776	3.9%

4.4 Discussion

Marker assisted breeding (MAB) is increasingly becoming a crucial part of modern plant breeding in Africa. Genetic diversity using various marker platforms, but more commonly microsatellite markers, is slowly becoming a common molecular biology tool applied in plant breeding. The application of MAB increases the efficiency of breeding programmes and hence, reduces the time required to release superior varieties. Genetic diversity studies using molecular phylogenetics form one core application of MAB, most especially on major food crops. Such studies are very important in selecting parents for hybridisation or crossing experiments aimed at improving the varieties. Microsatellite-based genetic diversity studies on East African sweet potato genotypes have been done before (Gichuru *et al*., 2006; Yada *et al*., 2010b; Karuri *et al*., 2010). In this study 68 sweet potato genotypes were assessed for genetic diversity using 13 microsatellite primer pairs which amplified a total of 21 alleles.

In this study, both agro-morphological and SSR markers were used to study sweet potato germplasm variation with the aim of complementing each other in achieving reliable evaluation and characterization of species diversity (Galvan *et al*., 2006). Even though successful results can be obtained using DNA markers in the determination of genetic traits for variety improvement (Abbas *et al*., 2008; Tairo *et al*., 2008), molecular techniques do not evaluate the effect of the environment on the expression of genes of interest. Apart from agro-morphological markers, this study also evaluated the diversity of sweet potato germplasm in relation to the nutrition content. This was based on the fact that different sweet potato germplasm constitutes different quantities of nutrients (Tumwegamire *et al*., 2011). From the results of this study, it was noted that no single genotype was superior in all desirable traits (high dry matter content, high yield, high protein content and high carotenoids content). This could have been attributed to the fact that each genotype has a unique genetic constitution.

The results of this study showed that there was an interaction between location (site) and sweet potato genotypes in relation to both agro-morphological and nutrition characters. Various studies have indicated the sensitivity of sweet potato to genotype x environment interaction (G x E) (Manrique and Hermann, 2001; Gruneberg *et al*., 2005; Chiona, 2009; Osiru *et al*., 2009; Moussa *et al*., 2011; Tumwegamire *et al*., 2016; Kathabwalika *et al*., 2016; Gurmu *et al*., 2017). Tumwegamire *et al*. (2011) reported that there were more pronounced differences between locations for starch content in their study. The presence of significant G x E interaction creates serious problems in comparing sweet potato genotypes and for recommending for wider adaptation (Moussa *et al*., 2011). Amongst farmers' the selection criteria for sweet potato genotypes are high yields, early maturity, tolerance to diseases and pests, high dry matter content and tasty or sweetness (Kapinga *et al*., 2003; Masumba *et al*., 2005; Masumba *et al*., 2007; Tairo *et al*., 2008). Furthur, studies by Mwanga *et al.* (2007) in Uganda and Richardson (2012) in Nassau, Bahamas as well as Onunka (2006) in Nigeria indicated high dry

matter content and storage root yield as important characteristics of good sweet potato varieties.

Vine growth rate was significant ($p \leq 0.05$) at both KALRO –Embu and ATC –Miyare. Genotypes that exhibited intermediate or fast growth rate at KALRO –Embu and ATC –Miyare can be suitable for animal feed since the vines of sweet potato usually form an excellent source of green fodder for cattle (Nedunchezhiyan *et al.,* 2012). Such genotypes that exhibited intermediate or fast growth rate at both sites in this study included Kenspot 1, 91/2187, Kenspot 3, Nyautenge, SPK 013, Kenspot 5, Ejumula, 56682-03, Santo Amaro, Fundukhusia and Mwavuli.

Root yield was significant ($p \leq 0.001$) at both sites. However, most evaluated genotypes were not ideal in terms of root yield stability across the two sites except for genotype Nyautenge which yielded highly at both sites. Although genotype Nyautenge was stable in yield production, it recorded low values in all other nutrition traits tested in this study with an exception of dry matter content. Mohammed *et al.* (2009) demonstrated that dry matter production is an important determinant of storage root yield in root and tuber crops hence it's an important selection criterion in breeding programmes for enhanced yield. Yield unstability across the rest of the genotypes was due to the different agro-ecological conditions experienced at the two sites (GOK, 2013; KALRO, 2013). High yield is a product of genetic make up of the individual genotypes (Rukundo *et al*., 2013; Vimala and Hariprakash, 2011), increased dry matter content in the roots (Mbah and Eke-okoro, 2015), increased weight of the roots or increased number of roots per plant (Lowe and Wilson, 1975). A number of genotypes evaluated in this study exhibited heavy weight (≥ 0.7 kg) of the largest root at either ATC –Miyare or KALRO –Embu (Table 4.10). These genotypes included Naspot 1, Lungabure, Obugi, Wera, Mbita, Polo yiengo, Sinia, Kenspot 1, Kenspot 5, and Amina. These means that there was a high potential for these mentioned genotypes to yield more if all the roots harvested from each plot could equally weigh like the largest root.

Latex production from the roots was significant ($p \leq 0.01$) at both sites. The results of this study show that location (site) affected the amount of latex production from the genotypes. Several lines of evidence suggest that latex production in plants is phenotypically plastic (i.e. responsive to environmental conditions). For example, work on the rubber tree (*H. Brasiliensis*) showed that light levels, drought, and soil moisture conditions determine the amount of latex production (Raj *et al*., 2005). Further, Data *et al.* (1996) reported genetic and environmental differences in latex production in a broad cross section of 96 sweet potato germplasm. Latex is an important component of resistance to herbivores (Agrawal and Konno, 2009). For example, application of latex to root cores of sweet potato reduced feeding and oviposition by *Cylas formicarius* (Data *et al*., 1996). Anyanga *et al.* (2013) found that chemical compounds in the root latex were responsible for the host plant resistance to *Cylas* spp. damage of 'New Kawogo' sweet potato variety. In this study, some genotypes produced abundant latex at both sites as compared to the rest. These genotypes included Nangili, SPK 013, 9 Nduma and K117.

Length of the storage root stalk was significant ($p \leq 0.01$) at both sites. Some genotypes exhibited long storage root stalk than others at both sites. A long root stalk increases the rooting depth of the crop roots. Deep rooting can act as an escape mechanism to weevil infestation. According to Lima and Morales (1992), deep rooting and early maturing genotypes are about four times less susceptible to weevil infestation than shallow rooting and late maturing genotypes. Also, Alghali and Munde (2001) reported that root clones that were heavily damaged were characterized by short necks (stalks). Therefore, genotypes found in this study to possess longer storage root stalks (including Naspot 1, 9 Nduma, 24 Kampala at ATC -Miyare and Kenspot 5, SPK 013, Mogesi Gikenja at KALRO –Embu) could be used as sources for weevil resistance.

The influence of G x E on root dry matter content was reported by various authors (Janssens 1983; Nasayao and Saladaga 1988; Gruneberg *et al.*, 2005; Chiona 2009).

Dry matter content varies due to a number of factors such as variety, location, climate, incidence of pests and diseases, cultural practices and soil types (Jones *et al*., 1986; Manrique and Hermann, 2000; Shumbusha *et al*., 2010; Vimala and Hariprakash, 2011). In a participatory rural appraisal conducted in Tanzania, it was learned that, low dry matter content is amongst the attribute that has led to abandonment of many varieties by famers (Ngailo *et al.*, 2016). All sweet potato genotypes evaluated in this study (with an exception of Tainung and Sinia) had a root dry matter content of >25%. The results of this study agree with those by Gichuki *et al*. (2003) that high dry matter content is a common phenomenon to east African sweet potato genotypes. According to Shumbusha *et al*. (2010), genotypes that have a root dry matter content >25% are acceptable by farmers. The use of sweet potato as a raw material for the biofuel and processing industries requires genotypes with a dry matter content that is above 35% of the fresh weight (Gruneberg *et al.*, 2009). Hence according to the results of this study, only six genotypes (Kenspot 3, Nyamuguta, Kenspot 2, Odinga, 12 Marooko and Ejumula x New Kawogo 3) are suitable to serve as effective raw material for processing industry. These genotypes had >35% root dry matter content at both sites.

Even though genotype Tainung (an orange-fleshed sweet potato) is rated in this study as unacceptable to farmers due to its low root dry matter content and yield, it was the best performer in total carotenoids content at both sites hence rated as nutritious. Other evaluated genotypes scored high carotenoids content at one site and low carotenoid content at another site due to G x E interaction. Therefore, genotype Tainung is suitable for addressing the vitamin A deficiency needs of women and children (CIP, 2010b). The quality of such a genotype (Tainung) can be improved by increasing its root dry matter content and yield to make it acceptable to farmers.

Sweetness is amongst farmers' selection criteria for sweet potato genotypes. Most farmers prefer genotypes that are sweet (contain high contents of sucrose) but some prefer genotypes that are less sweet. The genotypes with high content of sucrose can enhance carbohydrate uptake by individuals while the less sweet genotypes like Polo

yiengo, Fundukhusia, Kenspot 1 and Kenspot 2 (at ATC -Miyare) and 292-H-12, 5 Nyandere and K/KA/2002/12 (at KALRO –Embu) can be used as alternative food to the people who have diabetes. Diabetes is a disease in which too little or no insulin is produced or insulin is produced but cannot be used normally resulting in high levels of sugar in the blood. Hence people having diabetes are advised to consume foods with relatively low sugars.

The dendrograms drawn in this study (Figures 4.9, 4.10, 4.11, 4.12, 4.13 and 4.14) produced 2 major clusters but the genotypes did not cluster together uniformly in all the trees. The trees could only give the general germplasm relatedness and diversity. The probable reason as to why the clustering of the genotypes was not uniform across all the dendrograms drawn in this study is that the expressions of both agro-morphological and nutritional characters are environmental dependant while molecular characters are not. For instance, the root composition of genotypes grown at ATC –Miyare was different from the root composition of the same genotypes grown at KALRO –Embu. This is because of different agro-ecological regions presented by the two regions (GOK, 2013; KALRO, 2013). Considering that SSR –based data are more accurate than agro-morphological data Koussao *et al*. (2014), in relation to the results of this study, breeders can rely more on the SSR phylogenetic tree to determine the duplicates during their choice of parental line for crop improvement.

The weak agreement between the agro-morphological based dendrogram and the SSR dendrogram (Table 4.18) was also confirmed by different clustering of genotypes by each of these approaches. The findings of the current study that the agro-morphological and molecular characterization produced different clusterings agrees with those of Karuri *et al*. (2010) and Koussao *et al*. (2014) who compared agro-morphological and SSR-based evaluation of diversity. However, in all these studies, the sweet potato genotypes that were being evaluated were different.

A low consensus found between agro-morphological and molecular based trees in the current study was reported in other studies (Koehler-Santos *et al*., 2003; Ferriol *et al*., 2004; Bushehri *et al.,* 2005 and Koussao *et al*., 2014). The suggested reasons were that it could be as a result of the independent nature of agro-morphological and molecular variations. According to Vieira *et al*. (2007), this low correlation could also be due to the fact that a large portion of variation detected by molecular markers is non-adaptive as compared with phenotypic characters, which are influenced by the environment. In this study, type of leaf lobing, number of lobes, shape of the central lobe, plant type and abaxial leaf vein pigmentation are among the qualitative characters that were used to draw one of the dendrograms. According to Huaman (1992) type of leaf lobing, number of lobes and shape of the central lobe are not affected by the environment. According to the results of this study and the findings by Karuri *et al.* (2010), vine colour is a character that can be influenced by the environment. The high ploidy level in sweet potato may also be responsible for the variability in qualitative traits due to increased mutation rates associated with polyploidy (Mogie, 1992).

The results of this study showing that genotypes that shared a common name did not show genetic similarities could be as a result of evolution that takes place in the plants as they continue to interact with the environment. This was more pronounced in the F_1 clones. It is possible that the F_1 clones clustered in different groups because they are not yet genetically stable hence still undergoing rapid evolution.

4.5 Conclusion

1. Sweet potato germplasm presented high diversity based on agro-morphological, molecular and nutritional assessment approaches.
2. Based on yield, dry matter content and nutrition content;
   (i) Genotypes Odinga and Obugi are suitable for ATC –Miyare.
   (ii) Genotypes Naspot 1 and Alupe-or are suitable for Embu.

3. Each of the dendrograms based on agro-morphological, molecular and nutritional characters gave two major clusters, but the genotypes did not cluster uniformly in all the trees.

CHAPTER FIVE
EVALUATION OF SWEET POTATO GENOTYPES FOR RESISTANCE TO *Cylas puncticollis*

5.1 Introduction

The sweet potato weevil, *C. puncticollis,* is thought to have originated in Africa and has still yet to establish itself outside the continent. Today, this weevil occurs in 24 African countries namely, Burundi, Cape Verde, Cameroon, Chad, Congo, Central African Republic, DR Congo, Ethiopia, Ghana, Ivory Coast, Kenya, Madagascar, Malawi, Mali, Mozambique, Nigeria, Senegal, Sierra Leone, Somalia, Sudan, Tanzania, Uganda, Rwanda and Zambia (Okonya *et al.,* 2016a).

Damage by *Cylas puncticollis* Boheman and *Cylas brunneus* Fabricius constitutes a major constraint upon sweet potato (*Ipomoea batatas* (L.) Lam.) production in East Africa (Bashaasha *et al.* 1995; Kapinga *et al*., 1995; Kapinga *et al*., 2000; Smit 1997). The female sweet potato weevil lays eggs singly in cavities excavated in either the vines or the accessible roots of sweet potato (Stathers *et al.,* 2013). The developing larvae tunnel while feeding within the vine or root and are the most destructive stage. Plants may wilt or even die because of extensive stem damage, and damage to the vascular system can reduce the size and number of storage roots. While external damage to roots can affect their quality and value, internal damage can lead to complete loss. Even low levels of infestation can reduce root quality and marketable yield because the plants produce unpalatable terpenoids in response to weevil feeding (Chalfant *et al.,* 1990; Ames *et al.,* 1996).

Immunity to weevil infestation may not exist, but factors that adversely affect survival or development of *Cylas* spp. may drastically affect the dynamics of the weevil population (Mullen *et al.,* 1981). A lack of appropriate farm-level control options has led researchers to search for cultivars with resistance to *Cylas* spp. damage. Resistant

cultivars to weevils are environmentally friendly as they leave no toxic chemical residues in the soil and water ways. They are effective, simple, cheap and easy to adopt. Once resistant cultivars are identified, they can easily be made available to farmers, who only need to plant the materials to attain some measure of pest control.

Various authors have found differences in *Cylas* spp. damage among cultivars (Mwanga *et al*., 2001; Stathers *et al*., 2003a, b; Muyinza *et al.*, 2012). No variety has been reported to be completely resistant in field or laboratory experiments to *Cylas* spp. but some varieties have been reported to be more tolerant to weevils than others (Stathers *et al*., 2003a; Muyinza *et al.*, 2012, Gruneberg *et al.*, 2015). New Kawogo and Santo Amaro are examples of moderately resistant varieties (Stevenson *et al*., 2009; Gruneberg *et al*., 2015).

Under field conditions, many factors could potentially affect the susceptibility of a variety to sweet potato weevil damage, e.g. maturation date, root depth, root shape, root arrangement, plant canopy and root attraction (Stathers *et al*., 2003a, b). It is likely that any weevil resistance that exists is probably due to a combination of host resistance mechanisms such as antibiosis, tolerance, escape and non-preference which may be difficult to isolate (Stathers *et al*., 2003a). It is logical to expect plants to maximize their chances of avoiding insect damage by using a number of different resistance traits. Assessing resistance among a number of sweet potato genotypes can incorporate laboratory investigations and endeavour to measure every potential attribute which may confer resistance. However, laboratory studies may be of more use in the assessment of cultivar suitability for long-term post-harvest storage, as the storage of roots of sweet potato genotypes with reduced or delayed progeny emergence would slow the spread of infestation within a store (Stathers *et al*., 2003a).

Weevil larvae feed and develop within the storage root in which the egg is laid and do not migrate to other roots (Sutherland, 1986). Thus, their developmental potential

depends on the ovipositional site selected by the adult female. Root depth, root neck length, root latex production, root cortex thickness, root skin colour and shape of leaves are some of the morphological characters of sweet potato that can influence the infestation by *Cylas* spp. For instance, genotypes with pink and red coloured tubers as well as lobed leaves and thin foliage were considered less susceptible to *Cylas* spp. compared to brown and white coloured tubers (Teli and Salunkhe, 1996). Recent findings of compounds in the latex of the Ugandan variety, New Kawogo and the effect of these compounds on weevils may be of interest for breeding investment (Stevenson *et al*., 2009). Anyanga *et al*. (2013) found that chemical compounds in the root latex were responsible for the host plant resistance to *Cylas* spp. damage of "New Kawogo" sweet potato variety. Also, the reduced weevil infestation of Santo Amaro is associated with the latex in the storage root skin (Gruneberg *et al.,* 2015).

Different sweet potato genotypes have got different quality traits that make them preferred by sweet potato weevils and consumers. Stimuli attracting insects to a crop are usually visual and olfactory while those rendering the crop susceptible are tactile, phagostimulatory and nutritive (Painter, 1951). Therefore, though the weevils may find clones attractive enough for infestation, the rates of consumption may thus be different for the different clones (Alghali and Munde, 2001; Waldbauer, 1968). Thus, clonal suitability for infestation appears to be different from clonal susceptibility for damage. It is the feeding by the pest that invariably leads to damage and in turn determine the level of susceptibility (Alghali and Munde, 2001). Factors such as high dry matter and starch contents have been associated with lower insect damage (Cockerham and Deen, 1947; Hahn and Leuschner, 1981) although Anota and Odebiyi (1984b) found no evidence of this relationship. Contradictory findings of a link between carotene content and resistance to *Cylas* spp. exist. High carotene content was linked to *Cylas* spp. susceptibility in laboratory investigations by some authors (Hahn and Leuschner 1981, Anota and Odebiyi 1984b), but correlated with *Cylas* spp. resistance by other researchers during field trials (Cockerham and Deen 1947). As a consequence, it is

probable that root chemistry is intimately involved in modulating adult and larval feeding as it is with oviposition (Son *et al.,* 1991). However, little about this behaviour has been demonstrated. Likewise, the nutritional requirements of the larvae and adult weevils are not fully understood. As a consequence, information is needed on the type and concentation of constituents that promote feeding in adults and larvae which make certain genotypes more susceptible to *C. puncticollis* more than others. This study aimed at determining the effect of sweet potato morphological characters and root composition on the tolerance to the sweet potato weevil (*C. puncticollis*). This would allow documentation of information that could be used by breeders in the future when selecting genotypes for weevil (*Cylas* spp.) resistance.

5.2 Materials and Methods

5.2.1 Experimental site, design and layout

The experiment was carried out in KARLO –Embu from June to December, 2015. The region receives an average annual rainfall of 1250 mm, average temperature of 25˚C and is found in an altitude of 1497 m above sea level. The soils are well draining nitisols. Fifty-four genotypes were set in a Randomized Complete Block Design (RCBD) replicated three times (Appendix 4). Each genotype was planted in a 3.75 x 1.5 m plot. Genotypes Santo Amaro and Naspot 1 (Gruneberg *et al.,* 2015) were used as resistant and susceptible checks respectively. Sweet potato vines were planted at a spacing of 30 cm within rows and 75 cm between rows which were ridged. The gross plot had five rows each with five plants resulting in 25 plants per plot with the net plot having 9 plants per plot. Hand weeding was done six weeks after planting. A growing site that had not been planted with sweet potato was used, and planting material was produced on-station.

Five morphological/phenotypic traits on the planted sweet potato genotypes were evaluated using descriptors as developed by International Potato Center (CIP) (Huaman, 1992). The data was used to investigate the correlation between morphological traits

and weevil infestation parameters. The morphological characters included storage root length, diameter of the largest tuber, weight of largest tuber, oxidation of roots and root latex production. The morphological evaluation based on aerial parts began at 100 days after planting (dap). The evaluation was done on the nine plants of each genotypye excluding the border plant of each plot. The morphological evaluation based on root characteristics was done after harvest of the roots (160 dap) by use of the sweet potato descriptor by CIP (Huaman, 1992).

Sweet potato roots were harvested 160 days after planting (dap), were washed with clean water soon after lifting from the ground to remove all soil particles and foreign matter. The roots were then rinsed in water and treated with 50 ppm chlorine to avoid any fungal build up in the water and to sterilize the surface of the roots. They were then dried and taken to the laboratory to be infested by *C. puncticollis* adults. Medium sized roots (about 40 – 60 mm diameter at the widest part of the root), uninfested, undamaged roots were targeted for weevil infestation.

5.2.2 Weevil rearing

A sweet potato weevil colony of *C. puncticollis* was established from a field collected population and was maintained in an enclosed room on storage roots of Kemb 10 in artificially made netted bags at 28 ± 2 ˚C. Weevil collection started in August, 2015 to end of September, 2015. Collection was done daily from an old sweet potato farm in KALRO-Embu site. The adult insects were removed after 14 days, and the bags were subsequently checked daily for emergence. After another 14 days, the 0-14 day old adults that had emerged were removed and placed in a new netted bag with fresh Kemb 10 roots for a further 14 days. Hence, 14-28 days old *C. puncticollis* were used in this study.

5.2.3 Behavioral assays

The experiment was set up using a protocol by Anonymous (1998). The experiment was set in a Completely Randomized Design (CRD) with 3 replications and 51 genotypes. The genotypes were considered as the treatments. The unsexed adult weevils were separated into female and male sexes by use of hand lenses. The females were identified by use of their clubbed antennae (male weevil's antenna is straight while female weevil's antenna is round). Three pairs of *C. puncticollis* weevils (3 males and 3 females that were 14-28 days old) were put in a clear plastic jar with a single root of each of the 51 genotypes. Three clean roots (free from weevil infestation) per genotype per plot (in a block) were used. This resulted into a total of nine roots per genotype subjected to test with every replicate comprising three roots per genotype. Each container was covered with a net which was fastened by a rubber band to hinder the escape of adult weevils. After 12 days of infestation, both the male and female *C. puncticollis* adults were removed from the containers and those that were alive recorded. The experiment was carried out in a controlled environment of about 28 ± 2 $^{\circ}$C and a relative humidity of 85 ± 10%. An electrical heater and a humidifier were used to regulate the temperature and humidity respectively. The plastic jars were checked daily for adult emergence 20 days after set-up. The number of adult weevils emerging daily in the containers from 20 days after set-up were recorded daily and discarded after recording. This was done for a period of 22 days. After the 22 days recording period, each root was assessed for the percentage of external damage using the scale (1=0%; 2=1-10%; 3=11-25%; 4=26-50%; 5=51-75%; 6=>75%). The final evaluation of the roots for weevil infestation was done on the 42nd days after set-up. Adults and larvae of the weevils were exracted from the tubers by chipping them into small bits to facilitate removal and counting. The number of adults, larvae and pupae inside the roots were recorded. The resistance of the sweet potato roots to *C. puncticollis* was determined using the scale shown in Table 5.1.

Table 5.1: Rating of resistance of sweet potato roots to *C. puncticollis*

Score (in relation to sum of emerged adult weevils)	Description (ranking)
0	Completely resistant genotypes
1 – 5	Highly resistant genotypes
6 – 10	Medium resistant genotypes
11 – 15	Slightly resistant genotypes
16 – 20	Susceptible genotypes
21 – 25	Most susceptible genotypes

5.2.4 Data analysis

Analysis of variance was done using Statistical Analysis System programme (SAS Institute Inc, 1997) and means were separated using LSD at $p \leq 0.05$. Cluster analysis was done on weevil infestation data (total adult counts, total larvae counts and external root damage) based on the Euclidian distance co-efficient and UPGMA using NCSS -pc version 11 (Jerry, 2000). Hierarchical programme in Number cruncher statistical systems (NCSS) was used to generate dendrograms. Correlations among quantitative morphological and nutrition characters were carried out by SAS procedure CORR and the optional statement PEARSON. A chi-squared test (Appendix 5) was done to test the hypothesis that there was no significant ($p \leq 0.05$) effect of qualitative characters (latex production and oxidation) on the resistance of sweet potato genotypes to *C. puncticollis* using the following equation.

$$\chi^2 = \sum \frac{(O-E)^2}{E}$$

Where: χ^2 = Calculated Chi-squared

O = Observed frequencies

E = Expected frequencies

5.3 Results

At the end of the experimental period (42 days after set-up), sweet potato genotypes had been infested differently by *C. puncticollis*.

5.3.1 *C. puncticolis* emergence

Adult weevils of *C. puncticollis* began to emerge from roots of all genotypes 24-34 days after set-up except for a few (Mogesi Gikenja, 9-Nduma, Wera, 5 Nyandere, Kenspot 3, 292-H-12, Obugi, Santo Amaro, Bungoma, 1-Ujili and Mugande) which exhibited delayed emergence (Appendix 6). Mogesi Gikenja, 9-Nduma, Wera, 5 Nyandere, Kenspot 3, 292-H-12, Obugi, Santo Amaro, Bungoma, 1-Ujili and Mugande had *C. puncticollis* start emerging at 34 and 35 days after set-up (Appendix 6). For most genotypes tested in this study, there was a low emergence of adult *C. puncticollis* at 27 days after set-up (Appendix 6). As days progressed, the rate of emerged adult *C. puncticollis* from many genotypes increased with highest emergence recorded on the 35th and 39th days after set-up (Appendix 6). At the 42nd day after set-up, *C. puncticollis* emergence from most of the genotypes had droped (Appendix 6).

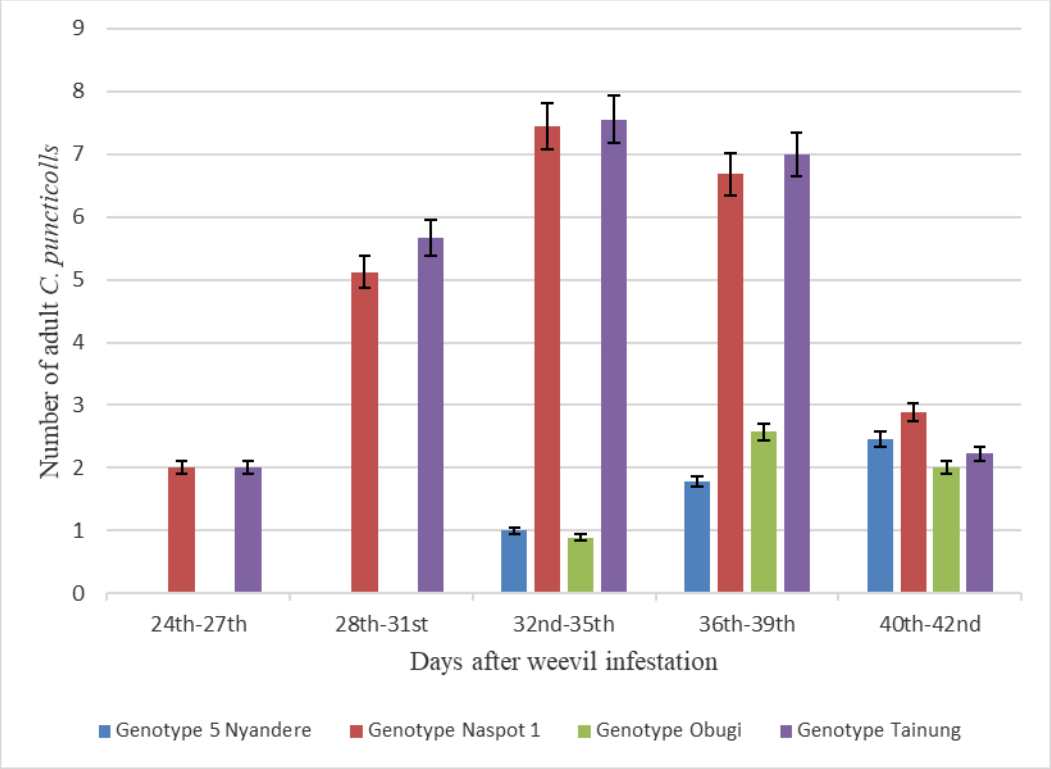

Figure 5.1: Number of *C. puncticollis* adults emerging from the most susceptible and highly resistant genotypes

At 24 to 31 days after weevil infestation, two genotypes (Tainung and Naspot 1) that were rated later in this study as "most susceptible" had recorded some weevil emergence while two genotypes (Obugi and 5 Nyandere) that were regarded in this study as "highly resistant" had not recorded any weevil emergence then (Figure 5.1). At about 36 to 39 days after weevil infestation, two of the "most susceptible" genotypes (Tainung and Naspot 1) had recorded a total of more than twenty emerged adult *C. puncticollis* while two of the "highly resistant" genotypes (Obugi and 5 Nyandere) had recorded less than four emerged *C. puncticollis* adults (Figure 5.1). For the susceptible genotypes, the rate of *C. puncticollis* emergence increased with time, reached optimum within 32-35 days after set-up and started declining while for one of the resistant genotypes (5 Nyandere), *C. puncticollis* emergence started within 32-35 days after set up and increased with time (Figure 5.1). However, for genotype obugi, *C. puncticollis* emergence started within 32-35 days after set up and the rate significantly decreased after the 39^{th} day (Figure 5.1).

5.3.2 Average total counts of *C. puncticolis* adults, larvae and external sweet potato root damage evaluation

The genotype effect on the sum of emerged *C. puncticollis* in the entire experimental period was significant at $p \leq 0.0001$ (Table 5.2). Tainung was one of the most susceptible genotypes with the highest average sum of the developed *C. puncticollis* adults (25) at 42 days after set-up (Table 5.2). Other genotypes that showed high numbers of adult *C. puncticollis* and ranked as most susceptible included Naspot 1 (24.33), Kenspot 5 (22.67), Fundukhusia (22.67), 62 Odhiogo (22.33), Alupe-or (21.67) and SPK 013 (21.67) (Table 5.2). The highly resistant genotypes to weevil infestation had low values for the sum of *C. puncticollis* adults at 42 days after set-up. These genotypes included Obugi and 5 Nyandere and had an average sum of 5 emerged adult weevils each (Table 5.2). Genotypes Mogesi Gikenja, Bungoma, 292-H-12, Santo Amaro, 9 Nduma, Kenspot 3, Wera, 1-ujili, Mugande and Kenspot 2 were ranked as "medium resistant"

having an average sum of 5.67, 6.33, 6.67, 7, 7.33, 7.67, 7.67, 7.67, 8.33 and 9 adults respectively (Table 5.2).

Many of the genotypes that showed high level of weevil tolerance (by having few *C. puncticollis* adults by the 42th day) had the highest average numbers of larvae at 42 days after set-up (Table 5.2). The genotypes that were having the highest average number of total larvae were Kenspot 3, obugi and 1 Ujili (0.67) followed by Bungoma, Wera, Santo Amaro, Karunde, Amina, Kenspot 5, 9 Nduma, Mogesi Gikenja, 292-H-12, Kenspot 2, Kenspot 1, Odinga and 5 Nyandere (all at average of 0.33) (Table 5.2). The rest of the tested genotypes did not have larvae at 42 days after set-up (Table 5.2).

At 42 days after set-up, genotypes Naspot 1, Kenspot 5, K117 and 62 Odhiogo had the highest number of external root damage which meant that >75% of the roots was damaged by weevils (Table 5.2). Other genotypes that recorded high numbers of external root damage included Tainung, Fundukhusia, SPK 031, Alupe-or and Kenspot 1 which also showed >75% damage (Table 5.2). On the other hand, genotypes obugi, 5 Nyandere and Mogesi Gikenja had the least number of external root damage having ≤10% of the damage (Table 5.2). Other genotypes that showed ≤ 25% of external root damage included Bungoma, 292-H-12, Santo Amaro, 9 Nduma, Kenspot 3, Wera, 1 Ujili, Mugande, Kenspot 2, Nyamuguta and Nyautenge (Table 5.2).

Table 5.2: Average number of *Cylas puncticollis* adults, larvae and external root damage on sweet potato genotypes at 42 days after set-up

S/N	Names of sweet potato genotypes	Sum of emerged *C. puncticollis* adults on sweet potato roots	Sum of observed *C. puncticollis* larvae on sweet potato roots	External root damage (external root damage on sweet potato roots)	Ranking in relation to weevil tolerance
1	Tainung	25 a	0.00 b	5.67 ab	Most susceptible
2	Naspot 1	24.33 a	0.00 b	6.00 a	Most susceptible
3	Kenspot 5	22.67 ab	0.00 b	6.00 a	Most susceptible
4	Fundukhusia	22.67 ab	0.00 b	5.67 ab	Most susceptible
5	62 Odhiogo	22.33 abc	0.00 b	6.00 a	Most susceptible
6	SPK 013	21.67 abcd	0.00 b	5.00 bcd	Most susceptible
7	Alupe or	21.67 abcd	0.00 b	5.67 ab	Most susceptible
8	SPK 031	21.67 abcd	0.00 b	5.67 ab	Most susceptible
9	K 117	20.33 bcde	0.00 b	6.00 a	Susceptible
10	Polo yiengo	20.00 bcdef	0.00 b	5.33 abc	Susceptible
11	Kenspot 1	19.67 bcdef	0.00 b	5.67 ab	Susceptible
12	Nyawo Nyathiodiewo	19.33 bcdefg	0.00 b	5.00 bcd	Susceptible
13	Kuny kibuonjo	19.33 bcdefg	0.00 b	5.33 abc	Susceptible
14	Nyakagwa	19.00 cdefgh	0.00 b	5.00 bcd	Susceptible
15	SPK 004	18.67 defgh	0.00 b	5.33 abc	Susceptible
16	Fumbara jikoni	18.33 defgh	0.00 b	5.33 abc	Susceptible
17	Saly boro	18.33 defgh	0.00 b	5.00 bcd	Susceptible
18	Kemb 10	17.33 efghi	0.00 b	4.67 cde	Susceptible
19	12 Marooko	17.33 efghi	0.00 b	5.00 bcd	Susceptible
20	Mbita	17.00 efghi	0.00 b	4.67 cde	Susceptible
21	K/KA/2004/215	16.83 efghij	0.00 b	5.00 bcd	Susceptible
22	56682-03	16.67 fghij	0.00 b	5.00 bcd	Susceptible
23	Sinia	16.00 ghijk	0.00 b	4.33 def	Susceptible
24	Lungabure	15.67 hijkl	0.00 b	5.00 bcd	Susceptible
25	Gachaka	14.67 ijklm	0.00 b	4.33 def	Medium tolerant
26	Mwavuli	14.67 ijklm	0.00 b	4.33 def	Medium tolerant
27	24 Kampala	14.33 ijklmn	0.00 b	4.33 def	Medium tolerant
28	36 Kalamb Nyerere	14.00 ijklmno	0.00 b	4.33 def	Medium tolerant
29	29 Kuny kibuonjo	13.33 jklmno	0.00 b	4.33 def	Medium tolerant
30	Amina	13.33 jklmno	0.33 ab	4.00 efg	Medium tolerant
31	Kenspot 4	13.33 jklmno	0.00 b	4.00 efg	Medium tolerant
32	Vitaa	13.00 klmno	0.00 b	4.00 efg	Medium tolerant
33	52 Nyakisumu	12.67 klmno	0.00 b	3.67 fgh	Medium tolerant
34	Nangili	12.67 klmno	0.00 b	4.00 efg	Medium tolerant
35	Nyautenge	12.33 lmnop	0.00 b	2.67 ijk	Medium tolerant
36	Karunde	12.33 lmnop	0.33 ab	3.67 fgh	Medium tolerant
37	Odinga	11.33 mnopq	0.33 ab	3.67 fgh	Medium tolerant
38	91/2187	11.00 nopqr	0.00 b	3.67 fgh	Medium tolerant
39	Nyamuguta	10.67 opqrs	0.00 b	3.33 hij	Medium tolerant
40	Kenspot 2	9.00 pqrst	0.33 ab	3.00 hij	Tolerant
41	Mugande	8.33 qrstu	0.33 ab	3.00 hij	Tolerant
42	1-ujili	7.67 rstu	0.67 a	2.67 ijk	Tolerant
43	Wera	7.67 rstu	0.33 ab	3.00 hij	Tolerant
44	Kenspot 3	7.67 rstu	0.67 a	3.00 hij	Tolerant
45	9 Nduma	7.33 stu	0.33 ab	3.00 hij	Tolerant
46	Santo Amaro	7.00 tu	0.33 ab	3.00 hij	Tolerant
47	292-H-12	6.67 tu	0.33 ab	3.00 hij	Tolerant
48	Bungoma	6.33 tu	0.33 ab	2.67 ijk	Tolerant
49	Mogesi Gikenja	5.67 tu	0.33 ab	2.33 jk	Tolerant
50	5 Nyandere	5.00 u	0.33 ab	2.33 jk	Most tolerant
51	Obugi	5.00 u	0.67 a	2.00 k	Most tolerant
	LSD Value	3.59	0.48	0.98	
	Mean	14.82	0.11	4.32	
	p Value	<0.0001	<0.0001	<0.0001	
	CV	15.05	21.2	13.90	

Means with the same letters and in same case along a column are not significantly different according to LSD test *(p*≤0.05*)*.

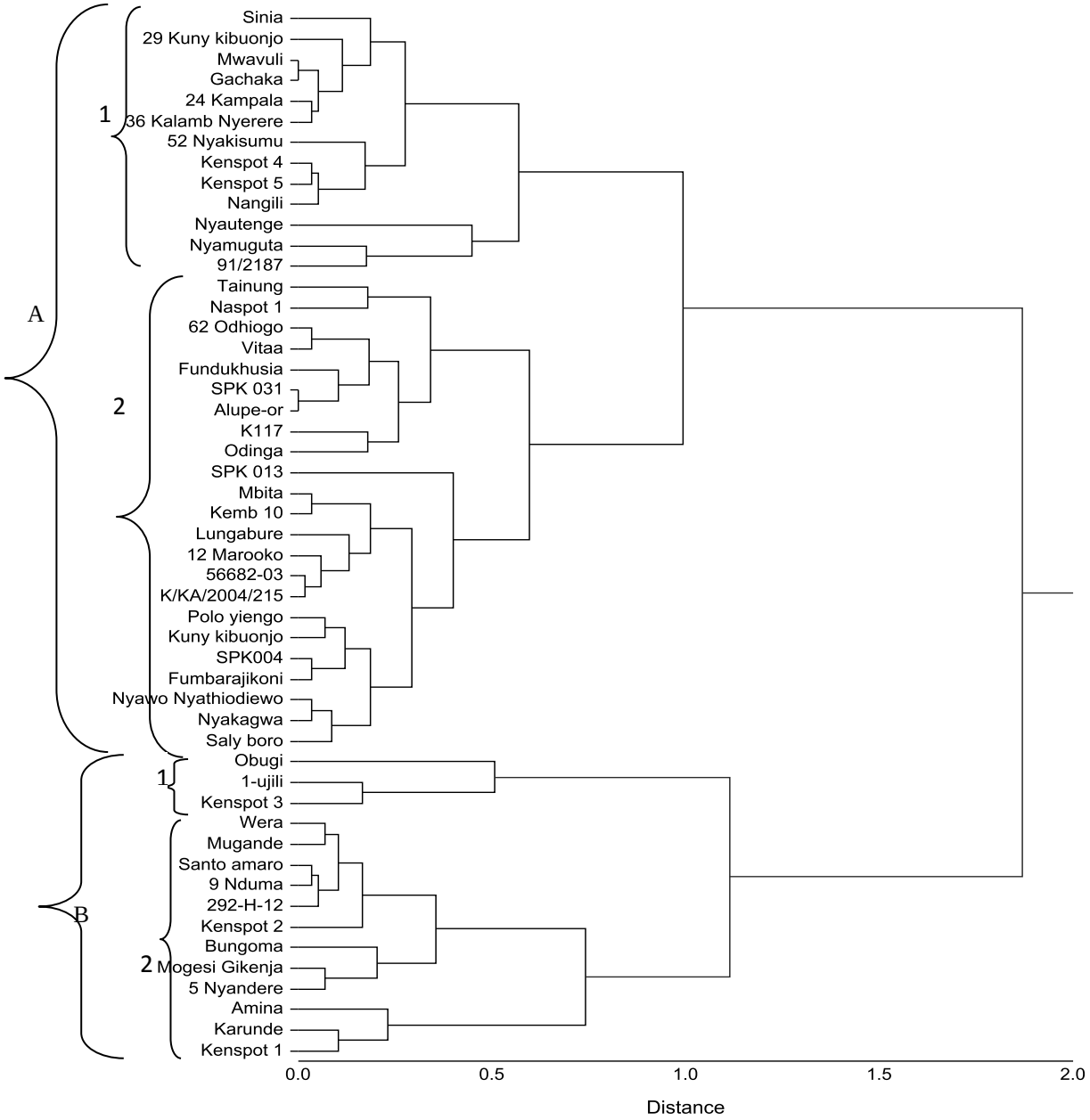

Figure 5.2: Dendrogram (based on Euclidean distance coefficient) of 51 genotypes based on average number of *Cylas puncticollis* adults, larvae and external root damage

Using the average number of emerged *C. puncticollis* adults, larvae and external root damage on sweet potato genotypes presented in Table 5.2, a dendrogram was derived (Figure 5.2) based on Euclidean distance coeeficient. The dendrogram separated the genotypes into two major clusters (A and B) within a Euclidean distance ranging from 0.0 to 1.9 (Figure 5.2). Cluster A contained 36 genotypes and consisted of 2 sub-clusters (Figure 5.2). Cluster B contained 15 genotypes and formed 2 sub-clusters (Figure 5.2). Majority of the genotypes in cluster B (sub-cluster 3 and 4) were among those that recorded lowest numbers of emerged *C. puncticollis* adults 42 days after set-up hence rated as 'medium resistant" or 'highly resistant' to *C. puncticollis* while majority of the genotypes in cluster A (sub-cluster 2) were among those that recorded highest numbers of emerged *C. puncticollis* adults hence regarded as 'very susceptible' or 'susceptible' (Figure 5.2). Some of the genotypes in cluster A (sub-cluster 1) were among those that recorded moderate numbers of emerged *C. puncticollis* adults hence regarded as 'slightly resistant' (Figure 5.2).

5.3.3 Correlation between sweet potato agro-mophological traits and weevil infestation

5.3.3.1 Association between sweet potato quantitative agro-mophological traits and weevil infestation

All the tested phenotypic traits did not correlate significantly ($p>0.05$) with the sum of emerged adult weevils (Table 5.3) except weight of largest tuber which was significant. The results of this study show that the heavier and wider the roots, the less the emerged *C. puncticollis* from the genotypes (Table 5.3). Further, this study established a significant and positive correlation between the total larvae counts and the sweet potato genotypes diameter of largest root ($p\leq0.001$; r = 0.66451), the total larvae counts and weight of largest tuber ($p\leq0.001$; r = 0.99055), external root damage and storage root length ($p\leq0.05$; r = 0.31887) as shown in Table 5.3. However, there was a significant negative correlation between the total larvae counts and sweet potato genotypes length

of storage root ($p \leq 0.001$; r = -0.58767); and external root damage and the diameter of the largest root ($p \leq 0.05$; r= -0.29566) as shown in Table 5.3.

5.3.3.2 Association between sweet potato qualitative agro-mophological traits and sum of emerged adult weevils

As concerns the association between qualitative traits (latex production and oxidation) and sum of emerged weevils, the calculated χ^2 (8.6588) was less than the distribution χ^2 (23.685) at 95% confidence level ($p \leq 0.05$). This showed that there were no significant ($p \leq 0.05$) effects of the evaluated qualitative traits (latex production and oxidation) on weevil resistance of the genotypes.

Table 5.3: Correlation coefficients for morphological traits and weevil infestation parameters in sweet potato

	Storage root length	Diameter of largest root	Weight of largest root	Root cortex
Sum of emerged *C. puncticollis* adults	0.19833^{ns}	- 0.17177^{ns}	- 0.27443*	- 0.08799^{ns}
Total larvae count	- 0.58767***	0.66451***	0.99055***	0.08194^{ns}
External root damage	0.31887*	- 0.29566*	- 0.44599***	- 0.04822^{ns}

Key: * means significant ($p \leq 0.05$) *** means significant ($P \leq 0.001$) ^{ns} means not significant

5.3.4 Correlation between sweet potato root nutrition characters and *C. puncticollis* infestation

Correlation coefficients between sweet potato root nutrition and *C. puncticollis* infestation parameters are presented in Table 5.4. All the traits were positively correlated with the sum of the recovered adult weevils counted in the entire experimental period except for the dry matter content.

The results of this study showed a significant strong negative correlation ($p \leq 0.001$; r = -0.70881) between the dry matter content and the emerged adult weevils (Table 5.4). This therefore meant that the higher the dry matter, the lower the level of infestation by weevils and vice versa. Further, the results of this study showed a significant positive correlation ($p \leq 0.0001$; r = 0.61390) between the dry matter content and the total larvae counts. There was also a significant negative correlation ($p \leq 0.001$; r = -0.66929) between the dry matter content and the external root damage. Among the 51 genotypes evaluated for weevil infestation, most of the genotypes that showed high number of adult weevil emergence had very low contents of dry matter (Table 5.5) as compared to their counterparts that showed low levels of adult weevil emergence (Table 5.6). For instance, the dry matter content for the genotypes that recorded high numbers of emerged adult weevils ranged from 24.39% to 34.11% (Table 5.5) while the dry matter

content for the genotypes that recorded few numbers of emerged adult weevils ranged from 33.34% to 46.44% (Table 5.6).

The results of this study showed a significantly positive very weak correlation ($p \leq 0.05$; r =0.28907) between total root carotenoids and the sum of emerged adult weevils (Table 5.4). The genotypes that recorded high numbers of emerged adult weevils had their total carotenoids ranging from 5.52 µg/g to 34.55 µg/g (Table 5.5) while those with low numbers of emerged adult weevils had their total carotenoids ranging from 6.13 µg/g to 22.61 µg/g (Table 5.6).

The results of this study showed a significant postive correlation between root sucrose and the emerged adult weevils ($p \leq 0.001$; r =0.48424), root sucrose and external root damage ($p \leq 0.001$; r =0.49316) as shown in Table 5.4. The genotypes that recorded high numbers of emerged adult weevils had their sucrose ranging from 36.63 ppm to 123.43 ppm (Table 5.5) while those with low numbers of emerged adult weevils had their sucrose ranging from 1.57 ppm and 81.10 ppm (Table 5.6).

The results of this study showed a significant postive correlation ($p \leq 0.001$; r = 0.46341) between root starch and the emerged adult weevils (Table 5.4). Further, there was a positive correlation ($p \leq 0.001$; 0.47101) between root starch and external root damage (Table 5.4). The genotypes that recorded high numbers of emerged adult weevils had their starch range from 32.97 ppm to 111.07 ppm (Table 5.5) while those with low numbers of emerged adult weevils had their starch range from 1.40 ppm to 75.93 ppm (Table 5.6). This means that the higher the content of starch, the more susceptible the sweet potato genotype becomes.

Root protein was not correlated with sum of emerged adult weevils (r = 0.20393), total larvae counts (r = -0.18624) and external root damage (r = 0.18362) (Table 5.4). The protein content of genotypes which recorded high numbers of emerged adult weevils

ranged from 3.08% to 10.92% (Table 5.5) while that of genotypes with few emerged adult weevils ranged from 2.21% to 11.27% (Table 5.6).

Table 5.4: Correlation among root nutritional content and weevil infestation parameters in sweet potato

	Dry matter	Root protein	Total root carotenoids	Root sucrose	Root starch
Sum of emerged *C. puncticollis* adults	-0.70881**	0.20393ns	0.28907*	0.48424**	0.46341**
Total larvae count	0.61390***	-0.18624ns	-0.12255ns	-0.22238ns	-0.19634ns
External root damage	-0.66929**	0.18362ns	0.24946ns	0.49316**	0.47101**

Key: * means significant ($p \leq 0.05$) ** means significant ($P \leq 0.001$) *** means significant ($P \leq 0.0001$) ns means not significant

Table 5.5: Means for root nutritional content of sweet potato genotypes which recorded highest numbers of emerged *C. puncticollis* adults

Sweet potato genotypes	**Dry matter (%)**	**Root Protein (%)**	**Root total Carotenoids (µg/g)**	**Root Sucrose (ppm)**	**Root total starch (ppm)**	**Sum of emerged *C. puncticollis***
Tainung	24.39 y	3.08 vw	30.57 d	65.53 l	59.00 l	25 a
Naspot 1	34.11 h	9.42 b	7.07 zAB	123.43 b	111.07 b	24.33 a
Kenspot 5	28.06 y	4.06 pqrstuv	32.22 c	59.30 n	53.37 n	22.67 ab
Fundukhusia	29.01 rst	8.52 cd	5.52 GH	72.33 j	65.10 ij	22.67 ab
Vitaa	32.35 klm	4.47 nopqrst	8.40 st	34.53 C	38.53 wx	22.67 ab
62 Odhiogo	26.57 x	4.48 nopqrst	8.18 tu	36.63 zAB	32.97 BCD	22.33 abc
SPK 013	29.98 q	8.48 bcd	6.37 CDE	71.63 j	64.47 j	21.67 abcd
Alupe-or	30.30 pq	5.15 klmnopq	34.55 b	52.40 srt	47.17 rst	21.67 abcd
SPK 031	28.90 stu	10.92 a	13.55 j	84.73 f	76.27 fg	21.67 abcd
K117	32.02 mn	2.62 w	9.21 qr	73.63 ij	66.27 ij	20.33 bcde
Polo yiengo	29.20 rs	7.35 def	7.09 yzAB	37.53 zA	33.77 ABC	20.00 bcdef
LSD Value	2.81	0.67	1.54	4.01	4.95	3.59
***p* Value**	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
CV	0.94	12.53	1.89	2.33	2.69	15.05

Means with the same letters (in the same case) along a column are not significantly different according to LSD test ($p \leq 0.05$).

Table 5.6: Means for root nutritional content of sweet potato genotypes which recorded lowest numbers of emerged *C. puncticollis* adults

Sweet potato genotypes	**Dry matter (%)**	**Root Protein (%)**	**Root total Carotenoids (µg/g)**	**Root Sucrose (ppm)**	**Root total starch (ppm)**	**Sum of emerged *C. puncticollis***
Obugi	38.50 c	4.01 qrstuv	7.40 xy	42.27 w	49.03 pqr	5.00 u
5 Nyandere	34.54 h	5.07 lmnopqr	12.66 k	15.63 G	14.07 J	5.00 u
Mogesi Gikenja	37.08 e	4.07 pqrstuv	6.55 C	35.63 ABC	32.07 CD	5.67 tu
Bungoma	35.60 g	5.31 klmno	7.43 xy	34.57 C	32.30 CD	6.33 tu
292-H-12	34.40 h	3.34 tuvw	6.60 C	1.57 H	1.40 K	6.67 tu
Santo amaro	34.17 h	8.51 cd	8.23 tu	47.00 u	42.27 vu	7.00 tu
9 Nduma	46.44 a	5.31 klmno	7.01 AB	81.10 g	75.93 fg	7.33 stu
Kenspot 3	41.20 b	3.85 ustv	9.08 r	56.90 o	51.20 o	7.67 rstu
Wera	33.34 i	11.27 a	7.50 wx	38.53 yz	34.67 zAB	7.67 rstu
1-ujili	33.61 i	5.09 lmnopq	7.43 x	51.20 t	46.07 t	7.67 rstu
Mugande	35.53 g	4.07 pqrstuv	6.13 DEF	51.60 st	46.43 st	8.33 qrstu
Kenspot 2	41.17 b	2.21 w	22.61 g	56.60 opq	50.07 opq	9.00 pqrst
LSD Value	2.81	0.67	1.54	4.01	4.95	3.59
***p* Value**	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
CV	0.94	12.53	1.89	2.33	2.69	15.05

Means with the same letters (in the same case) along a column are not significantly different according to LSD test ($p \leq 0.05$)

5.4 Discussion

The current study showed significance differences in *C. puncticollis* damage in respect to the nature of the genotype. Genotypes Obugi and Tainung incurred the least and the highest infestation respectively. This is similar to the findings by Parr *et al.* (2016) and Stathers *et al.* (2003a) who reported that different sweet potato cultivars had varied levels of feeding damage when *C. puncticollis* adults were offered free food and oviposition choices. The variability in the mean number of adults, larvae and external damage on the roots of different genotypes indicated that sweet potato weevils prefer particular genotypes even when not presented with a choice.

The results of this study showed that there was no genotype that was completely resistant to the weevils. Plant host resistance is important in management of insect pest (Rajasekhara, 2005). Despite years of intensive research, varieties with resistance to *C. puncticollis* are not available but there is progress in finding weevil resistant components in some varieties (Stevenson *et al*., 2009). Weevil resistance breeding characters in sweet potatoes are identified under polygenic inheritance. For instance, field research findings by Alghali and Munde (2001) reported a number of root characters (neck length, placement depth, width, length, cortex thickness, dry matter contents, colour of skin and flesh, shape and number per plant) that appear to influence the levels of *C. puncticollis* damage observed among clones.

Some of the genotypes recorded in this study as having high level of resistance or susceptibility have been reported in some other findings of other studies. For instance, in a field experiment, Kwach *et al*., (2008) recorded 292-H-12, Mugande and Bungoma as more resistance to weevil damage among eleven improved varieties while in the same study Nyathi Odiewo and Kemb 10 had high levels of weevil damage. Also, some studies have reported Naspot 1 and SPK 031 as susceptible varieties amongst others (Anyanga *et al*., 2013; Gruneberg *et al*., 2015; Kivuva *et al*., 2015). This means that there could be a positive correlation between the infestation of these genotypes in the

field and in the controlled environment after harvest. However, genotype Bungoma was reported by Kivuva *et al.* (2015) as a susceptible variety to weevils which contrasted the findings of this study. Further, the same researchers reported that genotype Kuny kibuonjo was a moderately weevil resistant variety but the results of this study show that it was one of the genotypes whose roots was susceptible to weevils. The reason behind these contradicting results could be that the attributes contributing to the two genotypes tolerance or susceptibility to weevils are not yet stable across different agro-ecological zones.

In this study *C. puncticollis* began to emerge from roots of all genotypes 24-35 days after set-up while peak emergence for most genotypes occurred at 24-34 days after set-up except for some resistant genotypes (Mogesi Gikenja, 9-Nduma, Wera, 5 Nyandere, Kenspot 3, 292-H-12, Obugi, Santo Amaro, Bungoma, 1-Ujili and Mugande) which exhibited delayed emergence (34-35 days after set-up). The delay in adult emergence may probably indicate that the environment was not ideal for the development of the weevil. This is supported by a study by Anota and Odebiyi, (1984b) who indicated that *C. puncticollis* raised on resistant cultivars had a low survival rate in all life stages, smaller body weights and a longer developmental period. Similarly, Hahn and Leuschner (1981) found that in resistant varieties, oviposition was reduced, hatching delayed, larval mortality increased and male adult weight gain reduced. Further, delayed adult pest emergence in some cultivars can indicate some levels of antibiosis (Stathers *et al*., 2003a). The beginning of *C. puncticollis* emergence from roots in the present study is almost in the same time frame as the study findings by Stathers *et al.* (2003a). They reported that *C. puncticollis* adults started emerging at 22-23 days after set-up and 22-25 days after set-up in two different sites (Stathers *et al*., 2003a). The slight differences could be as a result of the difference in experimental conditions (particularly temperature). Further, the results of this study on the first adult emergence is similar to Smit and Van Huis (1999) findings who reported that the first adult *C. puncticollis* emergence was 24 days after set-up with peak emergence at 28-31 days after set-up in

one of their experimental sites. However, the results of this study contradict the findings by Parr *et al*., (2016) who reported that *C. puncticollis* adults started emerging at 36-45 days after set-up with peak emergence at 46-55. The differences in the adult emergence time bracket between this study and the later could have been as a result of different genotypes tested in these studies.

In this study, dry matter content among the evaluated genotypes was significant and negatively correlated with *C. puncticollis* damage (r = -0.70881; $p \leq 0.001$). This is congruent with the findings of Mansaray *et al*., (2015) who reported a strong significant negative correlation (r = -0.91, p=0.0001) between dry matter content and the number of tubers damaged by *C. puncticollis*. High dry matter content probably makes it difficult for *C. puncticollis* to puncture the roots and hence confers some form of resistance. Additionally, Alghali and Munde, (2001) reported that cultivars with high dry matter contents suffered least *C. puncticollis* damages and vice versa. The results of this study also conform to the findings of Jackson and Bohac (2006) who reported strong evidence of resistance among the improved dry-fleshed cultivars.

The findings of this study agree with results reported by Cockerham and Deen (1947) that carotene positively correlates with variety susceptibility to *Cylas* spp. but contradicts some studies (Hahn and Leuschner 1981; Anota and Odebiyi 1984b) who reported that carotene negatively correlates with weevil resistance. For instance, Anota and Odebiyi reported that carotene content was a major factor in tuber resistance of *C. puncticollis* of five resistant sweet potato cultivars tested in Nigeria. The contradiction between these results could be caused by the evaluation of different genotypes in these two studies.

Starch is an important nutritional requirement of insects (Nottingham *et al.*, 1988). This can explain why the findings of this study showed a significant positive (r = 0.46341; $p \leq 0.001$) correlation between starch content and *C. puncticollis* damage on the sweet

potato genotypes tested. However, Anota and Odebiyi (1984b) found no evidence that starch played a role in tuber resistance of five resistant sweet potato cultivars tested in Nigeria. The contradiction between the results observed by Anota and Odebiyi (1984b) and the findings of this study could be caused by the evaluation of different genotypes in these two studies under dissimilar agro-ecological zones.

The results of this study showing that total larvae count positively correlated with dry matter and negatively correlated with all other biochemical traits tested in this study may not be credible. This is because, larvae count was done only once (at 42 days after set-up) and hence it was not a reflection of what happens in the normal circumstances of an infested sweet potato root. Credible results of the same could have been obtained if larvae counts could have been done on daily basis. The presence of larvae in this study could reflect the effect of genotype in the development of *C. puncticollis* with highly resistant genotypes recording the presence of larvae at 42 days after set-up.

5.5 Conclusion

1. No sweet potato genotype was completely resistant to *C. puncticollis* although some genotypes were more resistant to infestation than others.
2. Among the 51 sweet potato genotypes evaluated in this study, the highly resistant genotypes were Obugi and 5 Nyandere; the medium resistant ones were Mogesi Gikenja, Bungoma, 292-H-12, Santo Amaro, 9 Nduma, Kenspot 3, Wera, 1-Ujili, Mugande and Kenspot 2; while genotypes Tainung, Naspot 1 were the most susceptible among others.
3. Root dry matter content was negatively correlated with resistance to sweet potato weevil.
4. Starch and sucrose were positively correlated with resistance to sweet potato weevil.

CHAPTER SIX
GENERAL DISCUSSION, CONCLUSION AND RECOMMENDATIONS

6.1 General discussion

Sweet potato (*Ipomea batatas* [L.] Lam.) is an economically important crop in East Africa mainly grown by small holder farmers. Firstly in this study, the distribution of the sweet potato weevil (*cylas* spp.) and farmers coping strategies with the weevil in Homa Bay County, Kenya, was evaluated. The results indicated that 93.3% of the farmers identified *Cylas* spp. as the most problematic pest that affect sweet potato. In some previous studies, *Cylas* spp. was equally identified as the most problematic pest (Ashebir, 2006). For instance, in Southern Ethiopia 68.3% of the interviewed farmers identified *Cylas* spp. to be the most important pest in sweet potato production (Ashebir, 2006). The results of this study show that the varieties identified by farmers for resistance to *Cylas* spp. were region specific. This may be attributed to the fact that planting genotyes readily available to farmers are adapted to different agro-ecological conditions exhibited by the two sub-Counties (GOK, 2009a; GOK 2009b). The farmers in the two sub-Counties planted different genotypes and therefore their observation on the resistance of the genotypes to *Cylas* spp. could not be the same. The results from three out of six groups that rated the infestation of the sweet potato by *Cylas* spp. as the most serious problem continues to emphasize the economic importance of the pest in the study region. Therefore, identification of factors limiting production and provision of environmentally-friendly options for integrated crop management is inevitable if sweet potato production among the small-scale farmers is to be increased (Okonya and Kroschel, 2013). The most popular *Cylas* spp. management method was found to be earthing-up of ridges (re-ridging) during weeding. This is an important strategy to deter weevil infestation during drought conditions. It can be achieved by hilling (ridging) a small area around the sweet potato plant in order to prevent the entry of weevils into roots and oviposition by female weevils' (Hue and Low, 2015). However, re-ridging works best only when performed at the root formation stage.

Secondly in the study, 68 sweet potato (*Ipomea batatas* [L.] Lam.) genotypes were evaluated for diversity with respect to agro-morphological, molecular and nutritional characters. Among the genotypes studied, most of the agro-morphological and nutrition characters were highly variable. High agro-morphological variability in sweet potato genotypes has been previously reported by several researchers (Karuri *et al*., 2009; Karuri *et al*., 2010; Maquia *et al*., 2013) and it could be attributed to the fact that majority of the farmers grow landraces. In contrast to the results of this study, Tairo *et al.* (2008) observed low diversity of 0.52 among 280 sweet potato accessions in Tanzania. Similarly, and Gichuru *et al.* (2006) reported low diversity in East African sweet potato cultivars. The reason for the low diversity reported by Thompson *et al.* (1997) and Tairo *et al.* (2008) could have been attributed to narrow geographic zone of collection of the cultivars. The gene diversity values followed the same pattern implying low marker polymorphism. This could be due to the low genetic diversity of sweet potato considering the fact that it's a clonally propagated crop. Another explanation is that farmers in different regions tend to give a particular genotype different local names, hence when a breeder collects genotypes they might be the same genotype under different names. It is therefore important to do germplasm characterization before making crosses to determine the degree of variability between genotypes. The UPGMA trees (dendrograms) drawn in this study produced 2-5 major clusters but the genotypes did not cluster together uniformly in all the trees. The trees could only give the general germplasm relatedness and diversity. The overlapping of the genotypes as an identification of duplicates, and the outstanding of genetically distinct genotypes can help in selecting parents for hybridization experiments. A low consensus was found between agro-morphological and molecular based trees in this study. The results agreed with other studies whereby low correlation between morphological and molecular markers in many crops were found (Koehler-Santos *et al.,* 2003; Ferriol *et al.,* 2004; Bushehri *et al.,* 2005 and Koussao *et al.,* 2014). According to Vieira *et al.* (2007), this low correlation could be due to the fact that a large portion of variation

detected by molecular markers is non-adaptive as compared with phenotypic characters, which are influenced by the environment.

Thirdly in the study, sweet potato genotypes were evaluated for tolerance to *Cylas pnucticollis* (Boheman). The study showed significant differences in *C. puncticollis* damage in respect to the nature of the genotype. The variability in the mean number of adults, larvae and external damage on the roots of different genotypes indicated that sweet potato weevils prefer particular genotypes even when not presented with a choice. This result corroborates with the findings of Muyinza *et al.*, (2010). These authors reported that *C. puncticollis* can actively differentiate between sweet potato parts or have preference for some genotypes over others. The nature of the genotypes used in this study had influence on damage of *C. puncticollis*; as such Obugi and 5 Nyandere incurred the least infestation while Tainung incurred the highest infestation. The reason for this could be related to differences in the root genetic make up of the genotypes tested. Significantly a smaller number of adults, larvae and external root damage was recorded in some genotypes indicating that these genotypes had some form of resistance. Some of the genotypes recorded in this study having high level of resistance/susceptibility have been mentioned in some other findings of other studies. For instance, during a field experiment in some sites, Kwach *et al*., (2008) recorded 292-H-12, Mugande and Bungoma as having more tolerance to weevil damage among eleven improved genotypes while in the same study Nyathi Odiewo, and Kemb 10 had high levels weevil damage. This means that there could be a positive correlation between the infestation of these genotypes (292-H-12, Bungoma and Nyathi odiewo) in the field and in the controlled environment after harvest. Also, from the findings of a survey by Ochieng *et al.,* (2017) it was noted that genotypes Kalamb Nyerere, Wera, Amina and Mugande were perceived by farmers as resistant genotypes. Those findings conform to the findings of this study. However, farmers' perceptions that genotypes Kemb 10 and Sinia are resistant to weevils (Ochieng *et al.,* 2017) contradicts the findings of this study as the mentioned genotypes were found to be susceptible. The

contradiction could be due to the fact that weevil resistance in sweet potato is identified under polygenic inheritance (Hahn and Leuschner, 1982; Allard *et al.*, 1991).

6.2 General conclusion

1. Majority of the farmers were aware of the sweet potato weevil (*Cylas* spp.) as a major pest of sweet potato. Although farmers use several methods to manage the sweet potato weevil, re-ridging was the most commonly used.
2. Sweet potato genotypes presented high diversity based on molecular, agro-morphological and nutritional assessment approaches.
3. Some sweet potato genotypes were more resistant to *C. puncticollis* infestation than others. Genotypes Obugi and 5 Nyandere were the most resistant to the weevil while genotypes Tainung, Naspot 1, Kenspot 5, Fundukhusia, 62 Odhiogo, SPK 031, SPK 013 and Alupe-or, were the most susceptible genotypes to *C. puncticollis*.

6.3 Recommendations

1. Agricultural extension officers should train farmers on the existence of sweet potato genotypes resistant to weevils and management practices of reducing infestation. This is because 90.7% of the farmers in Homa Bay County did not know about the existence of resistant genotypes even though they existed while 35.7% of the farmers in Homa Bay County did not control weevils.
2. Genotypes that were reported by farmers to be resistant to weevils such as Tombra, Zapallo and Ndege oyiejo need to be studied further as they may provide potential sources of resistance to the pest.
3. The results obtained in this study on the agro-morphological, molecular and nutritional characterization can serve as a source of information for scientists and other stakeholders working on this crop.

4. Plant characters like high dry matter, low starch and sucrose contents that were associated with resistance of the crop to weevil infestation could be used for indirect selection of resistant cultivars.
5. This study recommends four genotypes (5 Nyandere, Santo Amaro, Nyautenge and Amina) to farmers residing at Embu County and its surrounding. Further, the study recommends four genotypes Obugi, Nyautenge and Gachaka to farmers residing at ATC –Miyare and its surrounding.
6. Genotypes such as 56682-03 and 1-Ujili in ATC Miyare; and K/KA/2004/215 and Tainung in KALRO Embu were low yielding yet grown by several farmers. These genotypes need to be studied further as they may pocess other valuable characteristics that are desired by farmers.

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APPENDICES

Appendix 1: Questionnaire on sweet potato production in Homa Bay County of Kenya

1. GENERAL INFORMATION ON FARMER, FARM SIZE, CROPS GROWN AND AREA COVERED.

Farmer

Name of interviewee……
Relation to household head…… (Code 1)
Farmers' age……sex……..
Marital status…… (Code 2) Level of Education……(Code 3)
Occupation…….. (Code 4)
Professionally trained? Yes or No……..
Are you able to read and write? Yes or No…….
Address……..Province……District……
Location……..Sub-location……..Village……...
Date of interview……..

Code1:
1=Household head
2=Wife
3=Son or daughter
4=Father or mother
5=Grand child
6=Grand parents
7=Mother-,father-, son-, and daughter-in-law
8=Other relatives
9=Non-relative

Code 2:
1=Single
2=Married
3=Widow/Widower
4=Divorced/separated

Code 3:
1=Never attended
2=Nursery
3=Primary
4= secondary
5=A-level
6=Middle level college
7=University

Code 4:
1=Self employed in Agriculture
2=Salaried worker in Agriculture
3=Self employed in non-farm enterprise
4=Salaried worker in non-agriculture
5=Unemployed

Who is responsible for the overall management of sweet potato in the farm? .....

Farm size

Crops grown and area covered:
Which crops did you plant in your farm this year?

Crop	Area (ha)

Total farm size……...
Cultivated area: 1) Rented…….
2) Owned…….

2. INFORMATION ON SWEETPOTATO VARIETIES GROWN

Distance to the field	
Size of the field	
Planting period	

Which variety are you going to plant?

Variety	Reason for planting (Code 5)	Problems experienced (Code 6)	Yield (Kg/ha)

Code 5:
1=Sweetness
2=Good skin colour of the tuber
3=Good flesh colour of the tuber
4=Good marketability
5=Good storage potential of the tuber
6=High percentage of dry matter
7=Disease resistance
8=pest resistance
9=Good tuber yield
10=Less fibre content
11=Drought resistance
12=Nutritious
13= Early maturing
14=Others

Code 6:
1=No problem
2=Low drought resistance
3=Poor tuber yield
4=Poor storage potential
5=Not sweet
6=Poor marketability
7=Low percentage of dry matter
8=Disease susceptibility
9=Pest susceptibility
10=Lodging susceptibility
11=High fibre content
12=Others

How did you come to know about the variety you are using?

TV	radio	research	extension	relative	Other farmers	traders	Others (specify)

When did you know about the variety? ……
From where did you get seed/vines when you first planted this variety?

Gene bank	Research	Extension	Relative	Other farmers	NGO	Seed company

From where did you obtain the vines/seeds you are planting now?

Gene bank	Research	Extension	Relative	Other farmers	NGO	Seed company

Do you have information on new varieties and their management?
How did you get that information?

TV	radio	research	extension	relative	Other farmers	Others (specify)

3. CROP PRODUCTION
What method do you use for land preparation?

Hand hoeing	Animal plough	Tractor plower	Others (specify)

How do you prepare your land before planting sweet potatoes? ……
……
……
Do you plant on a flat field? Yes/No?
If yes, why do you use this method?
……
What spacing do you use for the crop?
……
Do you know about the recommended spacing? ——————————
How did you get this information?

TV	Radio	Extension	Relative	Traders	Research	Other farmers	Others

Do you use agricultural inputs for sweet potato? Yes/No
If 'Yes' indicate type, rate, method

Input	Usage	Type	Rate (Kg/ha)	Method of application	Time of application
Fertilizer	Yes/No				
Herbicide	Yes/No				
Fungicide	Yes/No				
Insecticide	Yes/No				

Do you weed the crop? Yes/No
If 'Yes' how many times do you weed before harvesting?
……
……
Which method of weeding do you use?

Hand pulling	Hoeing	Herbicide	Others (specify)

What are the most problematic pest(s) in the field?

1	2	3	4

How do you control them?
……
……
……
……
Are sweet potato weevils amongst the problematic pests to your crop? Yes/No
If No, Why?
……
……
……..
If Yes, Why and how do you particularly deal with this problem?
……
……
……
……..
Have you ever grown sweet potato varieties resistant to sweet potato weevil? Yes/No?
If yes
(i) What is the name of the variety?
(ii) Do you still grow it? Yes/No. If No, why?
……
……
……..
(iii) How does the resistant variety look like?
……
…….
Have you ever heard of resistant varieties to sweet potato weevils? Yes/No
If yes, what are the names of those varieties?
……
……..
What are the symptoms of infected plants by the sweet potato weevil?

……
……
……
……..

Describe the type of weevil that affects your crop or give the local name if known to you.

……
……
……
……

What are the most problematic pest(s) in storage?

1	2	3	4

How do you avoid infestation of storage pests?

Sanitation	Chemical spray	Fumigation	Traditional practices	Others (specify)

How do you control storage pests?

Cleaning	Sun drying	Fumigation	Traditional practices	Others (specify)

Are sweet potato weevils amongst the problematic pests to your crop in storage? Yes/No

If No, Why?

……
……
……..

If Yes, Why?

……
……
……

What is (are) the most prevalent disease(s) of this crop in this area?

1	2	3	4

How do you control it/ them? _____

What are the indicators of maturity of the crop?

……
……
……
Do you select the vines for future planting? Yes/No

- If 'Yes' what is your criteria for selection?

……
……
……
……..

How do you store your sorted vine or how do you ensure the continuity of the variety you have chosen?

……
……
……..

Are improved varieties readily available? Tick where appropriate

Always	Sometimes	Not at all

Is the "Availability" adequate, timely and affordable?

Adequate quantity	Right time	Reasonable price
Yes/No	Yes/No	Yes/No
Yes/No	Yes/No	Yes/No
Yes/No	Yes/No	Yes/No

Is credit available for purchase improved sweet potato varieties?

- If 'Yes' what are the conditions for credit? _____
- If 'No' how do you obtain the sweet potato varieties?

NGO	Government	Other farmers	Others (specify)

Have you ever observed any pest control failure due to weevil infestation? Yes/No

- If 'Yes' when and where? _____

Name of interviewer……

Signature……

Appendix 2: Selected ANOVA tables

1.1a Vine growth rate combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	14679.5			
Block	2	4266.9			
Site	1	3620.5	3620.5	1437.1	<0.0001
Genotype	67	2183.7	32.6	12.9	<0.0001
Site*Genotype	67	3928.2	58.6	23.3	<0.0001
Error	270	680.2	2.5		

1.1b Vine growth rate ATC Miyare

Source	DF	SS	Mean square	F value	P value
Total	158	1129.2			
Block	2	453.6			
Genotype	67	537.4	8.0	5.2	0.047
Error	89	138.2	1.6		

1.1c Vine growth rate KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	1127.6			
Block	2	353.6			
Genotype	67	437.2	6.5	1.7	0.045
Error	89	336.8	3.8		

1.2a Vine internode length combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	13910.4			
Block	2	3267.2			
Site	1	510.1	510.1	36.9	<0.0001
Genotype	67	3000.3	44.8	3.2	0.002
Site*Genotype	67	3400.5	50.8	3.7	0.004
Error	270	3732.3	13.8		

1.2b Vine internode length ATC Miyare

Source	DF	SS	Mean square	F value	P value
Total	158	1025.6			
Block	2	421.2			
Genotype	67	394.6	5.9	2.5	0.048
Error	89	209.8	2.4		

1.2c Vine internode length KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	979.4			
Block	2	392.3			
Genotype	67	355.2	5.3	2.0	0.046
Error	89	231.9	2.6		

1.3a Vine internode diameter combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	1010.4			
Block	2	355.6			
Site	1	121.4	121.4	435.9	<0.0001
Genotype	67	225.6	3.4	12.1	<0.0001
Site*Genotype	67	232.6	3.5	12.5	<0.0001
Error	270	75.2	0.3		

1.3b Vine internode diameter ATC Miyare

Source	DF	SS	Mean square	F value	P value
Total	158	952.3			
Block	2	344.6			
Genotype	67	299.5	4.5	1.3	0.044
Error	89	308.2	3.5		

1.3c Vine internode diameter KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	953.1			

Block	2	255.3			
Genotype	67	544.4	8.1	4.7	0.039
Error	89	153.4	1.7		

1.4a Storage root cortex thickness combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	1002.2			
Block	2	375.1			
Site	1	120.8	120.8	474.1	<0.0001
Genotype	67	305.1	4.6	17.9	<0.0001
Site*Genotype	67	132.4	2.0	7.8	0.003
Error	270	68.8	0.3		

1.4b Storage root cortex thickness ATC Miyare

Source	DF	SS	Mean square	F value	P value
Total	158	833.4			
Block	2	433.6			
Genotype	67	299.4	4.5	4.0	0.001
Error	89	100.4	1.1		

1.4c Storage root cortex thickness KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	953.2			
Block	2	510.2			
Genotype	67	301.4	4.5	2.8	0.001
Error	89	141.6	1.6		

1.5a Storage root stalk combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	979.6			
Block	2	289.4			
Site	1	133.6	133.6	297.1	<0.0001
Genotype	67	299.4	4.5	9.9	0.001
Site*Genotype	67	135.8	2.0	4.5	0.005
Error	270	121.4	0.4		

1.5b Storage root stalk ATC Miyare

Source	DF	SS	Mean square	F value	P value

Total	158	679.3			
Block	2	221.1			
Genotype	67	356.1	5.3	4.6	0.01
Error	89	102.1	1.1		

1.5c Storage root stalk KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	701.2			
Block	2	240.1			
Genotype	67	239.2	3.6	1.4	0.001
Error	89	221.9	2.5		

1.6a Mature leaf size combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	1789.5			
Block	2	654.3			
Site	1	254.3	254.3	232.8	<0.0001
Genotype	67	303.6	4.5	4.1	0.002
Site*Genotype	67	282.4	4.2	3.9	0.002
Error	270	294.9	1.1		

1.6b Mature leaf size ATC Miyare

Source	DF	SS	Mean square	F value	P value
Total	158	1235.1			
Block	2	655.2			
Genotype	67	351.2	5.2	2.0	0.049
Error	89	228.7	2.6		

1.6c Mature leaf size KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	1186.4			
Block	2	384.9			
Genotype	67	577.8	8.6	3.4	0.05
Error	89	223.7	2.5		

1.7a Storage root length combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	2457.3			

Block	2	733.1			
Site	1	332.8	332.8	712.0	<0.0001
Genotype	67	973.1	14.5	31.1	<0.0001
Site*Genotype	67	292.1	4.4	9.3	0.0005
Error	270	126.2	0.5		

1.7b Storage root length ATC Miyare

Source	DF	SS	Mean square	F value	P value
Total	158	1899.4			
Block	2	1023.6			
Genotype	67	856.5	12.8	59.0	0.047
Error	89	19.3	0.2		

1.7c Storage root length KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	1585.1			
Block	2	953.2			
Genotype	67	533.5	8.0	7.2	0.045
Error	89	98.4	1.1		

1.8a Largest storage root diameter combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	1111.5			
Block	2	232.2			
Site	1	198.6	198.6	147.0	<0.0001
Genotype	67	200.1	3.0	2.2	0.04
Site*Genotype	67	115.8	1.7	1.3	0.05
Error	270	364.8	1.4		

1.8b Largest storage root diameter ATC Miyare

Source	DF	SS	Mean square	F value	P value
Total	158	955.3			
Block	2	452.1			
Genotype	67	322.5	4.8	2.4	0.05
Error	89	180.7	2.0		

1.8c Largest storage root diameter KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	879.2			

Block	2	422.1			
Genotype	67	299.6	4.5	2.5	0.05
Error	89	157.5	1.8		

1.9a Petiole length combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	877.9			
Block	2	122.3			
Site	1	200.7	200.7	220.6	<0.0001
Genotype	67	199.1	3.0	3.3	0.03
Site*Genotype	67	110.2	1.6	1.8	0.04
Error	270	245.6	0.9		

1.9b Petiole length ATC Miyare

Source	DF	SS	Mean square	F value	P value
Total	158	521.6			
Block	2	213.4			
Genotype	67	251.2	3.7	5.9	0.001
Error	89	57.0	0.6		

1.9c Petiole length KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	439.2			
Block	2	189.3			
Genotype	67	201.5	3.0	5.5	0.001
Error	89	48.4	0.5		

1.10a Weight of largest tuber combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	799.4			
Block	2	122.2			
Site	1	105.7	105.7	250.6	<0.0001
Genotype	67	255.5	3.8	9.0	<0.0001
Site*Genotype	67	202.1	3.0	7.2	<0.0001
Error	270	113.9	0.4		

1.10b Weight of largest tuber ATC Miyare

Source	DF	SS	Mean square	F value	P value
Total	158	328.2			
Block	2	155.6			
Genotype	67	99.2	1.5	1.8	0.05
Error	89	73.4	0.8		

1.10c Weight of largest tuber KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	401.2			
Block	2	152.5			
Genotype	67	102.1	1.5	0.9	0.05
Error	89	146.6	1.6		

1.11a Yield combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	701.2			
Block	2	155.2			
Site	1	110.4	110.4	626.2	<0.0001
Genotype	67	234.9	3.5	19.9	<0.0001
Site*Genotype	67	153.1	2.3	13.0	<0.0001
Error	270	47.6	0.2		

1.11b Yield ATC Miyare

Source	DF	SS	Mean square	F value	P value
Total	158	328.2			
Block	2	155.6			
Genotype	67	99.2	1.5	1.8	0.001
Error	89	73.4	0.8		

1.11c Yield KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	321.2			

Block	2	132.6			
Genotype	67	105.2	1.6	1.7	0.001
Error	89	83.4	0.9		

1.12a Dry matter combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	11488.5			
Block	2	3765.1			
Site	1	626.2	626.2	444.1135	<0.0001
Genotype	67	4667.2	69.6597	49.40404	<0.0001
Site*Genotype	67	2049.3	30.58657	21.6926	<0.0001
Error	270	380.7	1.41		

1.12b Dry matter ATC Miyare

Source	DF	SS	Mean square	F value	P value
Total	158	7488.5			
Block	2	2626.8			
Genotype	67	4667.2	69.7	31.9	<0.0001
Error	89	194.5	2.2		

1.12c Dry matter KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	7490.4			
Block	2	2934.1			
Genotype	67	3998.4	59.7	9.5	<0.0001
Error	89	557.9	6.3		

1.13a Protein combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	8778.6			
Block	2	2766.2			
Site	1	620.5	620.5	927.6578	<0.0001
Genotype	67	2283.1	34.07612	50.94436	<0.0001
Site*Genotype	67	2928.2	43.70448	65.33892	<0.0001
Error	270	180.6	0.668889		

1.13b Protein ATC Miyare

Source	DF	SS	Mean	F value	P value

			square		
Total	158	9669.4			
Block	2	5368.5			
Genotype	67	4029.3	60.1	19.7	<0.0001
Error	89	271.6	3.1		

1.13c Protein KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	8969.4			
Block	2	4369.7			
Genotype	67	4121.4	61.5	11.4	<0.0001
Error	89	478.3	5.4		

1.14a Total carotenoids combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	9012.3			
Block	2	2301.1			
Site	1	555.4	555.4	205.7602	<0.0001
Genotype	67	2081.4	31.06567	11.50896	<0.0001
Site*Genotype	67	3345.6	49.93433	18.49927	<0.0001
Error	270	728.8	2.699259		

1.14b Total carotenoids ATC Miyare

Source	DF	SS	Mean square	F value	P value
Total	158	27734.7			
Block	2	8419.9			
Genotype	67	17294.6	258.1	11.4	<0.0001
Error	89	2020.2	22.7		

1.14c Total carotenoids KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	23837.8			
Block	2	7819.3			
Genotype	67	15293.4	228.3	28.0	<0.0001
Error	89	725.1	8.1		

1.15a Sucrose combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	38215.1			

Block	2	5234.6			
Site	1	2134.6	2134.6	109.0545	<0.0001
Genotype	67	11215.4	167.394	8.551985	<0.0001
Site*Genotype	67	14345.6	214.1134	10.93883	<0.0001
Error	270	5284.9	19.5737		

1.15b Sucrose ATC Miyare

Source	DF	SS	Mean square	F value	P value
Total	158	32127.4			
Block	2	6328.2			
Genotype	67	23203.4	346.3	11.9	<0.0001
Error	89	2595.8	29.2		

1.15c Sucrose KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	31127.7			
Block	2	6329.5			
Genotype	67	23211.2	346.4	19.4	<0.0001
Error	89	1587.0	17.8		

1.16a Total starch combined sites

Source	DF	SS	Mean square	F value	P value
Total	407	32216.4			
Block	2	5039.3			
Site	1	2035.8	2035.8	14240.05	<0.0001
Genotype	67	11002.6	164.2179	1148.675	<0.0001
Site*Genotype	67	14100.1	210.4493	1472.054	<0.0001
Error	270	38.6	0.142963		

1.16b Total starch ATC Miyare

Source	DF	SS	Mean square	F value	P value
Total	158	37291.8			
Block	2	7568.9			
Genotype	67	28241.2	421.5	25.3	<0.0001
Error	89	1481.7	16.6		

1.16c Total starch KALRO EMBU

Source	DF	SS	Mean square	F value	P value
Total	158	38282.3			

Block	2	7268.8			
Genotype	67	28245.8	421.6	13.6	<0.0001
Error	89	2767.7	31.1		

1.17a Average number of *C. puncticollis* adults on sweet potato genotypes 42 days after set up

Source	DF	SS	Mean square	F value	P value
Total	152	5289.7			
Genotype	50	4756.9	95.1	18.2	<0.0001
Error	102	532.8	5.2		

1.17b Average number of *C. puncticollis* larvae on sweet potato genotypes 42 days after set up

Source	DF	SS	Mean square	F value	P value
Total	152	4523.6			
Variety	50	3184.2	63.7	4.8	<0.0001
Error	102	1339.4	13.1		

1.17c Average number of *C. puncticollis* external root damage on sweet potato genotypes 42 days after set up

Source	DF	SS	Mean square	F value	P value
Total	152	16.0			
Genotype	50	5.9	0.1	1.2	<0.0001
Error	102	10.1	0.1		

Appendix 3: Some attributes of common sweet potato genotypes in Kenya

Variety	Origin	Improved variety/Famer variety	Storage root flesh colour	Maturity time	Adaptation	Resistance to weevils	Taste type	Source of information.
Mugande	Rwanda	Modern variety	White	-	Mid and upper midland zone	-	Dry and starchy	Gruneberg *et al*., 2015
SPK 004	Kenya	Farmer variety	Light orange	Early maturing	Mid and upper midland zone	-	Dry and starchy	Gruneberg *et al*., 2015; Kivuva *et al*., 2015
Mwavuli	Kenya	Farmer variety	White	-	Mid and upper midland zone	-	Dry and starchy	Gruneberg *et al*., 2015
Bungoma	Kenya	Farmer variety	Yellow	Late maturing	Mid and upper midland zone	Susceptible to weevils	Dry and starchy	Gruneberg *et al*., 2015; Kivuva *et al*., 2015
K 117	Kenya	Farmer variety	Orange	-	Mid and upper midland zone	-	Dry and starchy	Gruneberg *et al*., 2015
Kenspot 1	Kenya	Modern variety	Yellow	Late maturing	Highland adaptaion	Moderate resistance	High dry matter	Gruneberg *et al*., 2015
Kenspot 2	Kenya	Modern variety	White	Late maturing	Highland adaptaion	Moderate resistance	Medium dry matter	Gruneberg *et al*., 2015
Kenspot 3	Kenya	Modern variety	Light Orange	Late maturing	Highland adaptaion	Moderate resistance	Dry and starchy	Gruneberg *et al*., 2015
Kenspot 4	Kenya	Modern variety	Orange	Late maturing	Highland adaptaion	Moderate resistance	Moderately dry and starchy	Gruneberg *et al*., 2015
Kenspot 5	Kenya	Modern variety	Orange	Late maturing	Highland adaptaion	Moderate resistance	Moderately dry and starchy	Gruneberg *et al*., 2015
New kawogo	Uganda	Farmer variety	White	Late maturing	Tall grassland savanna	Moderate resistance	Dry and starchy	Gruneberg *et al*., 2015
Kuny kibuonjo	Kenya	Farmer variety	White	-	-	Moderate resistance	-	Kivuva *et al*, 2015
Kemb 10	Kenya	Modern variety	Yellow	Medium maturing	Wide adaptation	Susceptible to weevils	Dry and starchy	Gruneberg *et al*., 2015; Kivuva *et al*, 2015
Vitaa	Kenya	Modern variety	Orange	-	Mid and upper midland zone	Susceptible to weevils	Dry and starchy	Gruneberg *et al*., 2015; Kivuva *et al*; 2015
SPK 031	Kenya	Modern variety	Light orange	Early maturing	-	Susceptible to weevils	-	Kivuva *et al*, 2015
Ejumula	Uganda	Farmer variety	Orange	-	Tall grassland savanna	Susceptible to weevils	Dry and starchy	Gruneberg *et al*., 2015
Naspot 1	Uganda	Modern variety	Pale yellow	Medium maturing	Wide adaptability	Susceptible to weevils	Dry and starchy	Gruneberg *et al*., 2015

Appendix 4*:* Field experimental layout in a Randomized Complete Block Design

Plot No.	Replication 1	Replication 2	Replication 3
1	Nyautenge	Kenspot 1	Kuny kibuonjo
2	SPK 013	Mbita	Mwavuli
3	Naspot 1	Mugande	Kenspot 3
4	Fundukusia	Kenspot 2	Naspot 1
5	24 Kampala	Kenspot 4	K 117
6	Saly boro	56682-03	Kemb 10
7	Lungabure	Fundukusia	Amina
8	Sinia	Wera	Polo yiengo
9	Gachaka	292-H-12	Kenspot 5
10	Karunde	Karunde	SPK 004
11	Odinga	Tainung	Nyawo Nyathiodiewo
12	292-H-12	62 Odhiogo	Mogesi Gikenja
13	Oduogo Jodongo	Ejumula	Fumbara jikoni
14	Alupe or	9 Nduma	Nyamuguta
15	K 117	SPK 031	1-Ujili
16	Santo Amaro	24 Kampala	36 Kalamb Nyerere
17	Kenspot 3	Sinia	56682-03
18	Mbita	Odinga	Karunde
19	Kenspot 5	Kenspot 5	Nyakagwa
20	12 Marooko	Mwavuli	K/KA/2002/12
21	Kenspot 1	Kuny kibuonjo	Nyautenge
22	Nangili	Nyawo Nyathiodiewo	Santo Amaro
23	Nyamuguta	K/KA/2002/12	SPK 013
24	Tainung	Nyautenge	5 Nyandere
25	36 Kalmb Nyerere	29 Kuny kibuonjo	Alupe or
26	K/KA/2004/215	Nyakagwa	Nangili
27	1-Ujili	Santo Amaro	Wera
28	Kuny kibuonjo	SPK 004	Odinga
29	Nyakagwa	Nyamuguta	Sinia
30	Mwavuli	Mogesi Gikenja	Oduogo jodongo
31	5 Nyandere	Naspot 1	Bungoma
32	K/KA/2002/12	Gachaka	Kenspot 2
33	62 Odhiogo	Kenspot 3	24 Kampala
34	Kenspot 4	K 117	62 Odhiogo
35	Kenspot 2	12 Marooko	Fundukusia
36	Amina	5 Nyandere	Kenspot 4
37	91/2187	Vitaa	29 Kuny kibuonjo
38	Polo yiengo	Fumbara jikoni	12 Marooko
39	Nyawo Nyathiodiewo	SPK 013	91/2187
40	Kemb 10	Alupe or	Saly boro
41	SPK 004	Nangili	Obugi
42	Obugi	K/KA/2004/215	Kenspot 1
43	9 Nduma	36 Kalmb Nyerere	Lungabure
44	Mogesi Gikenja	91/2187	Mbita
45	Mugande	Obugi	Ejumula
46	Ejumula	Polo yiengo	52 Nyakisumu
47	Fumbara jikoni	Bungoma	Mugande
48	SPK 031	Saly boro	SPK 031
49	56682-03	Oduogo jodongo	9 Nduma
50	Wera	Lungabure	Gachaka
51	Vitaa	1-Ujili	K/KA/2004/215
52	52 Nyakisumu	Amina	Vitaa
53	29 Kuny kibuonjo	Kemb 10	Tainung
54	Bungoma	52 Nyakisumu	292-H-12

Appendix 5*:* Association between qualitative characters (latex production and oxidation) and sum of emerged weevils

5.1. Obseved frequencies

S/N	Resistance level	Amount of latex or oxidation observed	Latex production	Oxidation	Total
			Observed	Observed	
1	Susceptible	Little	6	4	**10**
2	Susceptible	Some	8	10	**18**
3	Susceptible	Abundant	2	2	**4**
4	Most susceptible	Little	1	4	**5**
5	Most susceptible	Very little	0	1	**1**
6	Most susceptible	Some	5	1	**6**
7	Most susceptible	Abundant	2	2	**4**
8	Tolerant	Little	4	2	**6**
9	Tolerant	Some	4	5	**9**
10	Tolerant	Abundant	2	2	**4**
11	Tolerant	Very little	0	1	**1**
12	Medium tolerant	Little	6	4	**10**
13	Medium tolerant	Some	8	9	**17**
14	Medium tolerant	Abundant	1	2	**3**
15	Most tolerant	Some	2	2	**4**
Total			**51**	**51**	**102**

5.2. Expected frequencies

S/N	Resistance level	Amount of latex or oxidation observed	Latex production	Oxidation
			Expected	Expected
1	Susceptible	Little	5	5
2	Susceptible	Some	9	9
3	Susceptible	Abundant	2	2
4	Most susceptible	Little	2.5	2.5
5	Most susceptible	Very little	.5	.5
6	Most susceptible	Some	3	3
7	Most susceptible	Abundant	2	2
8	Tolerant	Little	3	3
9	Tolerant	Some	4.5	4.5
10	Tolerant	Abundant	2	2
11	Tolerant	Very little	.5	.5
12	Medium tolerant	Little	5	5
13	Medium tolerant	Some	8.5	8.5
14	Medium tolerant	Abundant	1.5	1.5
15	Most tolerant	Some	2	2

Chi-distribution [$\chi^2_{(0.05)}$] was recorded at (number of rows – 1) (number of columns – 1) degrees of freedom = 14

$$\chi^2 = \sum \frac{(O-E)^2}{E}$$

Where: χ^2 = Calculated Chi-squared

O = Observed frequencies

E = Expected frequencies

Appendix 6: Number of Adult *C. puncticollis* emerging from different genotypes on a daily basis

Genotype	Average number		Average of three replications (Number of adults) per day									
	Female	Male										
	13th day	13th day	24th day	25th day	26th day	27th day	28th day	29th day	30th day	31st day	32nd day	33rd day
Kenspot 1	2.89ab	2.89bc	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.67ij	0.67ijkl	0.44hij
Sally boro	2.89ab	2.78bc	0.00d	0.00e	0.67cd	0.33abc	0.89abc	0.22cde	1.11cdef	1.00ghij	1.67abcd	0.78fgh
91/2187	2.89ab	2.89bc	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.89hij	0.67ijkl	0.67ghi
5 Nyandere	2.78 ab	2.67c	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.00l	0.00m	0.00j
Odinga	3.00a	3.00b	0.00d	0.00e	0.67cd	0.11cd	1.00ab	0.56b	1.11cdef	1.78abcd	1.55abcde	1.67abc
Naspot 1	3.00a	3.00b	0.33ab	0.33bc	0.78bc	0.56a	1.11a	0.45bc	1.89ab	1.67abcde	1.78abc	1.22cdefg
Kenspot 3	3.00a	3.00b	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.00l	0.00m	0.00j
Nyamuguta	2.78 ab	3.00b	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.56jk	0.56jkl	0.67ghi
Nyautenge	2.89ab	2.78bc	0.00d	0.00e	0.00e	0.00d	0.56de	0.00e	0.44gh	1.44cdefg	0.78hijk	1.11cdefg
Nyakagwa	2.89ab	2.89bc	0.00d	0.00e	0.67cd	0.11cd	0.89abc	0.33bcd	1.11cdef	1.55bcdef	1.22defgh	1.11cdefg
Nangili	2.78 ab	2.78bc	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.22h	0.89hij	1.00fghij	0.67ghi
Kenspot 2	3.00a	2.78bc	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.11kl	0.44klm	0.67ghi
SPK 013	3.00a	3.00b	0.44a	0.33bc	0.89ab	0.33abc	1.00ab	0.33bcd	0.78fg	1.56bcdef	2.00a	1.11cdefg
K/KA/2004/215	3.00a	3.00b	0.22bc	0.22cd	1.00a	0.33abc	1.00ab	0.56b	1.56abc	1.67abcde	1.67abcd	1.22cdefg
Alupe or	2.89ab	3.00b	0.00d	0.00e	0.78bc	0.22bcd	1.00ab	0.56b	1.44bcd	1.89abc	1.78abc	1.67abc
12 Marooko	2.89ab	3.00b	0.00d	0.00e	0.00e	0.00d	0.78bcd	0.33bcd	1.00def	1.55bcdef	1.34cdefg	1.11cdefg
Kenspot 5	2.67 b	2.78bc	0.00d	0.00e	0.00e	0.00d	0.56de	0.00e	0.44gh	0.67ij	1.22defgh	1.34bcdef
36 Kalamb Nyerere	2.78 ab	3.00b	0.00d	0.00e	0.00e	0.00d	0.56de	0.00e	0.89efg	1.22efgh	1.00fghij	1.45bcde
292-H-12	3.00a	3.00b	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.00l	0.00m	0.00j
Mogesi Gikenja	2.78 ab	3.33a	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.00l	0.00m	0.00j
Lungabure	2.89ab	3.00b	0.00d	0.00e	0.00e	0.00d	0.44e	0.00e	0.78fg	1.00ghij	1.44bcdef	1.11cdefg
Kenspot 4	2.89ab	2.89bc	0.00d	0.00e	0.00e	0.00d	0.56de	0.00e	0.78fg	1.00ghij	1.22defgh	1.34bcdef
Vitaa	3.00a	3.00b	0.11cd	0.44ab	1.00a	0.56a	0.89abc	0.44bc	1.33cde	1.67abcde	1.67abcd	0.89efgh

9 Nduma	2.78 ab	2.78bc	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.00l	0.00m	0.00j
24 Kampala	2.89ab	3.00b	0.00d	0.00e	0.00e	0.00d	0.44e	0.22cde	1.00def	0.89hij	1.33cdefg	1.00defgh
Obugi	2.89ab	2.89bc	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.00l	0.00m	0.00j
56682-03	2.89ab	3.00b	0.00d	0.00e	0.67cd	0.11cd	0.78bcd	0.33bcd	1.00def	1.11fghi	1.33cdefg	1.22cdefg
NyawoNyathiodiewo	3.00a	3.00b	0.00d	0.00e	0.56d	0.22bcd	1.00ab	0.22cde	1.11cdef	1.56bcdef	1.33cdefg	1.56abcd
Gachaka	3.00a	3.00b	0.00d	0.00e	0.00e	0.11cd	0.56de	0.11de	0.78fg	1.22efgh	1.33cdefg	1.44bcde
Mugande	3.00a	3.00b	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.00l	0.22lm	0.00j
Amina	2.89ab	2.67c	0.00d	0.00e	0.00e	0.00d	0.56de	0.00e	0.89efg	0.67ij	1.22defgh	1.00defgh
Fumbara jikoni	3.00a	2.89bc	0.00d	0.00e	0.67cd	0.00d	0.78bcd	0.33bcd	1.00def	1.44cdefg	1.33cdefg	1.56abcd
Karunde	2.89ab	2.89bc	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	1.00ghij	1.44bcdef	0.67ghi
SPK 004	3.00a	3.00b	0.33ab	0.33bc	0.78bc	0.22bcd	0.89abc	0.45bc	1.11cdef	1.34defgh	1.44bcdef	1.55abcd
Kuny kibuonjo	3.00a	2.78bc	0.22bc	0.11de	0.78bc	0.00d	1.00ab	0.56b	1.44bcd	1.44cdefg	1.33cdefg	1.00defgh
1-Ujili	2.89ab	3.00b	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.00l	0.00m	0.11ij
Santo Amaro	2.89ab	3.00b	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.00l	0.00m	0.00j
Wera	2.78 ab	2.78bc	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.00l	0.00m	0.00j
Kemb 10	2.89ab	3.00b	0.00d	0.00e	0.78bc	0.33abc	0.89abc	0.00e	1.00def	1.45cdefg	1.33cdefg	1.34bcdef
Mbita	2.89ab	2.89bc	0.00d	0.00e	0.56d	0.11cd	0.56de	0.33bcd	0.89efg	1.22efgh	1.56abcde	1.11cdefg
29 Kuny kibuonjo	2.78 ab	2.78bc	0.00d	0.00e	0.00e	0.00d	0.00f	0.11de	0.22h	1.33defgh	1.11efghi	1.22cdefg
62 Odhiogo	2.89ab	3.00b	0.00d	0.00e	0.67cd	0.22bcd	0.89abc	0.22cde	1.33cde	2.00ab	2.00a	2.11a
52 Nyakisumu	3.00a	2.89bc	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.11h	1.00ghij	0.56jkl	1.00defgh
Bungoma	3.00a	3.00b	0.00d	0.00e	0.00e	0.00d	0.00f	0.00e	0.00h	0.00l	0.00m	0.00j
K 117	2.78 ab	2.89bc	0.00d	0.00e	0.56d	0.22bcd	0.89abc	0.33bcd	1.33cde	1.33defgh	1.67abcd	1.44bcde
Fundukhusia	3.00a	3.00b	0.22bc	0.00e	0.56d	0.33abc	1.00ab	0.22cde	1.45bcd	2.11a	1.89ab	1.34bcdef
SPK 031	3.00a	3.00b	0.22bc	0.33bc	0.78bc	0.44ab	1.00ab	0.33bcd	1.22cdef	1.56bcdef	1.11efghi	1.44bcde
Mwavuli	2.78 ab	2.89bc	0.00d	0.00e	0.56d	0.00d	0.78bcd	0.33bcd	1.11cdef	0.89hij	1.22defgh	1.00defgh
Polo yiengo	3.00a	3.00b	0.00d	0.00e	0.78bc	0.33abc	0.78bcd	0.44bc	1.33cde	1.78abcd	1.11efghi	1.89ab
Sinia	2.89ab	2.89bc	0.00d	0.00e	0.00e	0.11cd	0.67cde	0.22cde	1.22cdef	1.33defgh	0.89ghijk	1.45bcde
Tainung	3.00a	3.00b	0.45a	0.55a	0.67cd	0.33abc	1.11a	0.89a	2.00a	1.66abcde	1.89ab	1.55abcd

Mean	2.91	2.93	0.05	0.06	0.31	0.11	0.51	0.19	0.71	1.00	1.03	0.95
LSD (0.05)	0.25	0.27	0.18	0.19	0.20	0.29	0.22	0.32	0.46	0.46	0.53	0.57
CV	5.26	5.65	22.26	20.83	21.62	16.67	27.45	10.34	29.57	28.24	21.68	27.38
P value	0.46	0.06	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001

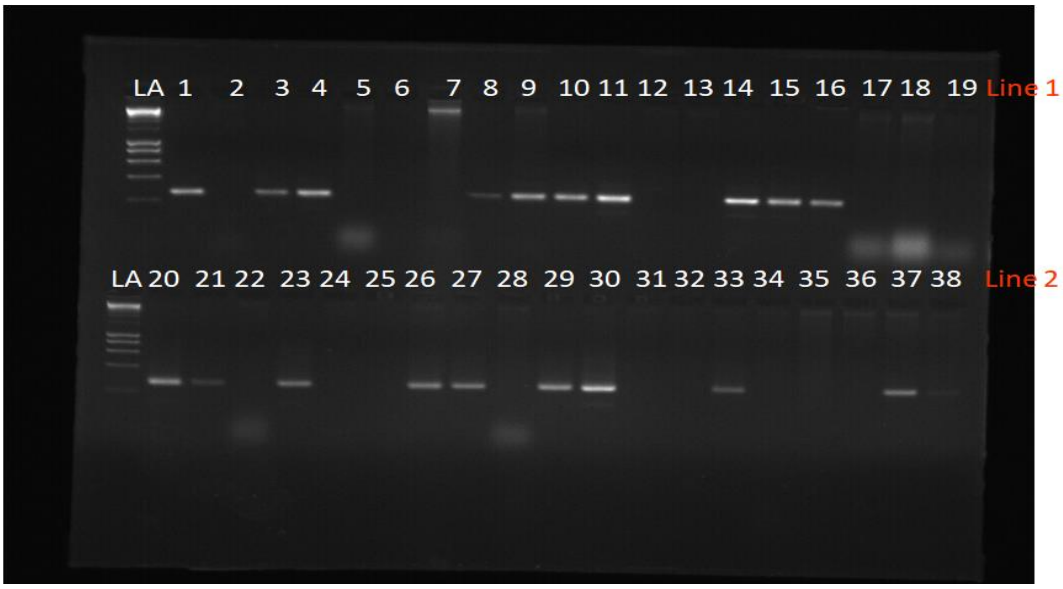
Continuation of number of adults emerging from different genotypes on a daily basis

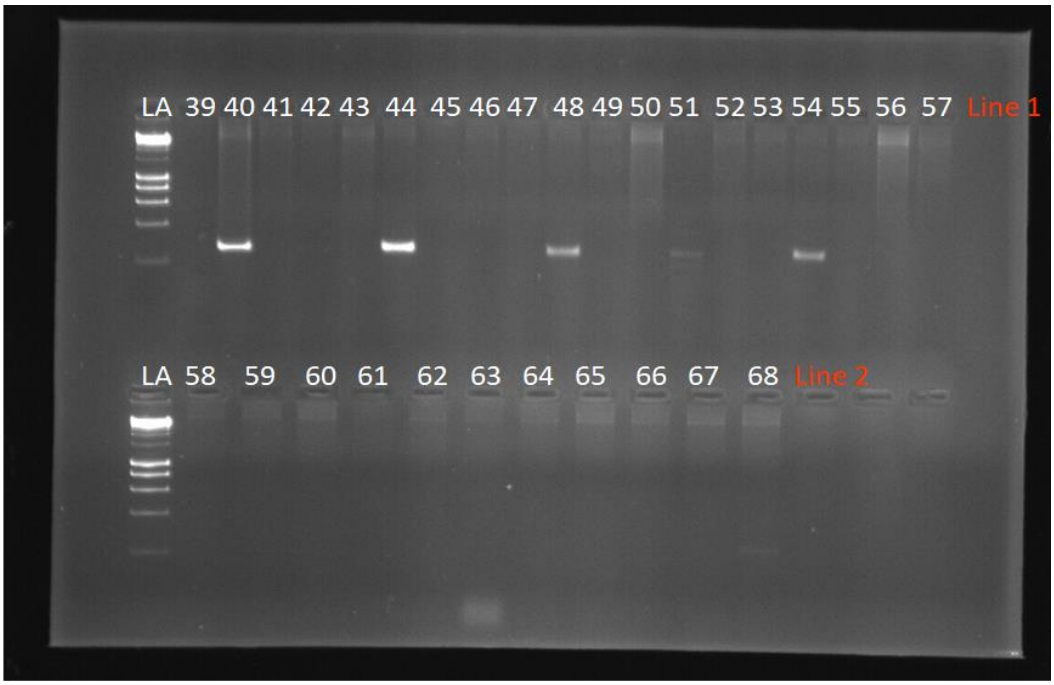
Genotype	**Average of three replications (Number of adults) per day**								
	34th day	**35th day**	**36th day**	**37th day**	**38th day**	**39th day**	**40th day**	**41st day**	**42nd day**
Kenspot 1	1.33defgh	1.11efgh	1.11defghi	1.33abcdef	0.22j	1.22abcde	1.22abcde	0.67fghijk	1.22abcde
Sally boro	1.78abcd	1.44cdef	1.44bcdef	1.33abcdef	0.89defghij	1.44abc	1.00cdef	1.22abcdefg	1.11abcdef
91/2187	1.22efghi	1.11efgh	1.00efghi	0.89defgh	0.89defghij	0.33f	1.34abcde	0.78efghijk	1.11abcdef
5 Nyandere	0.11mn	0.89fghij	0.67hij	0.45h	0.33ij	0.33f	1.00cdef	0.89cdefghij	0.56ef
Odinga	1.33defgh	1.34defg	1.56bcde	1.44abcde	1.33abcdef	1.00bcde	1.33abcde	0.89cdefghij	1.11abcdef
Naspot 1	2.11a	2.33a	1.78bc	1.56abcd	1.78ab	1.56ab	1.00cdef	1.22abcdefg	0.67def
Kenspot 3	0.11mn	0.45ijk	0.78ghij	0.89defgh	1.00cdefghi	1.22abcde	1.11bcde	1.56abc	0.56ef
Nyamuguta	1.11fghi	1.11efgh	1.11defghi	0.89defgh	0.89defghij	0.67ef	0.89def	0.78efghijk	1.66a
Nyautenge	0.78ijkl	1.22defgh	0.89fghij	1.00cdefgh	1.22abcdefg	1.44abc	0.44f	0.33jk	0.67def
Nyakagwa	1.67abcde	1.33defg	1.11defghi	1.67abc	1.22abcdefg	1.33abcd	1.33abcde	1.00cdefghij	1.11abcdef
Nangili	1.67abcde	1.11efgh	1.45bcdef	1.00cdefgh	0.67fghij	0.89cdef	0.89def	0.55hijk	1.33 abcd
Kenspot 2	0.44klmn	1.11efgh	0.89fghij	1.11bcdefgh	0.67fghij	0.78def	1.00cdef	0.89cdefghij	0.89bcdef
SPK 013	1.33defgh	1.22defgh	1.52bcde	1.89a	1.56abcd	1.44abc	1.55abc	0.89cdefghij	1.11abcdef
K/KA/2r004/215	1.44cdefg	0.78ghij	2.45a	1.67abc	1.67abc	1.00bcde	1.22abcde	0.89cdefghij	1.00abcdef
Alupe or	1.78abcd	1.22defgh	1.67bcd	1.89a	1.11bcdefgh	1.56ab	0.78ef	1.22abcdefg	0.89bcdef
12 Marooko	1.67abcde	1.22defgh	0.89fghij	1.45abcde	1.22abcdefg	1.33abcd	1.22abcde	1.22abcdefg	1.00abcdef
Kenspot 5	1.00ghij	1.00efghi	1.22cdefgh	0.78efgh	1.22abcdefg	0.89cdef	1.22abcde	0.44ijk	0.89bcdef
36 Kalamb Nyerere	1.11fghi	1.45cdef	0.67hij	1.33abcdef	1.00cdefghi	1.11bcde	1.00cdef	0.89cdefghij	0.44f
292-H-12	0.11mn	0.00k	0.78ghij	0.45h	1.00cdefghi	0.78def	1.44abcd	1.44abcde	0.67def

Mogesi Gikenja	0.00n	0.33jk	0.33j	0.67fgh	0.44hij	0.67ef	1.00cdef	0.67fghijk	1.44abc
Lungabure	1.33defgh	1.00efghi	1.33bcdefg	1.22abcdefg	1.33abcdef	0.67ef	1.11bcde	1.33abcdef	1.22abcde
Kenspot 4	1.00ghij	0.89fghij	0.78ghij	1.22abcdefg	0.89defghij	1.22abcde	0.78ef	0.78efghijk	0.78cdef
Vitaa	1.89abc	1.11efgh	1.56bcde	1.67abc	1.78ab	1.44abc	1.78a	1.44abcde	1.22abcde
9 Nduma	0.00n	0.44ijk	0.78ghij	0.78efgh	1.11bcdefgh	0.89cdef	1.11bcde	1.00cdefghij	1.33 abcd
24 Kampala	1.00ghij	1.33defg	1.33bcdefg	1.22abcdefg	1.11bcdefgh	1.33abcd	0.89def	0.33jk	0.66def
Obugi	0.11mn	0.78ghij	0.56ij	0.78efgh	0.56ghij	0.67ef	0.78ef	0.56ghijk	0.67def
56682-03	1.11fghi	1.11efgh	1.34bcdefg	1.11bcdefgh	0.89defghij	1.55ab	1.11bcde	1.00cdefghij	1.00abcdef
Nyawo	1.55bcdef	1.44cdef	1.11defghi	1.11bcdefgh	1.67abc	1.11bcde	1.67ab	0.89cdefghij	1.00abcdef
Nyathiodiewo Gachaka	0.89hijk	0.89fghij	1.22cdefgh	1.22abcdefg	1.34abcdef	0.67ef	1.00cdef	1.00cdefghij	1.00abcdef
Mugande	0.33lmn	0.67hij	1.00efghi	0.55gh	0.67fghij	0.89cdef	1.22abcde	1.89a	0.67def
Amina	1.55bcdef	0.89fghij	1.00efghi	0.67fgh	0.89defghij	1.22abcde	1.11bcde	0.89cdefghij	0.89bcdef
Fumbara jikoni	1.22efghi	1.56bcde	1.11defghi	1.44abcde	1.11bcdefgh	1.22abcde	1.22abcde	1.33abcdef	1.00abcdef
Karunde	1.56bcdef	1.44cdef	0.89fghij	1.33abcdef	0.78efghij	0.89cdef	0.78ef	0.33jk	1.11abcdef
SPK 004	1.00ghij	1.33defg	1.44bcdef	1.33abcdef	1.22abcdefg	1.44abc	0.89def	1.00cdefghij	0.78cdef
Kuny kibuonjo	1.33defgh	1.33defg	1.67bcd	1.33abcdef	1.44abcde	1.45abc	1.44abcd	1.22abcdefg	0.44f
1-Ujili	0.56jklm	0.67hij	0.67hij	0.89defgh	0.78efghij	1.00bcde	1.00cdef	1.55abcd	0.44f
Santo Amaro	0.44klmn	0.78ghij	0.78ghij	0.78efgh	0.56ghij	1.22abcde	0.89def	1.22abcdefg	0.44f
Wera	0.00n	0.33jk	0.33j	0.78efgh	1.11bcdefgh	1.00bcde	1.22abcde	1.44abcde	1.33 abcd
Kemb 10	1.22efghi	1.33defg	1.22cdefgh	1.44abcde	1.11bcdefgh	1.11bcde	1.33abcde	1.11bcdefghi	0.44f
Mbita	1.45cdefg	0.89fghij	1.33bcdefg	1.33abcdef	0.89defghij	1.56ab	1.00cdef	1.11bcdefghi	0.89bcdef
29 Kuny kibuonjo	1.56bcdef	1.55bcde	1.33bcdefg	0.89defgh	0.78efghij	1.33abcd	1.56abc	0.22k	1.44abc
62 Odhiogo	1.66abcde	1.78abcd	1.33bcdefg	1.33abcdef	1.45abcde	0.78def	1.67ab	1.78ab	1.33 abcd
52 Nyakisumu	1.22efghi	1.33defg	1.11defghi	1.33abcdef	0.44hij	1.34abcd	0.89def	0.44ijk	1.56ab
Bungoma	0.45klmn	0.44ijk	0.67hij	0.67fgh	0.55ghij	0.67ef	1.11bcde	1.00cdefghij	0.89bcdef
K 117	1.78abcd	0.89fghij	1.56bcde	1.78ab	1.22abcdefg	1.44abc	1.22abcde	1.34abcde	1.00abcdef
Fundukhusia	1.56bcdef	2.11ab	1.33bcdefg	1.78ab	1.22abcdefg	1.78a	1.78a	1.67ab	0.67def
SPK 031	1.78abcd	1.33defg	1.78bc	1.55abcd	1.33abcdef	1.56ab	1.56abc	1.00cdefghij	1.11abcdef

Mwavuli	0.78ijkl	1.33defg	1.00efghi	1.22abcdefg	1.00cdefghi	0.89cdef	1.11bcde	0.78efghijk	0.67def
Polo yiengo	1.11fghi	1.56bcde	1.22cdefgh	1.34abcdef	1.22abcdefg	1.11bcde	1.56abc	1.00cdefghij	1.45abc
Sinia	1.11fghi	1.33defg	1.00efghi	1.11bcdefgh	1.67abc	0.89cdef	1.11bcde	1.33abcdef	0.78cdef
Tainung	2.11a	2.00abc	1.89ab	1.67abc	1.89a	1.55ab	0.89def	0.67fghijk	0.67def
Mean	1.12	1.13	1.16	1.19	1.07	1.12	1.15	1	0.95
LSD (0.05)	0.55	0.58	0.60	0.70	0.76	0.66	0.65	0.67	0.68
CV	20.21	21.8	22.26	16.54	13.97	16.44	14.86	11.17	24.14
P value	0.0001	0.0001	0.0001	0.001	0.001	0.001	0.04	0.0001	0.01

Appendix 7: *Electrophoresis of DNA amplified by 13 primers*

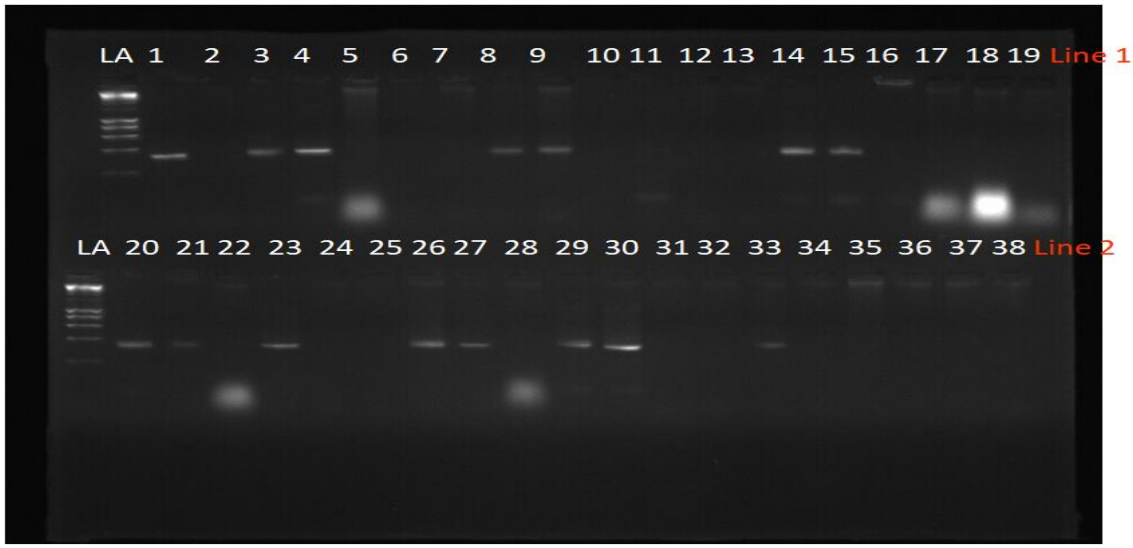




Electrophoresis of DNA Amplified by IBR03 Primer

Where:

LA = DNA Ladder 100 bp
Lines 1 to 68 = Sweet potato genotypes



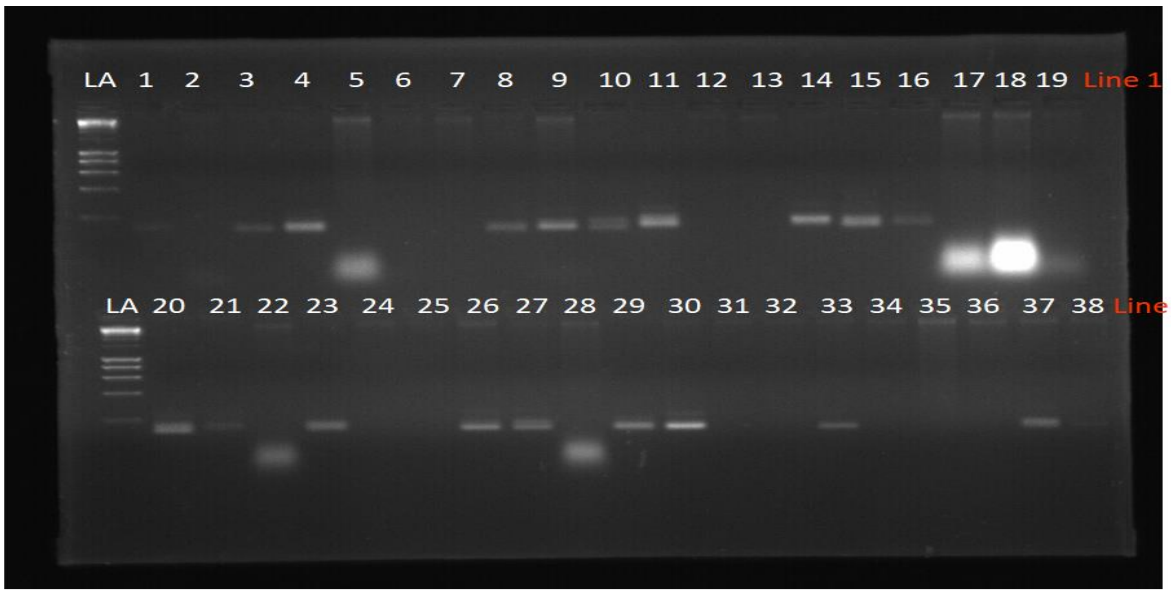
Electrophoresis of DNA Amplified by IBR12 Primer

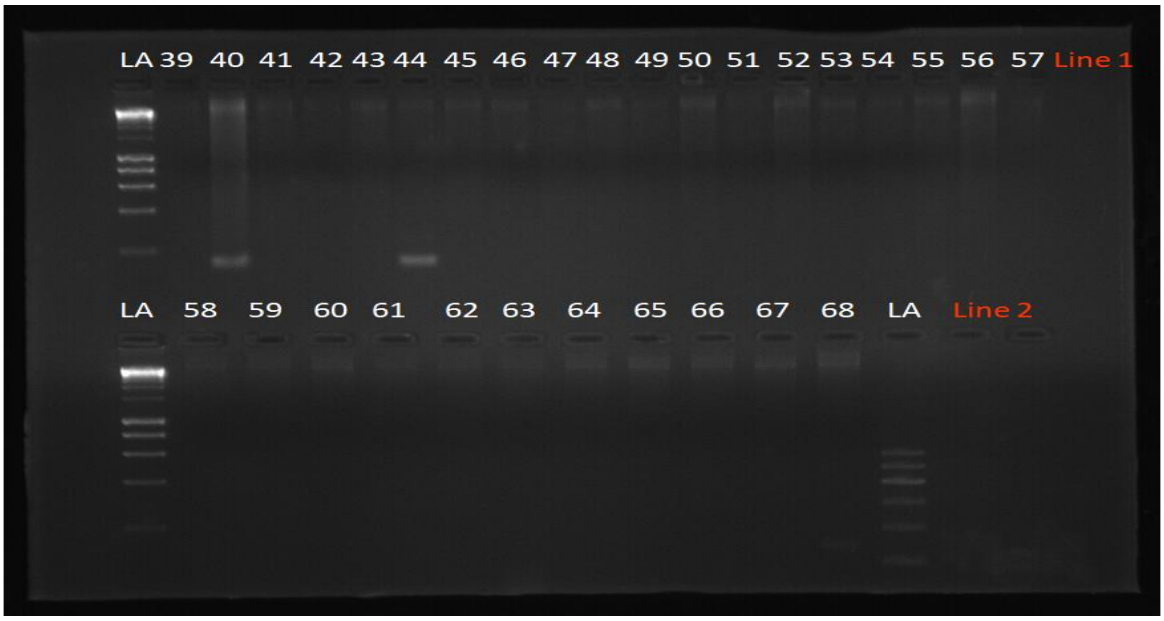
Where:
LA = DNA Ladder 100 bp

Lines 1 to 68 = Sweet potato genotypes

Electrophoresis of DNA Amplified by IB242 Primer

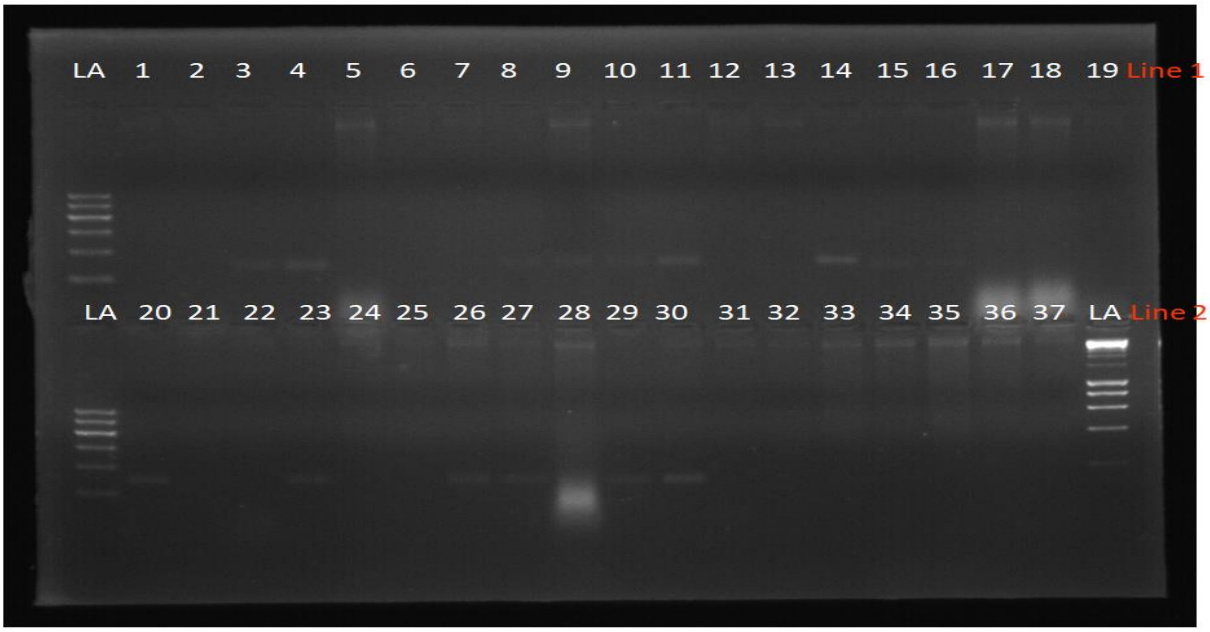
Where:
LA = DNA Ladder 100 bp
Lines 1 to 68 = Sweet potato genotypes

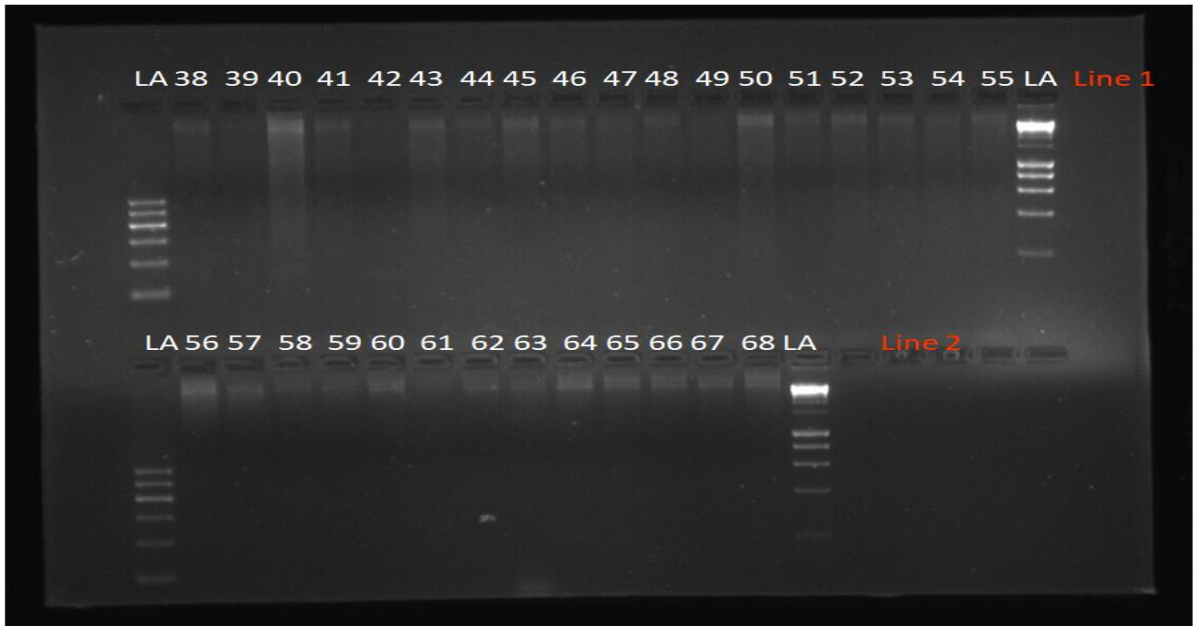




Electrophoresis of DNA Amplified by IB275 Primer

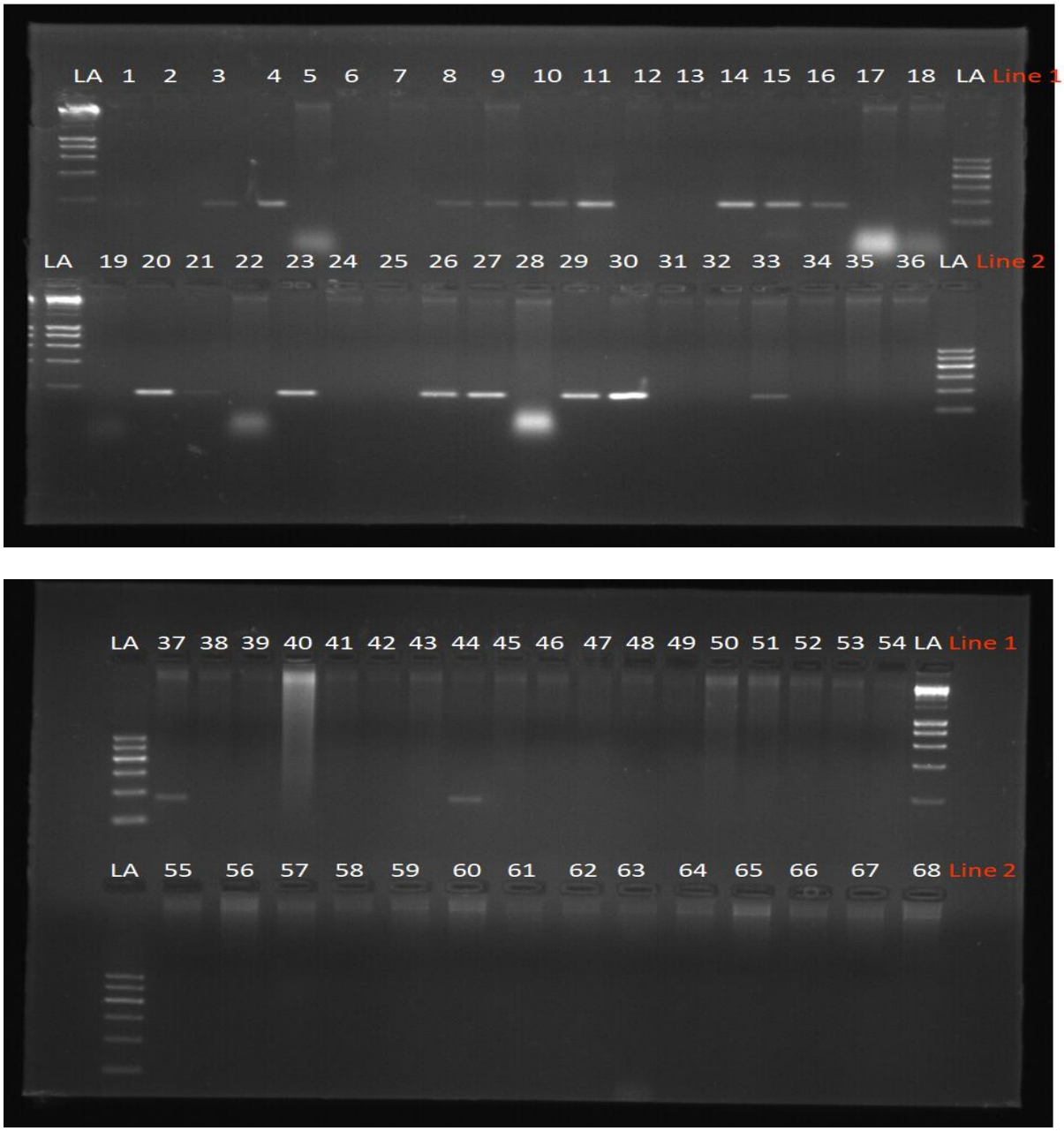
Where:
LA = DNA Ladder 100 bp
Lines 1 to 68 = Sweet potato genotypes





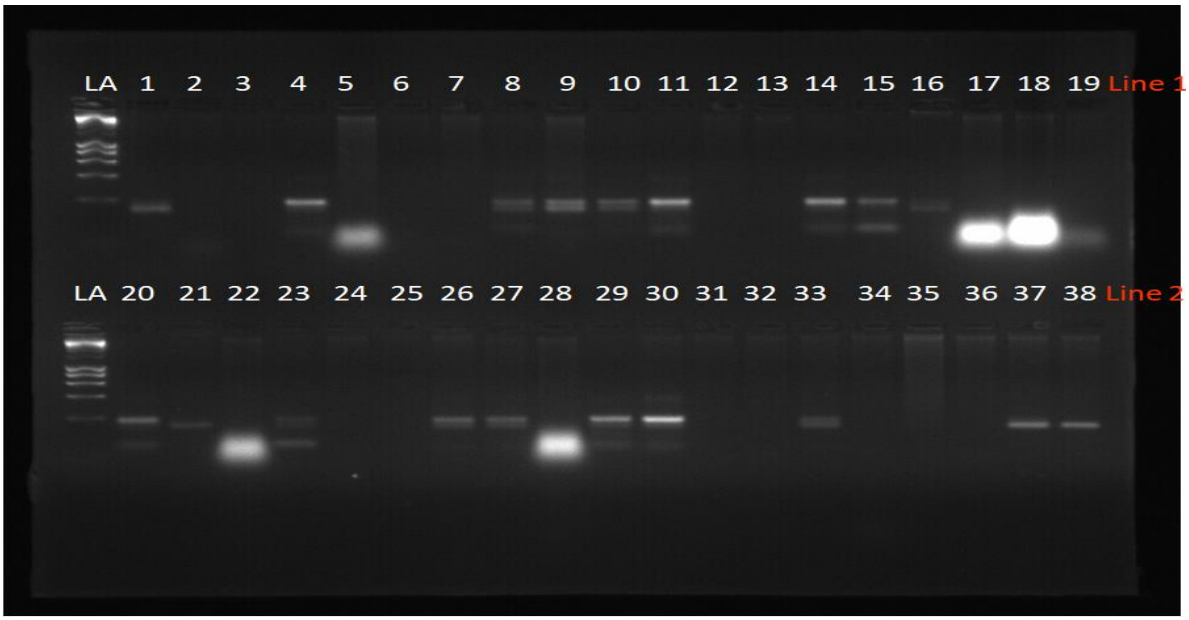
Electrophoresis of DNA Amplified by IB316 Primer

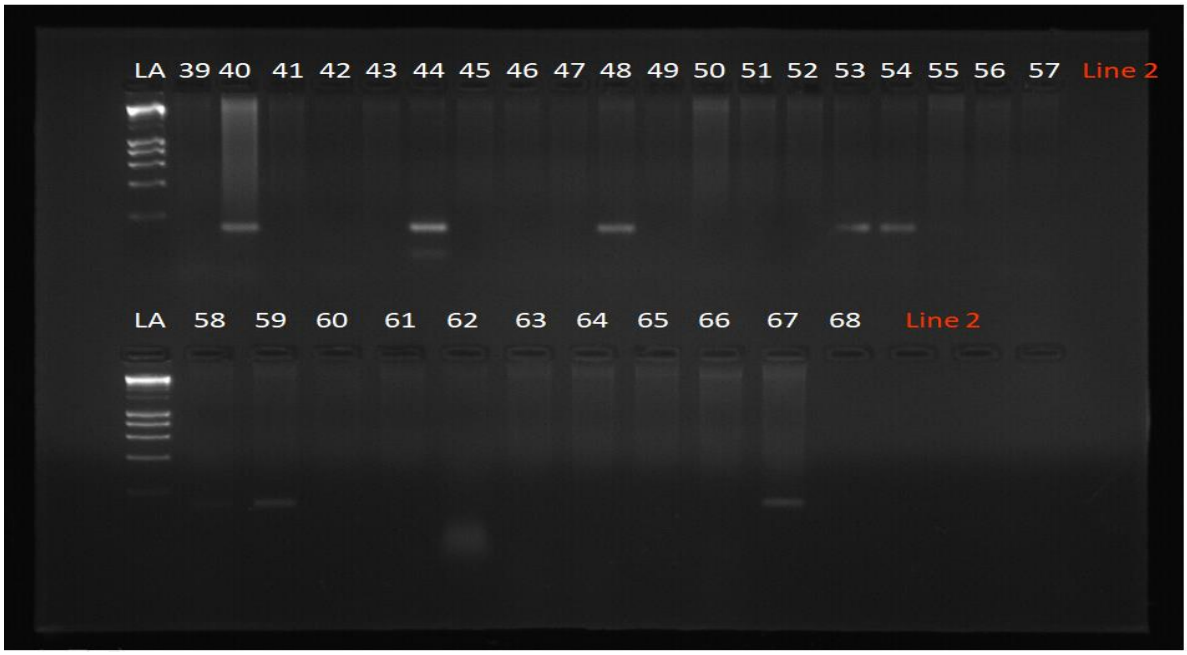
Where:
LA = DNA Ladder 100 bp
Lines 1 to 68 = Sweet potato genotypes



Electrophoresis of DNA Amplified by IB324 Primer

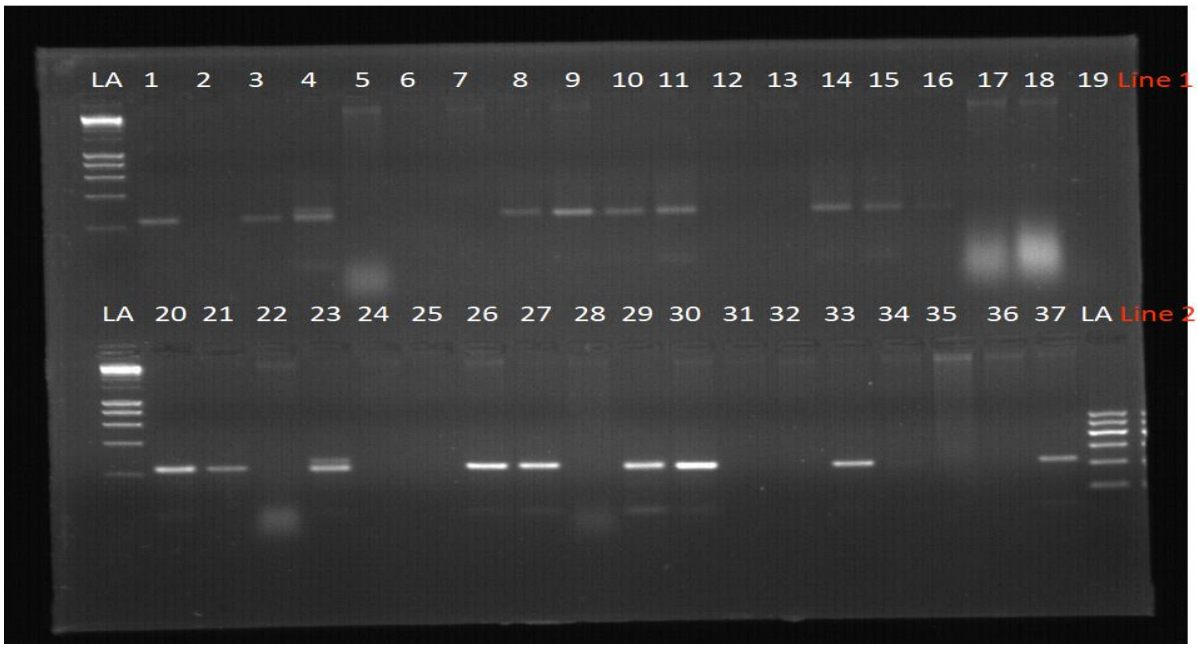
Where:
LA = DNA Ladder 100 bp
Lines 1 to 68 = Sweet potato genotypes

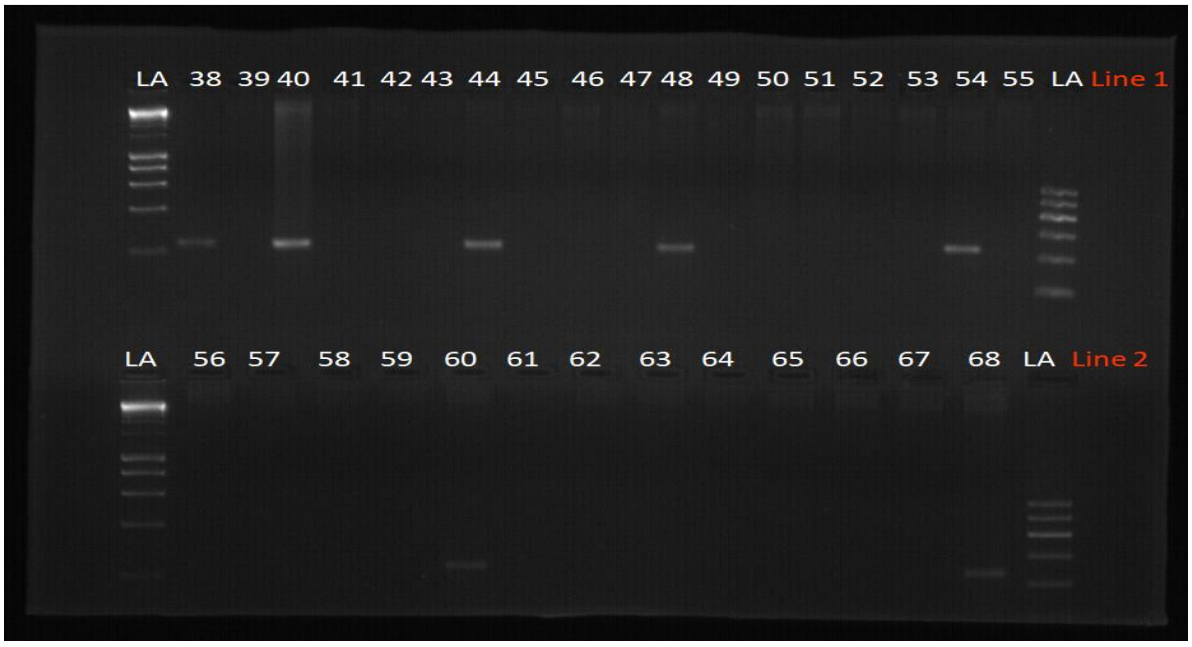




Electrophoresis of DNA Amplified by IBCIP Primer

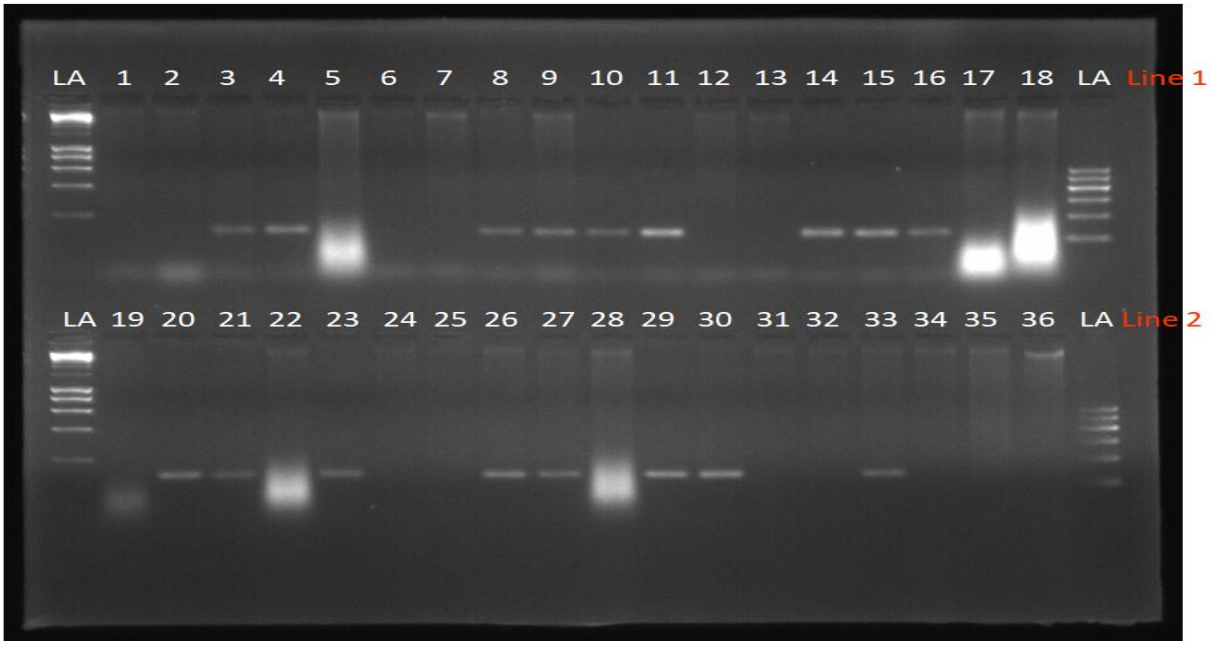
Where:
LA = DNA Ladder 100 bp
Lines 1 to 68 = Sweet potato genotypes

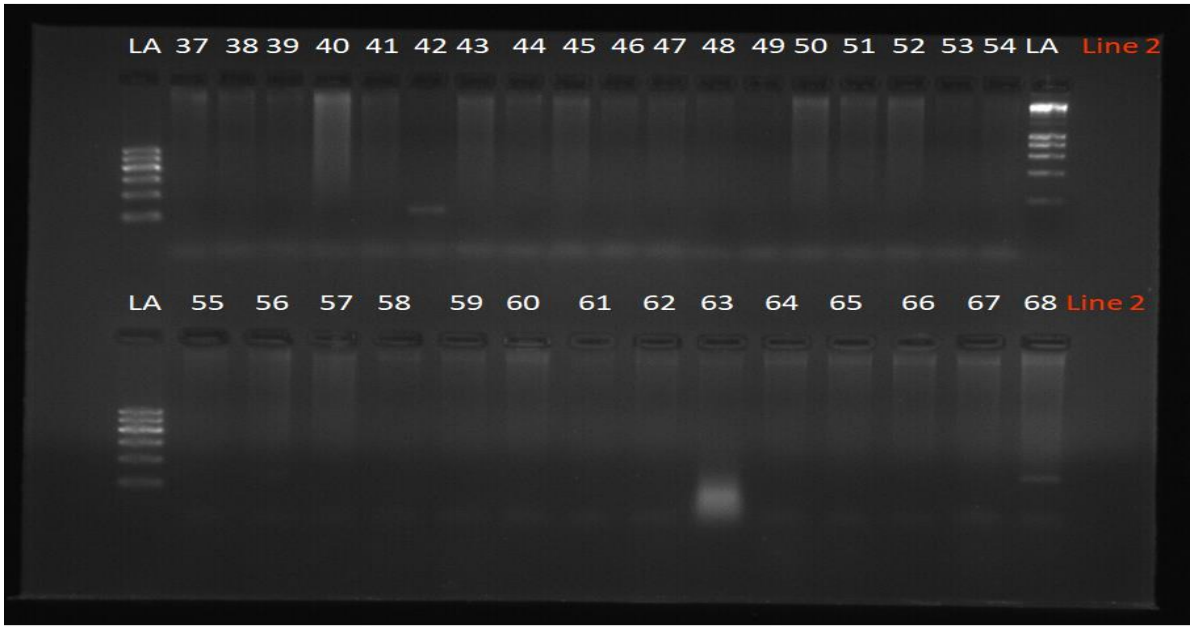




Electrophoresis of DNA Amplified by IBJ522 Primer

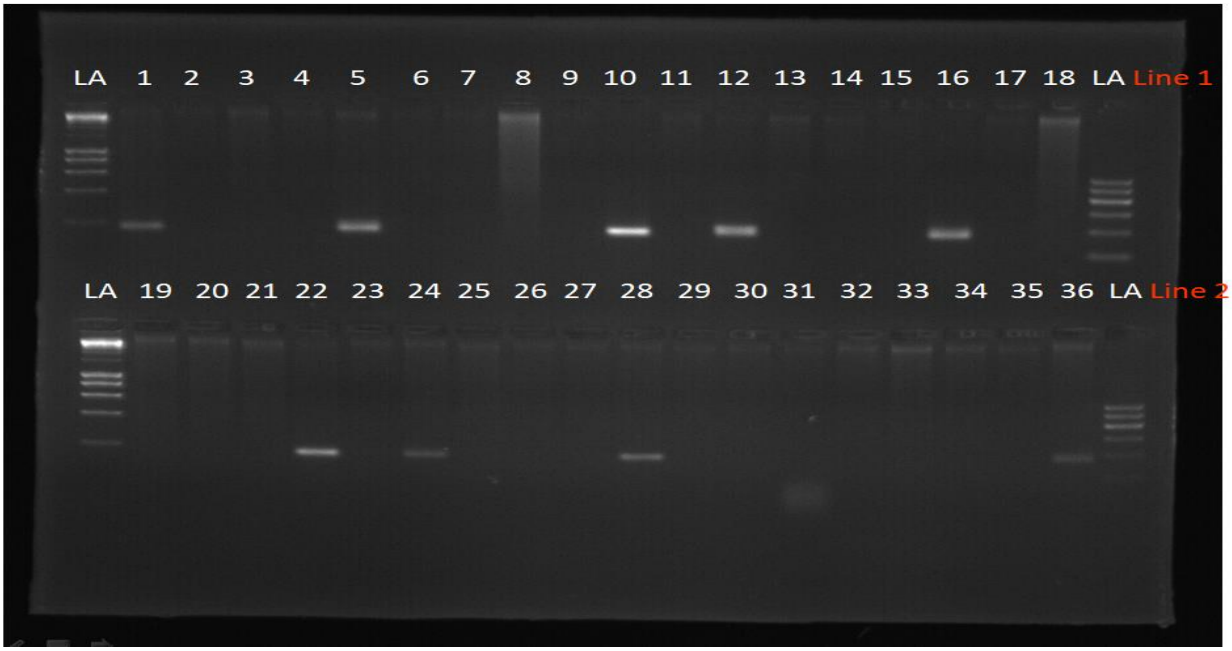
Where:
LA = DNA Ladder 100 bp
Lines 1 to 68 = Sweet potato genotypes

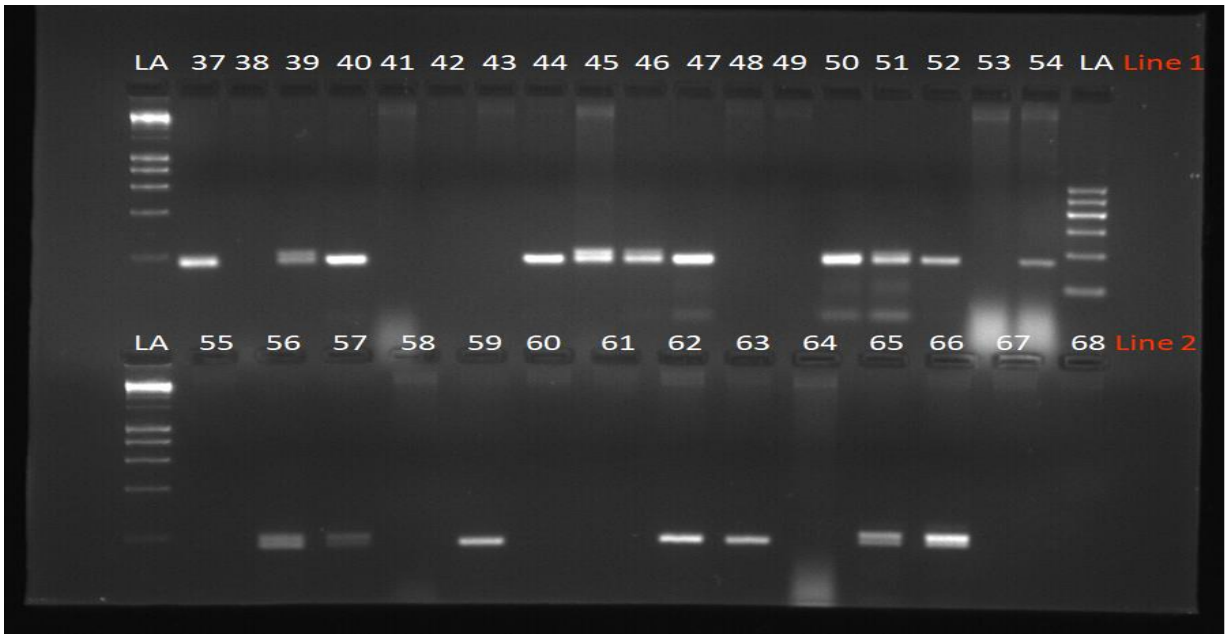




Electrophoresis of DNA Amplified by IBS07 Primer

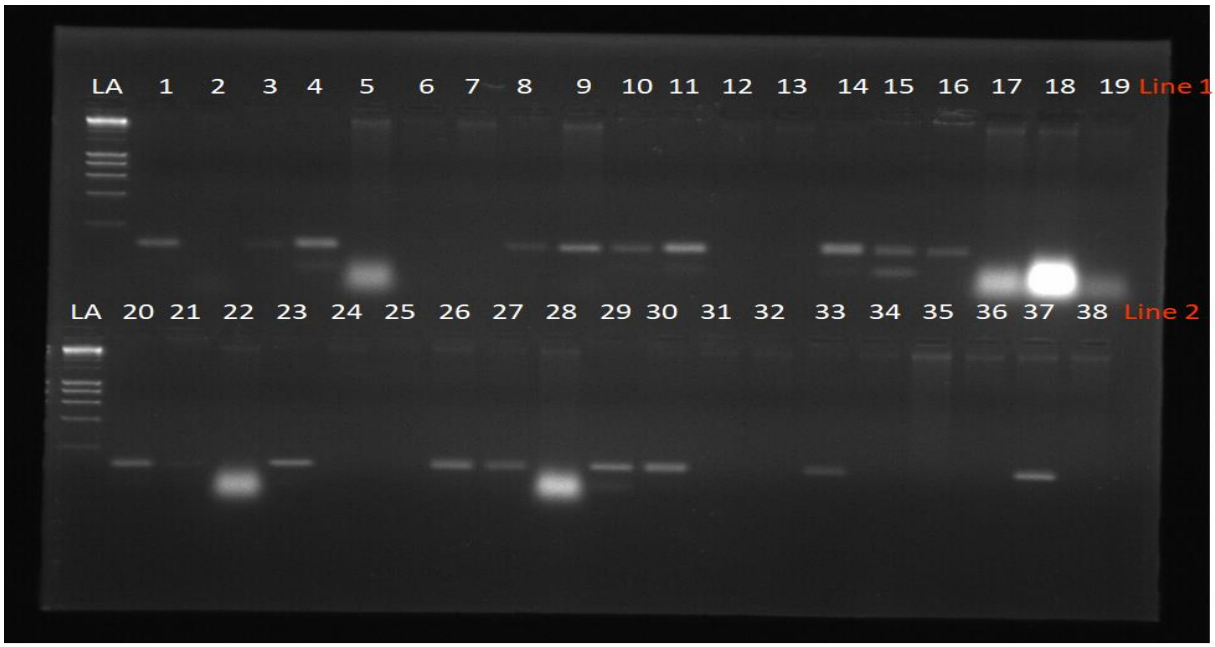
Where:
LA = DNA Ladder 100 bp
Lines 1 to 68 = Sweet potato genotypes

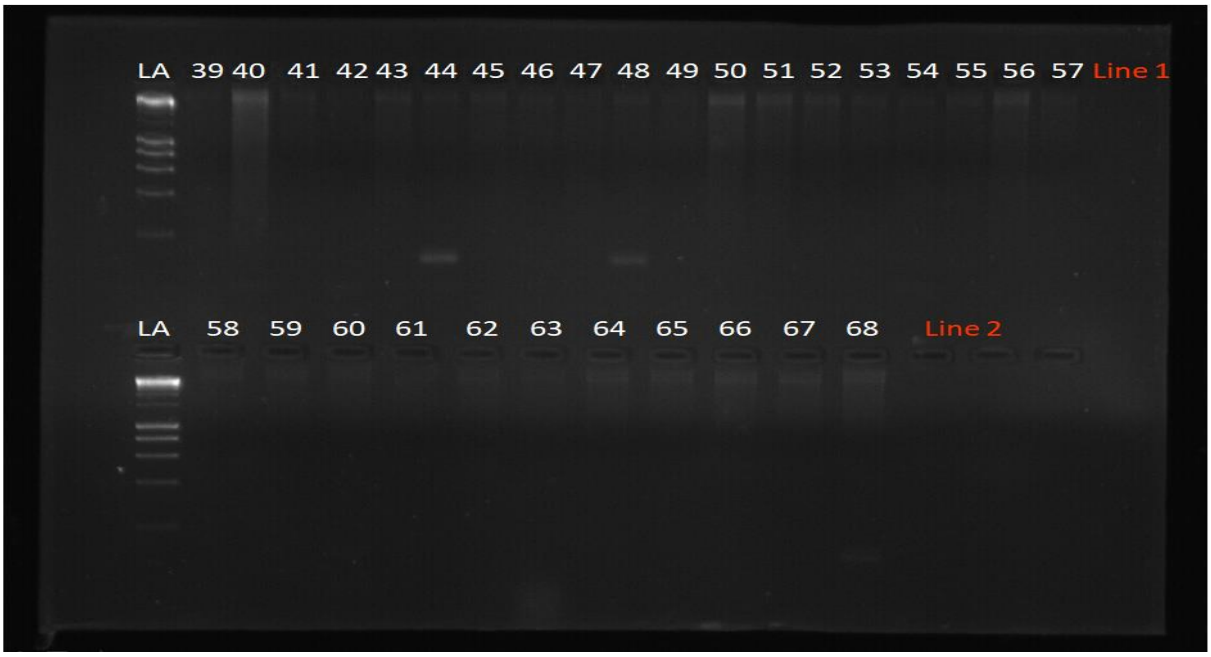




Electrophoresis of DNA Amplified by J67 Primer

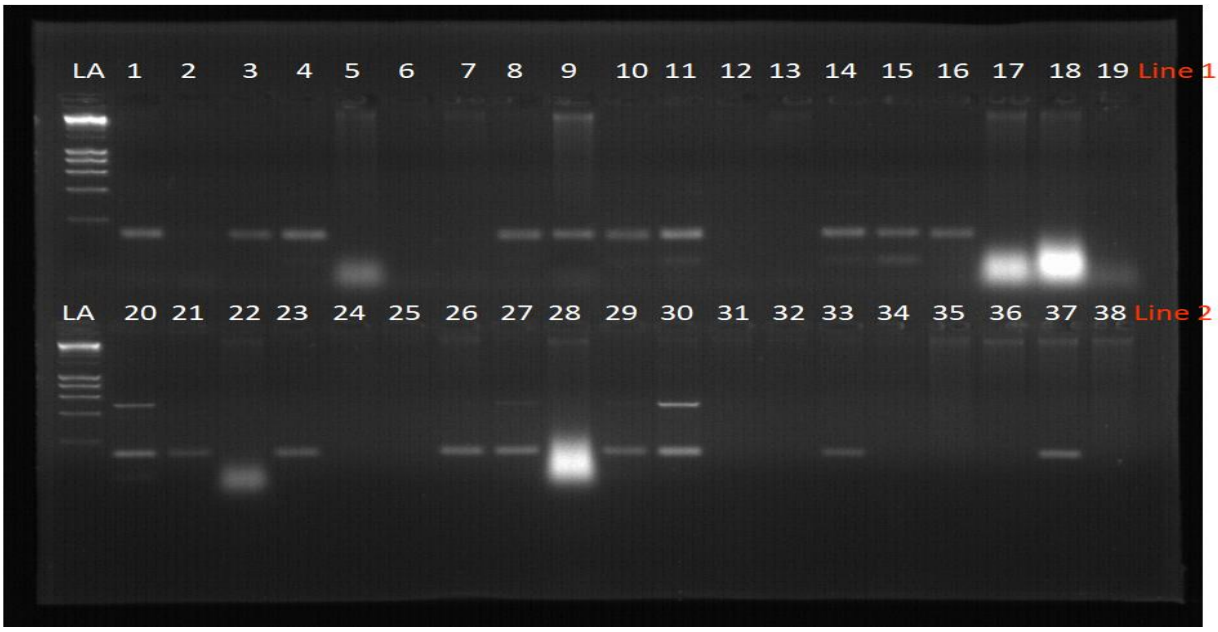
Where:
LA = DNA Ladder 100 bp
Lines 1 to 68 = Sweet potato genotypes

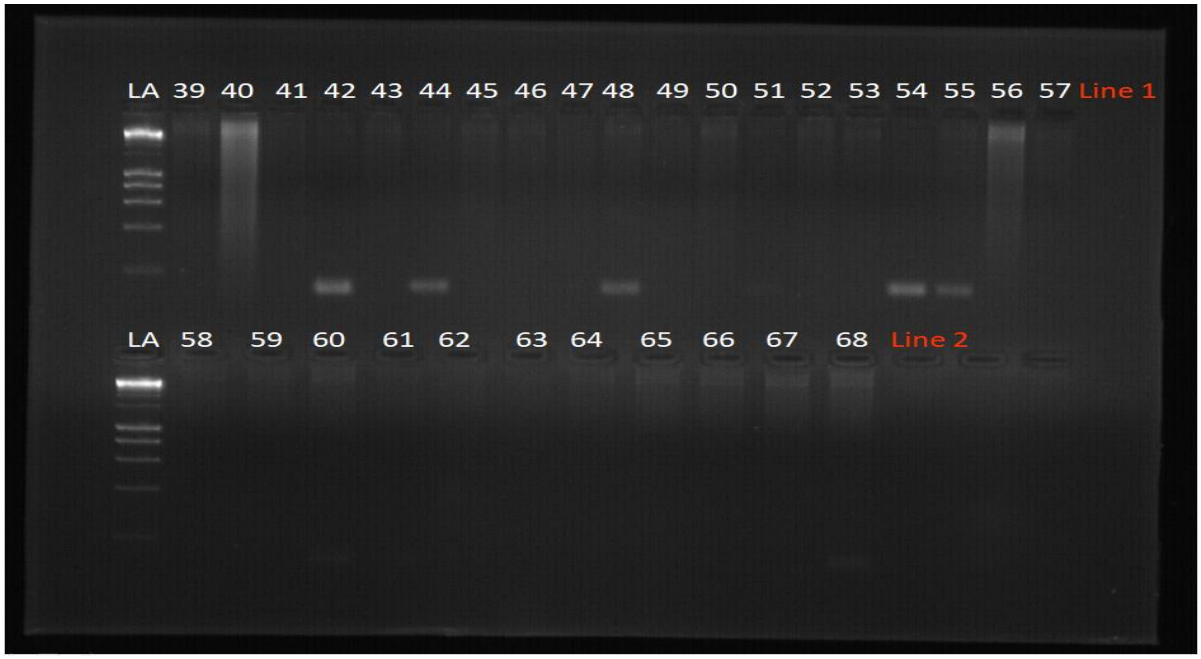




Electrophoresis of DNA Amplified by J175 Primer

Where:
LA = DNA Ladder 100 bp
Lines 1 to 68 = Sweet potato genotypes





Electrophoresis of DNA Amplified by JB1809 Primer

Where:
LA = DNA Ladder 100 bp
Lines 1 to 68 = Sweet potato genotypes

Key for sweet potato genotypes: 1 –52 Nyakisumu, **2** –56682-03, **3** -Kenspot 1, **4** – Ejumula x New kawogo 2, **5** –Obugi, **6** –Amina, **7** –Ejumula, **8** –Naspot x New kawogo 3, **9** Mugande x New kawogo 3, **10** –Mugande x New kawogo 4, **11** -36 Kalamb Nyerere, **12** –Kunyi kibuonjo, **13** –Lungabure, **14** –Polo yiengo, **15** –Saly boro, **16** – 1-Ujili, **17** –Mogesi Gikenja, **18** –Naspot x New kawogo 2, **19** –Mbita, **20** –5 Nyandere, **21** –Odinga, **22** –Nangili, **23** –Ejumula x New kawogo 3, **24** –Nyarambe, **25** –SPK 031, **26** –9 Nduma, **27** –Nyamuguta, **28** –Wera, **29** –Oduogo jodongo, **30** –K/K/2002/12, **31** –K/KA/2004/215, **32** –Fumbara jikoni, **33** –K117, **34** –292-H-12, **35** –Mwavuli, **36** – Mugande, **37** –SPK 004, **38** –29 Kuny kibuonjo, **39** –Santo Amaro, **40** – 62 Odhiogo, **41** –Naspot x New kawogo 1, **42** –Ejumula x New kawogo 4, **43** –Karunde, **44** – Kibuonjo, **45** –12 Marooko, **46** –Sinia, **47** –Kenspot 2, **48** –Kemb 10, **49** –Ejumula x New kawogo 1, **50** –Kenspot 5, **51** –55 Nganyomba, **52** –Kenspot 3, **53** –Nyakagwa, **54** –24 Kampala, **55** –91/2187, **56** –Nyawo Nyathiodiewo, **57** –Vitaa, **58** –Gachaka, **59** – Kenspot 4, **60** –Naspot 1, **61** –Mugande x New kawogo 1, **62** –SPK 013, **63** – Nyautenge, **64** –Tainung, **65** –Mugande x New kawogo 2, **66** –Bungoma, **67** –Alupe-or, **68** –Fundukusia