

**Breeding of Sweetpotato (*Ipomoea batatas* (L.) Lam.) for Storage Root Yield and Resistance to *Alternaria* Leaf Petiole and Stem Blight (*Alternaria* spp.) in Uganda**

**Godfrey Sseruwu**

**BSc. Agriculture, MSc. Crop Science, Makerere University, Uganda**

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**School of Agricultural, Earth and Environmental Sciences**

**College of Agriculture, Engineering and Science**

**University of KwaZulu-Natal**

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## Thesis Abstract

*Alternaria* leaf petiole and stem blight is an important disease of sweetpotato (*Ipomoea batatas* (L.) Lam.) causing yield losses in both landraces and improved cultivars. The most important species causing economic yield loss in Uganda are *Alternaria bataticola* and *A. alternate* with *A. bataticola* the most aggressive and widely distributed. The study was conducted to: i) establish farmer-preferred sweetpotato attributes, production constraints and *Alternaria* leaf petiole and stem blight awareness; ii) evaluate Ugandan sweetpotato germplasm for *Alternaria* leaf petiole and stem blight resistance; iii) determine the mode of inheritance of resistance to *Alternaria* leaf petiole and stem blight and storage root yield components of sweetpotato through estimation of the general combining ability (GCA) of the parents and the specific combining ability (SCA) of the parents for each cross; and iv) determine the adaptability and farmer acceptability of selected F<sub>1</sub> genotypes across environments. The participatory rural appraisal was conducted to establish farmer preferences and production constraints revealed that farmer preferred sweetpotato traits were high yield, sweetness (taste), early maturity, high dry mass, resistance to pests and diseases, and in-field root storability after maturity. A majority of the farmers considered *Alternaria* leaf petiole and stem blight a serious production constraint causing yield loss of over 50%. The main control measures against the disease were roguing of infected plants, spraying with fungicides, use of healthy planting materials and planting resistant genotypes. Thirty sweetpotato landraces and improved cultivars were evaluated for *Alternaria* blight severity; yield, dry mass, harvest index, sweetpotato weevil (*Cylas* spp.) damage and sweetpotato virus disease at two sites (Namulonge and Kachwekano) over three seasons (2010B, 2011A, 2011B) under *Alternaria* inoculum and fungicide spray treatments. Landrace Shock was more resistant to *Alternaria* blight than Tanzania, the resistant check. Genotypes NASPOT 1, NASPOT 7, New Kawogo and Dimbuka were the most susceptible. Thirty two F<sub>1</sub> families were generated from 16 parents in two sets in a North Carolina II mating scheme. The families were evaluated at two sites using a 5 x 7 row-column design with two replications. There were significant ( $P < 0.05$ ) differences among the families in *Alternaria* blight severity. Both GCA and SCA mean squares (MS) for *Alternaria* blight were highly significant ( $P < 0.001$ ) but the predominance of GCA sum of squares (SS) for *Alternaria* blight at 67.4% of the treatment SS versus 32.6% for SCA SS indicated that additive effects were more important than the non-additive effects in controlling this trait. For the yield components, the GCA MS were significant ( $P < 0.05$ ) and accounted for more than 60% of the treatment SS except for percentage dry mass composition where SCA SS accounted for 53.0% of the treatment SS implying that non-additive genetic effects were slightly more important than additive for this trait. Some parents that had desirable high, negative GCA

effects for *Alternaria* blight produced families with undesirable positive SCA effects and the reverse was also true. This implied that the best parents should not be chosen based on GCA effects alone but also on SCA effects of their best crosses. The promising  $F_1$  genotypes selected from previously evaluated crosses together with one *Alternaria* blight resistant check (Tanzania) and one susceptible check (NASPOT 1) were evaluated at three sites (Namulonge, Kachwekano and Serere) using a randomised complete block design with three replications. Scientists and farmers evaluated the agronomic performance and also quality traits of the genotypes before and at harvest. Genotypes G14, G16, G24, G29, G49, G59 and G69 were the most stable across the sites for low *Alternaria* blight severity and can, therefore, be recommended for further evaluation under both low and high disease pressure areas. Genotypes G67, G13, G14, G24, G29 and G53 were the most high yielding and stable across the sites and were therefore the most widely adapted. In the participatory selection, before harvest and at harvest, Spearman's rank correlation of the scientists and farmers' mean ranking of the genotypes at each site was positive and significant. This indicated that the scientists in the study were capable of selecting for farmer preferred traits.

## Declaration

I, Godfrey Sseruwu, declare that:

The research reported in this thesis, except where otherwise indicated, is my original work.

The thesis has not been submitted for any degree or examination at any other university.

The thesis does not contain other persons' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from other persons.

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The thesis does not contain text, graphics or tables copied and pasted from the internet, unless specifically acknowledged, and the source being detailed in the thesis and in the references sections.

Signed ..... Date.....

Godfrey Sseruwu

As the candidate's supervisors, we agree to the submission of this dissertation for examination

Signed..... Date.....

Dr. Paul Shanahan (Principal supervisor)

Signed ..... Date .....

Prof. Rob Melis (Co-supervisor)

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## **Dedication**

I dedicate this thesis to my family; my wife Sarah and children, Christine, Shaun and Catherine. To my mother, Mrs Josephine Lunkuse, my brothers, sisters, nephews and nieces.

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## List of abbreviations

a <sup>-1</sup>	Per annum
AMMI	Additive main effects and multiplicative interaction
ASV	AMMI stability value
AUDPC	Area under disease progress curve
BPH	Best parent heterosis
CIP	International Potato Centre
DAO	District agricultural officer
DM%	Percentage dry mass composition
FAOSTAT	Food and Agricultural Organization Statistics
GCA	General combining ability
GCA <sub>f</sub>	General combining ability effects due to the female parent
GCA <sub>m</sub>	General combining ability effects due to the male parent
GEI	Genotype by environment interaction
GSI	Genotype selection index
HI	Harvest index
HPR	Host plant resistance
IPCA	Interaction principal component analysis
KAZARDI	Kachwekano Zonal Agricultural Research and Development Institute
MAP	Months after planting
MRN	Number of marketable storage roots
MRY	Mass of marketable storage roots
MS	Mean square
MUZARDI	Mukono Zonal Agricultural Research and Development Institute
NAADS	National Agricultural Advisory Services
NaCRRRI	National Crops Resources Research Institute
NARO	National Agricultural Research Organization
NaSARRI	National Semi Arid Resources Research Institute
NGO	Non-governmental organization
OFSP	Orange fleshed sweetpotato
PRAPACE	The regional network of potato and sweetpotato in eastern and central Africa
R <sup>2</sup>	Coefficient of determination
SAB	Severity of Alternaria blight
SCA	Specific combining ability
SI	Selection index
SPCFV	<i>Sweet potato chlorotic fleck virus</i>
SPCSV	<i>Sweet potato chlorotic stunt virus</i>

SPFMV	<i>Sweet potato feathery mottle virus</i>
SPLCV	<i>Sweet potato leaf curl virus</i>
SPLV	<i>Sweet potato latent virus</i>
SPVD	Sweetpotato virus disease
SS	Sum of squares
TRN	Total number of storage roots
TRY	Total storage root fresh mass
UMRN	Number of unmarketable storage roots
USD	Uganda sweetpotato database

## Introduction to thesis

Sweetpotato (*Ipomoea batatas* (L.) Lam.) is an important crop in many parts of the world. It is grown in over 100 countries and is the sixth most important food crop (Woolfe, 1992) after maize (*Zea mays* L.), rice (*Oryza sativa* L.), wheat (*Triticum aestivum* L.), potato (*Solanum tuberosum* L.), cassava (*Manihot esculenta* Crantz) with a total production of  $107 \times 10^6 \text{ t a}^{-1}$  (FAOSTAT, 2010). Asia is the world's largest sweetpotato producing continent with  $88 \times 10^6 \text{ t a}^{-1}$ . China is the world's leading sweetpotato producer with a production of  $81 \times 10^6 \text{ t a}^{-1}$  which accounts for 75% of the global sweetpotato production. A total of  $12 \times 10^6 \text{ t a}^{-1}$  is produced in sub-Saharan Africa (FAOSTAT, 2010), mainly grown around the great lakes region (Ewell, 1997). It is the second most important root crop in the region after cassava (Hakiza et al., 2000) and the great lakes regional production accounts for 62% of sub-Saharan Africa sweetpotato production (FAOSTAT, 2010). Uganda is the first and second largest sweetpotato producer in Africa and the world, respectively, with a production of  $2.8 \times 10^6 \text{ t a}^{-1}$  (Table 1) (FAOSTAT, 2010), followed by Nigeria with a production of  $2.7 \times 10^6 \text{ t a}^{-1}$ . Sweetpotato is one of the main staple crops in the food systems of Uganda, Rwanda, and Burundi with a per capita consumption of 72.6, 73.0 and 88.9 kg, respectively (FAOSTAT, 2010) and it is the second most important food crop after cassava in Uganda (Table 2).

In Uganda, sweetpotato is a major food crop grown throughout the country as a subsistence and food security crop (Bashaasha et al., 1995; Yanggen and Nagujja, 2006). The highest production is concentrated in the densely populated, mid- to high altitude regions ranging between 1000 to 2000 m above sea level (Bashaasha et al., 1995). It is principally grown for its edible storage roots mostly by low-income, smallholder farmers predominantly women for household consumption (Bashaasha et al., 1995; Karyeija et al., 1998) and is sometimes referred to as the "poor person's food" (Low et al., 2009). It is an important source of carbohydrates, vitamin C, fibre, iron, potassium and protein (Woolfe, 1992). In the dry areas of Uganda, sweetpotato storage roots are processed by slicing and drying. The dried chips are eaten during periods of food scarcity (Scott et al., 1998; Kapinga and Carey, 2003).

In addition to sweetpotato being an ideal staple crop, the orange-fleshed genotypes are an invaluable source of  $\beta$ -carotene, a precursor for vitamin A, and are making a significant contribution towards alleviating vitamin A deficiency in Uganda and other countries where sweetpotato is an important food crop for human nutrition (Yanggen and Nagujja, 2006).



**Table 1: Sweetpotato production in Uganda for 2002-2010**

Year	Area harvested (ha)	Yield (kg ha <sup>-1</sup> )	Total production (t)
2010	620 000	4577.4	2 838 000
2009	609 000	4541.9	2 766 000
2008	599 000	5519.2	2 707 000
2007	578 000	4501.7	2 602 000
2006	584 000	4500.0	2 628 000
2005	590 000	4413.5	2 604 000
2004	595 000	4401.9	2 650 000
2003	595 000	4386.5	2 610 000
2002	589 000	4400.6	2 592 000

Source: FAOSTAT (2010)

**Table 2: Comparison of sweetpotato production with other major staple crops in Uganda**

Crop	Area harvested (ha)	Production quantity (t)
Cassava	415 000	5 282 000
Sweetpotato	620,000	2 838 000
Maize	890 000	1 373 000
Millet	470 000	850 000
Potato	102 000	695 000
Banana	143 000	600 000
Rice	140 000	218 000

Source: FAOSTAT (2010)

Despite ranking second in the world for sweetpotato production, Ugandan sweetpotato productivity is still very low. The relatively high sweetpotato production in the country is due to an increase in the area under production from 589 000 ha in 2002 to 620 000 ha in 2010, and not to increased productivity (FAOSTAT, 2010). Yields of up to 25 t ha<sup>-1</sup> for improved cultivars have been obtained at research stations (Mwanga et al., 2011). However, these yields are obtained with proper crop management such as timely planting, weeding, and pest and disease control which farmers most often do not practice. The average yield of 4.6 t ha<sup>-1</sup> at farm level is still far below the world average of 13.3 t ha<sup>-1</sup> (FAOSTAT, 2010). The discrepancy between research station and farm yields is a result of both abiotic and biotic constraints. Of the biotic factors, sweetpotato weevils (*Cylas* spp.) (Stathers et al., 2003), sweetpotato virus disease (SPVD) caused by a synergistic interaction between a potyvirus, *Sweet potato feathery mottle virus* (SPFMV) and a crinivirus, *Sweet potato chlorotic stunt virus* (SPCSV) (Gibson et al., 1997;

Karyeija et al., 1998), and *Alternaria* leaf petiole and stem blight (*Alternaria* spp.) (Osiru et al., 2007a) commonly referred to as *Alternaria* blight, are the most important (Table 3).

**Table 3: Major sweetpotato agro-ecological zones in East Africa and associated production constraints**

<b>Agro-ecological zone</b>	<b>Major areas</b>	<b>Principal mode of utilization</b>	<b>Main identified constraint</b>
Moist, warm environments (bimodal rainfall)	Major production zones of Kenya, Uganda, western Tanzania, Rwanda, Burundi	Fresh consumption and forage	Sweetpotato virus disease and mole rats
Dry, warm environments (unimodal rainfall)	Northern Uganda, parts of Kenya, Tanzania	Fresh consumption and limited processing	Weevils, drought, scarcity of planting materials
Moist cool environments high elevation (bimodal rainfall)	South-west Uganda, Rwanda, Burundi	Fresh consumption and forage	<i>Alternaria</i> blight, low soil fertility

**Source: Kapinga and Carey (2003)**

Of the three major biotic constraints, *Alternaria* blight is still largely unstudied. Bashaasha et al. (1995) and Mwanga et al. (2007) confirmed *Alternaria* blight as the most important fungal disease of sweetpotato in Uganda. Surveys carried out by Osiru et al. (2007) further confirmed the disease as a major problem in most of the major sweetpotato growing districts, with several genotypes reported to be susceptible and yield losses of up to 54%. Of the available control options, the most economical is the use of genetically based host plant resistance. Attempts have been made by the National Sweetpotato Programme of Uganda to breed for resistance (Mwanga et al., 2007) but the incidence of the disease is still on the increase (Mwanga et al., 2011). Clearly, therefore, there is an urgent need to breed for new sweetpotato cultivars that are resistant to the disease.

Some lessons learnt during breeding for various aspects of sweetpotato are that farmers prefer their landraces to newly introduced cultivars regardless of whether they are higher yielding and have resistance to pests and diseases. This is because farmers have selected these landraces for specific attributes which may be lacking among the new introductions (Joshi and Witcombe, 1996). A lack of involvement of farmers in cultivar selection has led to low adoption rates for new cultivars. It is important to involve farmers at some stage during the breeding process so that the new clones are selected for attributes that are acceptable to the target farmers.

A good breeding program starts with identification of farmer preferred attributes, identification of the sources of the preferred attributes as well as sources of resistance to the target disease/s,

followed by the establishment of new genetic variation through hybridisation. In order to develop sweetpotato genotypes with appreciably higher levels of resistance to *Alternaria* blight combined with farmer preferred attributes, it is important to understand the nature of the inheritance of resistance to *Alternaria* blight and the underlying gene action controlling other important agronomic and consumer preferred traits in sweetpotato. This will enable the establishment of an appropriate and scientifically sound breeding strategy that will respond to both farmer and consumer needs.

### **Objectives of the study**

The aim of the study was to advance the development of high yielding, *Alternaria* blight resistant sweetpotato genotypes with farmer and consumer desired attributes that will enhance sweetpotato productivity and income generation among the resource poor farming communities in Uganda. Specifically the study aimed at:

- i. establishing farmer preferred sweetpotato traits, production constraints and *Alternaria* blight awareness;
- ii. evaluating Ugandan sweetpotato germplasm for *Alternaria* blight resistance;
- iii. studying the mode of inheritance of *Alternaria* blight resistance and storage root yield components of sweetpotato; and
- iv. determining the adaptability and general farmer acceptability of selected F<sub>1</sub> genotypes across environments.

### **Hypotheses**

The hypotheses adopted for the study were:

- i. sweetpotato farmers in the different regions of Uganda face the same production constraints and have the same preferred attributes;
- ii. there is no difference in the reaction of different Ugandan sweetpotato genotypes to *Alternaria* blight;
- iii. resistance to *Alternaria* blight in sweetpotato is mainly due to additive gene effects, more specifically quantitatively inherited additive gene effects; and
- iv. the F<sub>1</sub> progeny selected from the crosses conducted in this breeding programme are highly adaptable and have farmer preferred attributes.

## **Organisation of the thesis**

1. General introduction
2. Chapter one: Literature review
3. Chapter two: Farmers' awareness and perceptions of *Alternaria* leaf petiole and stem blight and their preferred sweetpotato traits in Uganda
4. Chapter three: Evaluation of sweetpotato genotypes for resistance to *Alternaria* leaf petiole and stem blight, and stability of agronomic traits in Uganda
5. Chapter four: Genetic analysis of resistance to *Alternaria* leaf petiole and stem blight, and inheritance of yield traits
6. Chapter five: Adaptability and farmer acceptability of selected F<sub>1</sub> genotypes across environments
7. Chapter six: General overview of the study

Chapters 2-5 are written as discrete research articles therefore there may be some repetition as well as overlap of content especially for introductory sections and references used.

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# Chapter 1

## Literature review

### 1.1 Introduction

This literature review provides a general perspective of the botany of sweetpotato (*Ipomoea batatas* (L.) Lam.), its origin and distribution, agronomic requirements, production constraints with an emphasis on *Alternaria* leaf petiole and stem blight in Uganda, Mendelian and quantitative genetics, breeding of sweetpotato, mating designs used in sweetpotato breeding, participatory breeding and genotype by environment interaction. The conclusions drawn from the review are provided at the end of the chapter.

### 1.2 Origin and distribution of sweetpotato

The origin of sweetpotato is not known with certainty. It is believed to have originated in tropical America where it was domesticated over 5000 years ago (Woolfe, 1992), but some archaeological evidence from dried roots found in the Chilca Canyon of Peru indicates that sweetpotato could have been domesticated over 8000 years ago (Engel, 1970; Yen, 1974; Ugent and Peterson, 1998). The exact centre of origin is not known up to now but it is postulated to be the central or South American lowlands (Austin, 1988; Woolfe, 1992). Austin (1988) postulated that the centre of origin of sweetpotato was between the Yucatan Peninsula of Mexico and the mouth of the Orinoco River in Venezuela. In addition, Zhang et al. (1998) provided stronger evidence using molecular markers that the geographical zone postulated by Austin is the primary centre of diversity.

Sweetpotato was widely established throughout the central and South American region as well as the Caribbean before the European explorers reached America (Woolfe, 1992) and Columbus is believed to have introduced sweetpotato to Spain after his first voyage to America. From Spain, sweetpotato was introduced to Africa and Asia by Spanish and Portuguese traders (Vaughan and Geissler, 2009).

Sweetpotato was introduced by missionaries to Uganda in the early 1900s and became well established in the central and parts of the western region of the country during the British administration (Akimanzi, 1982, cited by Yanggen and Nagujja, 2006). It is now a major crop grown throughout the country mostly as a subsistence food crop (Hakiza et al., 2000; Yanggen and Nagujja, 2006).

### **1.3 Taxonomy of sweetpotato**

Sweetpotato is a dicotyledonous plant which belongs to the family Convolvulaceae (morning glory), genus *Ipomoea*, subgenus *Eriospermum*, section *Eriospermum* (formerly *Batatas*), series *Batatas* and species *Ipomoea batatas* (Huaman, 1992). It is a perennial crop but is mostly cultivated as an annual for its succulent storage roots and vines. *Ipomoea batatas* is the main species that is of economic value as a food in its family out of the over 50 known genera (Purseglove, 1974; Woolfe, 1992). To a small extent, however, *I. aquatica* is used as a vegetable in Malaysia and China (Woolfe, 1992). There are several wild species in this family, estimated to be more than 400, and sweetpotato is the only one not known to survive in the wild and no direct ancestor is known (Purseglove, 1974; Woolfe, 1992). However, some genetic studies suggest that *I. trifida* is the closest relative of *I. batatas* and may be its progenitor (Kirst, 1997).

Sweetpotato is allogamous and therefore heterozygous, and as a hexaploid with a basic chromosome number of 15, it has a total of 90 chromosomes ( $2n=6x=90$ ) (Austin, 1988; Wilson et al., 1989). It is believed that sweetpotato or its progenitor, was derived from a cross between a tetraploid ( $2n=60$ ) and a diploid ( $2n=30$ ). The resulting triploid ( $3n=45$ ) underwent spontaneous chromosome doubling to form the hexaploid form (Purseglove, 1974; Austin, 1988). Jones (1990) suggested that unreduced gametes may be the likely origin of the hexaploid *I. batatas*. Bohac and Jones (1994) found that the formation of unreduced gametes is genetically controlled and occurred in 16% of the sweetpotato lines they studied providing further support for unreduced gametes as the likely mechanism for polyploidisation from lower ploidy levels rather than spontaneous doubling which occurs rarely in nature.

### **1.4 Sweetpotato genetics and flowering**

#### **1.4.1 Mendelian genetics**

Sweetpotato is not suitable for Mendelian genetics studies (MacDonald, 1967). The genetic inheritance of traits is complicated in sweetpotato because it is a hexaploid with a large chromosome number and because of its complex self- and cross-incompatibility systems (Jones, 1986). Since it is a hexaploid, each gene is represented by six alleles thus its genetic studies are complicated by several meiotic and cytological abnormalities (Tan et al., 2008). Jones (1967) presented theoretical segregation ratios for qualitative traits and presented four hypotheses (hexasomic, tetradisomic, tetrasomic, disomic) of inheritance. Since the simple ratios are artefacts due to homozygosity for some genes, inheritance studies often have shown discrepancies with respect to expected segregation patterns. Genetic studies by Poole (1955) showed that the inheritance patterns of some morphological traits, for example flowering vs. non-flowering, and red vines vs. green followed the normal Mendelian 3:1 ratio. Similarly,



Kumagai et al. (1990) tested four inheritance hypotheses i.e. hexasomic, tetradisomic, tetrasomic and disomic and showed that the  $\beta$ -amylase null trait in sweetpotato storage roots was controlled by one recessive gene that was inherited in a hexasomic or tetradisomic manner, but not disomically or tetrasomically. However, the majority of the important agronomic traits in sweetpotato are inherited quantitatively (Tan et al., 2008).

#### **1.4.2 Quantitative genetics and breeding**

Application of quantitative genetics principles has enabled an understanding of the inheritance of sweetpotato traits that otherwise would not have been possible. While studying the morphological variations in leaf type, stem colour and vine length in  $F_1$  seedlings, Hermon (1960) cited by Vimala (1993) found that all these traits were quantitatively inherited. Similarly, Jones (1969) found that additive variance was more important than non-additive genetic variance for leaf vein, leaf whorl and vine purpling. Chen et al. (1989) estimated the narrow-sense heritability for storage root yield and found that it was very low indicating the contribution of non-additive genetic variance, environmental and genotype x environment variance to the expression of the trait. In contrast, Vimala and Lakshmi (1991) found that additive genetic variance was more important than the non-additive variance for root yield. On the other hand, Pillai and Amma (1989) reported additive and non-additive variance to be equally important for root yield. In his study of 10 vine traits, Jones (1969) reported a large proportion of the phenotypic variance of all the traits to be accounted for by the genetic component i.e. additive and non-additive gene action. In their studies on root knot nematodes, Jones and Dukes (1980) reported high narrow-sense heritability estimates for resistance to two nematode species implying that additive genetic variance was more important than non-additive in the expression of the resistance mechanisms. Jones (1986) outlined the different methods for calculating heritability estimates and their use in sweetpotato breeding. He illustrated how heritability values can differ depending on the method used to calculate them. All of these studies confirm the degree of variability of the genetic variance components for the different traits and the requirement to carefully select the method/s used to calculate heritability estimates.

#### **1.4.3 Floral and reproductive biology**

Sweetpotato flowers occur in axillary inflorescences of 1 to 22 buds (Jones, 1966; Wilson et al., 1989). Each flower contains a pistil and stamen covered by a funnel shaped corolla. The colour of the corolla varies from white through various shades of lavender to complete lavender (Jones, 1966). The stamen consists of five filaments with anthers at the top. The filaments may be shorter, of the same length, or longer than the stigma. The length of the stamens relative to the stigma determines the ease with which such a flower can be hand-pollinated. Where the stamens are shorter than the stigma, hand pollination is easier whereas if the stamens are the

same length as, or longer than the pistil, it is difficult to locate the stigma during hand pollination (Wilson et al., 1989). The enlarged base of the pistil contains two ovaries, and each ovary has the potential of producing two seeds, thus each fruit, which is called a capsule, can contain a maximum of four seeds. Normally four seeds are obtained through natural pollination and controlled pollination yields one to two seeds only (Jones and Dukes, 1980; Wilson et al., 1989). At the base of the corolla, there are conspicuous yellow glands that contain insect attracting nectar (Jones et al., 1987). The flowers open in groups of two or more soon after day break and often fade by noon (Tuoutine, 1935; Jones and Dukes, 1980).

Following successful pollination, seeds take four to six weeks to mature depending on the prevailing environmental conditions (Tuoutine, 1935; Jones and Dukes, 1980; Jones et al., 1987). Germination is very irregular unless scarification is done using concentrated sulphuric acid (Steinbauer, 1937). Seed scarification can also be done by pricking the seed with a sharp instrument (Jones and Dukes, 1980). A small cut can also be made on the opposite side to the hilum of the seed using a sterile scalpel (Wilson et al., 1989) or sand paper can be used to wear down the testa until it is very thin (Huáman and Asmat, 1999).

#### **1.4.4 Flowering in sweetpotato**

Most sweetpotato genotypes flower naturally in most tropical countries but where natural flowering fails, especially in temperate regions, flowering has to be induced (Purseglove, 1974). Miller (1939) studied different techniques of inducing flowering in sweetpotato and found that staking or trellising, girdling the vine, and cultivar reaction to day length were important in sweetpotato flowering and subsequent seed set. Further studies carried out by Du Plooy (1982), showed that grafting onto different *Ipomoea* spp., and temperature and day-length regulation also induced flowering. He further noted that a short photoperiod of eight hours and low temperatures (15 - 20°C) are favourable for flowering while a long photoperiod (9 to 12 h) and high temperature (25 - 30°C) are favourable for vegetative growth.

In the tropics, most sweetpotato genotypes flower readily and produce both fruits and seeds but the rate of flowering depends on the genotype, prevailing environmental conditions and season (Wilson et al., 1989). Pollination can be by natural or controlled means. Natural cross-pollination is effected by insects especially bees while controlled pollination is done by emasculation and crossing appropriate parents. Dehiscence of the pollen starts 6 h before the flower opens and since the flowers open very early in the morning, controlled pollination is usually done between 06h00 and 09h00 (Tuoutine, 1935; Wilson et al., 1989; Lebot, 2009). Flowers that are not pollinated wither and fall off between 11h00 to 12h00 (Tuoutine, 1935; Purseglove, 1974; Jones and Dukes, 1980).

#### **1.4.5 Incompatibility in sweetpotato**

Self-fertilization in sweetpotato is rare because all genotypes have a high degree of self-incompatibility. Similarly, it may be difficult to obtain seed from crosses between certain parents because cross-incompatibility also occurs (Wilson et al., 1989). Incompatibility is the failure of viable pollen grains to germinate after landing on the stigma. It can also be the failure to set seed after germination of the pollen grains. This can arise as a result of meiotic abnormalities in some cultivars and cytological irregularities within the pollen mother cell (Martin and Cabanillas, 1966; Du Plooy, 1986) or can be as a result of abnormalities in meiosis associated with the hexaploid nature of sweetpotato ( $2n=6x=90$ ) (Oración et al., 1990). Poor seed set may also be attributed to sweetpotato producing large number of weak and imbalanced gametes (Martin, 1965). Despite these abnormalities, chromosomes may pair normally, but the gametes may not carry a well-balanced set of chromosomal material leading to poor seed germination, low seed vigour, abnormal plant types, reduced flowering, ovule abortion, ineffective pollen tube growth or embryo abortion and poor seed set (Martin and Ortiz, 1967). Incompatibility can be between genotypes (cross-incompatibility) or within a genotype (self-incompatibility) (Martin, 1965). Incompatibility mechanisms may involve the enzyme system failing to break down cutin covering the stigma, inhibition of the pollen tube growth in the style or non-fusion of gametes within the ovule after penetration by male nuclei leading to flower abortion (William and Cope, 1967).

William and Cope (1967) outlined the effects of incompatibility on breeding programs which include a reduction of the genetic base available for generation of seedling populations on which selection for improved types can be practised, restriction of the use of conventional techniques for parental evaluation such as progeny testing, and retardation of fixation of desirable and heritable traits because it limits inbreeding. Thus, incompatibility and low seed set are the major obstacles faced by sweetpotato breeders and it is through trial and error that they find compatible genotypes. Even then, the sparse flowering habits and poor seed set of many existing genotypes and landraces limit genetic variability, making it extremely difficult to develop new genotypes from them (Du Plooy, 1986).

#### **1.5 Agronomic requirements of sweetpotato**

Sweetpotato is a tropical and sub-tropical crop and grows very well under hot conditions. Most of the sweetpotato crop is grown between 48°N and 40°S of the equator and its maturity period varies from 3-6 months (Woolfe, 1992). In these regions, sweetpotato can grow at any elevation from sea level to 3000 m but most production is concentrated around 1000-1800 m above sea level (Hahn, 1984). The optimum growth temperature is 24°C but the crop can grow well in a temperature range of 10-35°C outside of which growth is retarded. The crop grows well under

relatively dry conditions but cannot survive long periods of drought and is mainly grown during the wet season. In the dry seasons, it is grown in wetland areas or can be grown under irrigation, which is not often economical for the resource poor farmers of Uganda (Adrich, 1963; Bashaasha et al., 1995; Karyeija et al., 1998). In areas that experience prolonged droughts, availability of planting materials is a major challenge since the vines cannot survive to the next season. Optimum rainfall requirement is 750-1000 mm (Tewe et al., 2003). Sweetpotato cannot tolerate water logging and is usually grown on mounds or ridges (Purseglove, 1974). It can grow in a wide range of soils but prefers well-drained, sandy loams with high organic matter content and can tolerate pH of 4.5 to 6.5. High soil density and poor aeration retard storage root formation (Woolfe, 1992) since the storage roots develop as adventitious roots. The adventitious roots can be sub-divided into thick and thin roots and under a conducive environment, the thick roots develop into storage roots (Kays, 1985). According to Villordon et al. (2009) adventitious roots that eventually turn into storage roots are initiated as early as five to seven days after transplanting. Therefore, it is important to have a well prepared seedbed before planting the sweetpotato vines.

## **1.6 Sweetpotato production constraints**

Sweetpotato production has both biotic and abiotic constraints (Kapinga and Carey, 2003). The abiotic constraints include low soil fertility, drought, limited range of processing and utilization options and post-harvest problems such as lack of storage facilities (Mwanga et al., 2007). The biotic constraints include pests such as weevils (*Cylas* spp.) (Stathers et al., 2003) and diseases, especially sweetpotato virus disease (SPVD) (Mwanga et al., 2007) and *Alternaria* leaf petiole and stem blight (*Alternaria* spp.) (commonly referred to as *Alternaria* blight) (Hakiza et al., 2000; Osiru et al., 2007a; Osiru et al., 2007b; Osiru et al., 2008). Other constraints include low yielding genotypes of low nutritive value (mainly low dry mass and low  $\beta$ -carotene content), genetic erosion, and shortage of high quality planting materials and marketing problems.

### **1.6.1 Sweetpotato pests**

Sweetpotato is attacked by several insect pests. The potential negative impact of a particular pest species depends on the agro-ecological zone and on the season (Ames et al., 1996). Sweetpotato weevils (*Cylas* spp.) are the most destructive insect pests of sweetpotato in Central America, Africa, and Asia causing yield losses of between 60 to 100% (Mullen, 1984; Chalfant et al., 1990; Jansson and Raman, 1991; Lenné, 1991). *Cylas formicarius*, *C. puncticollis* and *C. brunneus* are the three main species; whereas *C. puncticollis* and *C. brunneus* are confined to Africa, *C. formicarius* is found globally (Wolfe, 1991; Ames et al., 1996). *Cylas formicarius* is the most serious pest causing damage both in the field and in

storage. The principal form of damage to sweetpotato is mining of the storage root by the weevil larvae. The infested storage root is often riddled with cavities, spongy in appearance, and dark in colour. Such storage roots produce bitter tasting and toxic sesquiterpenes that render them unfit for human consumption (Andrade et al., 2009). Yield losses of up to 97% have been reported in some parts of the world (Capinera, 2006) and in Uganda, losses of up to 73% have been reported (Smit, 1997).

Another important category of pests is the virus transmitters: aphids (*Aphis gossypii*, *Myzus persicae* and *Aphis cracivora*) and whiteflies (*Bemisia tabaci*). The aphids suck sap from the growing shoots causing wrinkling, cupping, and downward curling of the young shoots. In the process of feeding, they transmit the *Sweetpotato feathery mottle virus* (*Potyviridae/Potyvirus*). The whiteflies cause yellowing and necrosis of infected leaves and also transmit the *Sweetpotato chlorotic stunt virus* (*Clesteroviridae/Crinivirus*) (Ames et al., 1996; Alicai et al., 1999).

## **1.6.2 Sweetpotato diseases**

### **1.6.2.1 Sweetpotato viruses**

Worldwide, at least 30 viruses are known to infect sweetpotato. These viruses are assigned to nine families namely: *Bromoviridae*, *Bunyaviridae*, *Caulimoviridae*, *Closteroviridae*, *Comoviridae*, *Flexiviridae*, *Geminiviridae*, *Luteoviridae* and *Potyviridae*. Most of these viruses are associated with symptomless infections in sweetpotato and their occurrence varies with geographical region (Clark et al., 2012). They occur singly or as mixed infections. In the temperate region, the crop is mainly affected by a complex of potyviruses and possibly other unknown viruses that cause yield reductions of 20-30% (Karyeija et al., 1998). In East Africa, a synergistic interaction of *Sweet potato feathery mottle virus* (SPFMV), a potyvirus transmitted by aphids, and *Sweet potato chlorotic stunt virus* (SPCSV), a *Crinivirus* transmitted by whitefly, causes sweetpotato virus disease (SPVD), the most important disease of sweetpotato (Gibson et al., 1998). It causes yield losses of 80-90% in many high yielding genotypes (Gibson et al., 1997; Karyeija et al., 1998) and despite all the research attention it has received over the years, it is still a very devastating disease (Gibson et al., 2008). Other important sweetpotato viruses include: *Sweet potato mild mottle virus* (SPMMV), *Sweet potato latent virus* (SPLV), *Sweet potato chlorotic fleck virus* (SPCFV) and *Sweet potato leaf curl virus* (SPLCV) (Aritua et al., 1998; Gibson et al., 1998). Aphids and whiteflies act as vectors of some of the viruses (Andrade et al., 2009) and the viruses are also transferred through planting materials. Infected plants have negligible yield, especially if symptoms manifest at an early stage in the development of the plant (Gibson and Aritua, 2002).

### **1.6.2.2 Non-viral sweetpotato diseases**

Sweetpotato production is affected by many non-viral diseases some of which cause yield losses. Many of these diseases have received little attention throughout Africa due to being regarded as low priority within research institutes (Skoglund et al., 1994). The non-viral leaf and stem diseases include: Alternaria blight (*Alternaria* spp.), Phomopsis leaf spot (*Phyllostica* leaf spot), and Fusarium wilt (*Fusarium oxysporium* sp. *batatas*). The storage root diseases include: foot rot (*Plenodomus destruens*), Java black rot (*Diplodia theobroma*), and soft rot (*Rhizopus stolonifer*) (Ames et al., 1996). Among these diseases, Alternaria blight is the most important both in East Africa (Stathers et al., 2005) and Brazil (Ames et al., 1996). Recently, it has progressively gained in importance in Ethiopia (van Bruggen, 1984), Kenya (Skoglund et al., 1994), India (Sivaprakasam et al., 1977), Brazil (Lopes and Boiteux, 1994), Rwanda (Ndamage, 1988), and Uganda (Osiru et al., 2007a).

### **1.6.3 Alternaria leaf petiole and stem blight**

#### **1.6.3.1 Occurrence and incidence of Alternaria leaf petiole and stem blight of sweetpotato**

Alternaria blight occurs in most of the major sweetpotato growing regions of the world. It has been reported in South America especially in Brazil where it has been considered endemic (Lopes and Boiteux, 1994) and in South East Asia (Lenné, 1991) and has for a long time been reported in Zimbabwe (Whiteside, 1966) and Nigeria (Arene and Nwankiti, 1978). It was recently reported in South Africa but no economic yield losses have so far been reported (Narayanin et al., 2010a). In sub-Saharan Africa, the disease is common within the tropics and has been a major production constraint in Ethiopia (van Bruggen, 1984), Kenya (Gatumbi et al., 1991; Skoglund et al., 1994; Anginyah et al., 2001) and Rwanda (Ndamage, 1988). In Uganda, it has been reported in all regions of the country with the highest incidence in the Central and South-western highland agro-ecologies and the lowest in the Northern warm region (Mwanga et al., 2007; Osiru et al., 2007a). In Kenya (Skoglund et al., 1994; Anginyah et al., 2001) and Rwanda (Ndamage, 1988), higher disease incidence was reported at higher altitude areas. However, Osiru et al. (2007a) recorded high disease incidence at both mid-altitude areas around Lake Victoria and at high altitude in south-western Uganda. The differences in occurrence and distribution of the disease are attributed to climatic conditions which are favourable for pathogen infection and disease development (Osiru et al., 2007a). According to Rotem (1994), the optimum temperature range for *Alternaria* species infection is 25-28°C and these are the prevalent temperatures in the Lake Victoria Crescent Zone. In other areas where the disease occurs at mid- to high altitude, incidence and lesion size increase with altitude and

relative humidity since leaf surface moisture is necessary for infection and sporulation (Ames et al., 1996).

From their survey, Osiru et al. (2007a) reported low incidences of the disease in Uganda both at district and regional levels and the disease was recorded on most of the landraces. Similarly, Rotem (1994) observed differences in disease incidences among genotypes. Similar results were reported by van Bruggen (1984) in Ethiopia, and Lopes and Boiteux (1994) in Brazil, Skoglund et al. (1994) and Anginyah et al. (2001) in Kenya, and Narayanin et al. (2010b) in South Africa. In Uganda, Kenya and Ethiopia, lower disease incidences were recorded in the landraces that were more locally adapted than the newly introduced cultivars. Among the cultivars released by the Ugandan National Sweetpotato Program before 2003, only five (Bwanjule, Sowola, NASPOT 3, NASPOT 5, and NASPOT 6) exhibited moderate to high field resistance to *Alternaria* blight and the rest were susceptible (Mwanga et al., 2007). The observed differences in reaction of the indigenous and introduced genotypes to the disease can be attributed to the differences in the genetic base whereby local genotypes exhibited higher disease resistance levels possibly due to their broader genetic base (Anginyah et al., 2001). In Uganda, however, Osiru et al. (2007a) further noted considerable differences in reaction to the disease among the local genotypes, indicating that selection for disease resistance within these genotypes is also possible. Owing to the increasing incidence of the disease, and the lack of genotypes that are resistant, these observed differences in both local and introduced genotypes provide a basis for breeding for improved resistance since host plant resistance is the key to disease management in subsistence agriculture and in low value crops like sweetpotato.

#### **1.6.3.2 Causal organism(s) of *Alternaria* blight of sweetpotato**

*Alternaria* blight of sweetpotato is caused by a fungus of the genus *Alternaria* but the species differ from site to site. The pathogen identified as *Alternaria capsici-annui* was first reported in India (Sivaprakasam et al., 1977), and *A. alternata* has been reported in Papua New Guinea (Lenné, 1991), while *A. bataticola* has been reported in Brazil (Lopes and Boiteux, 1994). In sub-Saharan Africa, *Alternaria* blight caused by *A. tax* sp. (IV) has been reported in Ethiopia (van Bruggen, 1984), *A. solani* in Burundi and Rwanda (Ndamage, 1988), *A. bataticola* and *A. alternata* in Kenya (Anginyah et al., 2001) and Uganda (Osiru et al., 2007a; Osiru et al., 2008; Osiru et al., 2009). In Uganda, the incidence of *A. bataticola* was higher than of *A. alternata* in samples collected from across the country, thus *A. bataticola* is the most important species of the two (Osiru et al., 2007a; Mwanga et al., 2011). Identification and description of *A. bataticola* in Uganda was done by Osiru et al. (2008).

### **1.6.3.3 Morphology of the *Alternaria* blight pathogens, *Alternaria bataticola* and *Alternaria alternata***

Owing to the similar appearance of the isolates of *A. bataticola* and *A. alternata*, characterisation is done based on colony appearance or morphology and conidia shape. The morphological characteristics considered are the number of longitudinal and vertical septae, conidiophores as well as conidia length and shape (Osiru et al., 2008).

According to the International Mycological Institute description (David, 1991), *A. bataticola* (Ikata ex W. Yamamoto) is characterised by mycelia that are “fuscous brown to almost hyaline, smooth-walled but occasionally rough-walled, septate, branched, 6-8  $\mu\text{m}$  in diameter and 10-30  $\mu\text{m}$  in length”. On potato dextrose agar, the colonies are grey-green with a large amount of fluffy pale green aerial mycelium. The conidiophores are “single or in bundles, unbranched, erect or slightly curved, two to seven septate, pale brown to fuscous-brown”. In culture, the conidia arise as short side-branches on the main mycelium, unbranched, with one or a few conidiogenous loci. According to Osiru et al. (2008), “The conidia are solitary, elongate-obclavate, muriform, transversely five to eight septate, longitudinally zero to eight septate, pale to fuscous-brown, and smooth walled. The dimensions of the conidia are 69 (34-160) x 24 (15-42)  $\mu\text{m}$ . The conidial beaks are long, filiform, colourless to pale brown, septate, and often branched with an average dimension of 8 (4-12) x 71 (32-129)  $\mu\text{m}$ ”. However, some exceptions have been reported in Brazil where some isolates differed from the conventional description, and the conidia did not form branching beaks. These differences suggest that *Alternaria* of sweetpotato may be a complex disease across the world whose morphology can vary depending on site and prevailing environmental conditions.

*Alternaria alternata* differs in conidia shape and size from *A. bataticola*. “The conidia are brown, ellipsoidal, 20-60 x 15  $\mu\text{m}$  (average 39 x 10.3) in size, short beaks, with two to six transverse septa, zero to four longitudinal septa and are catenulate at the apex of the conidiophores” (Anginyah et al., 2001). The conidia are small pigmented, with short beaks, and borne on chains (Rotem, 1994).

### **1.6.3.4 Symptoms of *Alternaria* blight disease of sweetpotato**

The common symptom of this disease is the formation of characteristic lesions. The lesions begin as small tan spots with light coloured centres that may enlarge up to several centimetres in diameter with concentric rings (Stathers et al., 2005). In carrot (*Daucus carota* L.), the ridge is slightly raised and thickened usually with concentric rings. Under favourable conditions, the lesions increase in number, expand and eventually coalesce and the affected leaf may shrivel and die. Large lesions on the petiole may also girdle and kill the leaf. Sometimes the infection originates on the leaf margin and progresses down the vein, petiole and stem (Gugino et al.,



2004). Manifestation of this disease varies with geographical location and several authors have described the symptoms differently depending on their location. According to Sivaprakasam et al. (1977), in India “the infected leaves show presence of dark brown to black irregular or more or less circular dead areas upon the leaves, which usually show concentric rings”. In a severe infection, a number of spots may coalesce to form large patches and the leaves get completely blighted and drop off prematurely. Furthermore, van Bruggen (1984) in Ethiopia described the symptoms as, “small, grey to black, oval lesions with a lighter centre on the stems and petioles”. These symptoms are sometimes visible on the veins commonly on the lower side of the leaves. Under humid weather conditions, the lesions on the stems enlarge into black areas and eventually become girdled and the leaves above the infected areas dry out. In dry conditions, the lesions become bleached. Skoglund et al. (1994) described the symptoms as “blackened lesions that occur on stems and petioles and later enlarge and coalesce until stems are girdled and killed”. Lesions occasionally occur on leaves and severe defoliation takes place especially on older vines. Stem blight manifests itself as stem necrosis and dieback is normally severe during the wet season and the soil beneath the diseased vines is carpeted with blackened leaf debris (Stathers et al., 2005; Osiru et al., 2008) (Figure 1.1).



**Figure 1.1 Sweetpotato infected with *Alternaria* leaf petiole and stem blight at the National Crops Resources Research Institute (NaCRRI), Namulonge, Uganda**

#### **1.6.3.5 Ecology and epidemiology of *Alternaria* leaf petiole and stem blight disease**

*Alternaria* blight can be differentiated from other leaf spots and blights because of its severity. No other foliage diseases, with the exception of leaf and stem scab caused by *Elsinoe batatas*, have been reported to be so destructive. *Alternaria* blight is frequently observed at various stages of growth of the sweetpotato crop and under severe infection the soil under the diseased vines is carpeted with blackened leaf debris (Stathers et al., 2005).

As temperatures increase, the duration of leaf wetness required for infection to occur decreases. Infections can occur within 8 to 12 h at temperatures of 16-25°C. Such lower temperatures favour disease development in the highlands where cool temperatures are

experienced (Stathers et al., 2005). The fungus sporulates readily on dead necrotic tissue and spores germinate readily in water droplets and dew. The disease is spread through infected planting material, wind, splashing rain, water and air currents (Skoglund et al., 1994; Mwanga et al., 2001; Gugino et al., 2004). The fungus survives as spores in plant debris and on volunteer plants (Stathers et al., 2005).

#### **1.6.3.6 Management of *Alternaria* leaf petiole and stem blight**

Healthy planting materials, field sanitation where infected crop materials are destroyed and burnt, crop rotation, and host-plant resistance are the common control measures at present. Fungicides are effective but not widely used by resource poor farmers because they are expensive. Some resistant genotypes have been identified. For example in Uganda, cultivar Tanzania is resistant and is consequently grown throughout the country (Osiru et al., 2007a).

### **1.7 Breeding sweetpotato**

#### **1.7.1 History of sweetpotato breeding in Africa**

In Africa, sweetpotato breeding started in South Africa in 1951 with the introduction of some cultivars and breeding lines from the USA (Du Plooy, 1986). Regional breeding efforts in Africa were spearheaded by the International Institute of Tropical Agriculture (IITA) in Nigeria in the 1970s and later by the International Potato Centre (CIP) (Carey et al., 1997). In Uganda, sweetpotato breeding started at Makerere University farm, Kabanyolo, in 1961 when two landraces, Bitambi and Magabali, were found to produce seed and could be crossed and several genotypes were subsequently developed from these and other landraces (MacDonald, 1965; 1967). However, it was not until 1982 through collaborative work between the Uganda Ministry of Agriculture and CIP that sweetpotato breeding gained importance and the sweetpotato improvement program was established at Namulonge in 1986 (Hakiza et al., 2000). Since then significant improvements in sweetpotato have been made under the Ugandan National Sweetpotato Program (Mwanga et al., 2007).

#### **1.7.2 Sweetpotato genetic improvement**

Sweetpotato has a broad genetic base and is therefore highly variable (Woolfe, 1992). Although this broad genetic base coupled with its highly heterozygous nature makes the genetics of sweetpotato very complicated (Magoon et al., 1970; Wilson et al., 1989), it provides plant breeders with a tremendous opportunity to exploit it for the genetic improvement (Woolfe, 1992). In the improvement of sweetpotato, different procedures are used depending on the objectives of the breeding program but the basic steps followed are the same (Wilson et al., 1989). Jones (1965) proposed a procedure through which intra- and inter-chromosomal recombination would increase the chances of the expression of favourable epistatic effects.

This meant that recurrent mass selection should be used instead of the pedigree breeding procedure. He further suggested that in order to achieve maximum variability in the progeny population, unrelated parents ranging from 4 to 20 should be used. Wilson et al. (1989) also agreed with Jones in terms of the number of unrelated parents to be used. Variability is achieved by crossing these parents in all possible combinations in a design known as polycross. Since each seed produced is genetically different from the others, through proper evaluation it may become a new improved cultivar and be increased vegetatively. The performance of the progeny is evaluated at different stages and the most promising ones are clonally advanced to the next stage. This is followed by recurrent selection where new genotypes are cross-pollinated to further improve the population (Wilson et al., 1989).

### **1.7.3 Sweetpotato breeding objectives**

The sweetpotato breeding objectives are determined by the target environment(s), ideally in consultation with the target farmer group(s), and taking into consideration the intended end use of the crop. The major, current breeding objective of the Ugandan National Sweetpotato Program is to develop germplasm with farmer and consumer desired traits, combined with multiple resistances to mainly sweetpotato virus disease, *Alternaria* blight and sweetpotato weevil (Mwanga et al., 2007).

## **1.8 Breeding for *Alternaria* blight resistance**

### **1.8.1 Inheritance of resistance to *Alternaria* blight**

The inheritance of resistance to *Alternaria* blight in sweetpotato is not very widely studied as more priority has often been given to SPVD, which so far has been the most devastating sweetpotato disease in East Africa (Gibson et al., 1998). However, *Alternaria* blight has gained importance in most of the sweetpotato producing areas. From previous studies, it is clear that both the landraces and improved cultivars have varying levels of resistance to *Alternaria* blight. It is, however, not clear, if this resistance is durable or non-durable. Efforts are also underway at the Ugandan National Sweetpotato Program to screen the germplasm and breeding populations for resistance to the disease. Quantitative approaches have been previously used to study different sweetpotato diseases. For example, quantitative inheritance studies of resistance to *Fusarium* wilt disease were carried out by Jones (1969). He observed that the entire variance for resistance to *Fusarium* wilt was accounted for by the additive component and that heritability was high. These results were further confirmed by Collins (1977) based on a diallel analysis of sweetpotato resistance to *Fusarium* wilt. There is limited information in the available literature about similar studies on *Alternaria* blight of sweetpotato and thus its mode of inheritance is not known. However, genetic studies have been carried out on two related diseases, *Alternaria* leaf

blight (*Alternaria dauci* (Kühn) Groves and Skolko) of carrot by Simon and Strandberg (1998), and *Alternaria* early blight (*Alternaria solani* Sorauer) of diploid potato (*Solanum tuberosum* L.) by Christ and Haynes (2001). Simon and Strandberg (1998) used the diallel and observed highly significant genotypic differences for resistance to *Alternaria* blight in carrot with both general combining ability (GCA) and specific combining ability (SCA) effects contributing significantly to the variation but the GCA sum of squares (SS) were 2.2 times greater than the SCA SS. Thus, the additive variance was more important than the non-additive variance. Christ and Haynes (2001) reported narrow-sense heritability of 61% for resistance to early blight in potato indicating that additive genetic variance predominates.

### **1.8.2 The polycross mating design**

Controlled crossing methods based on for example, diallel (Griffing, 1956) and North-Carolina II factorial (Comstock and Robinson, 1952) mating designs are very reliable for identifying superior parents and good cross-combinations. However, their use in sweetpotato and potato breeding is difficult, labour intensive and time consuming. In these methods, a set of crosses are required to be made in which selected female parents are crossed with selected male parents in a specific pattern based on the design (Gopal, 1994). With incompatibility and sterility in sweetpotato coupled with poor seed set, obtaining the required cross-combinations is usually very difficult. Therefore, controlled crossing can be avoided by exploiting random, open-pollination in a polycross design (Jones and Dukes, 1980; Stuber, 1980; Jones, 1986). A polycross is the natural inter-crossing of a group of plants in an isolated crossing block (Stuber, 1980; Nyquist and Santini, 2007). Jones (1986) recommended that a limited number of parents (not more than 30) should be used to establish a polycross and left to be randomly crossed by naturally occurring insects, usually honey bees. The parents in a polycross are arranged in such a way so as to provide an equal opportunity for each to cross with each and every other parent (Stuber, 1980; Nyquist and Santini, 2007). For a polycross arrangement to be perfect, each parent should have every other parent as the nearest neighbour once in all four compass directions i.e. south, north, east and west (Olesen and Olesen, 1973). Wright (1965) outlined a total of 12 field plans for systematically designed polycross arrangements starting with a 6 x 6 to a 46 x 46 genotype layout in which he clearly demonstrated the nearest neighbour principle. In all these arrangements, an important aspect of a polycross that can determine its success or failure is synchronisation of flowering. This may necessitate staggered planting of the parents so that they all bloom at the same time (Stuber, 1980). In addition, Tumana and Kesavan (1987) emphasised the need for self-incompatibility and cross-compatibility among parents if the polycross system of mating is to be effective. In this design, only the female parent of each family is known and the progeny are half-sibs (Stuber, 1980) and only the GCA effects can be generated (Olesen and Olesen, 1973; Saladago, 1989).

### 1.8.3 North Carolina mating designs

Comstock and Robinson (1952) suggested three mating designs, North Carolina mating design I, II and III (or simply Design I, II and III), and described their statistical analyses to study gene action affecting quantitative traits. In the North Carolina I mating design or hierarchical design, the non-common parents are divided into sets. Each set is mated to one common parent, which is the common parent for the progeny from that set. That is, each member of a group of parents used as males is mated to a different group of parents used as females and no female is involved in more than one mating with the pollen parents (Dabholkar, 1992). This design is useful in generating and evaluating half-sib and full-sib families for recurrent selection and also estimating additive and dominance variances (Acquaah, 2009).

North Carolina II design is a factorial mating design where each member of a group of parents used as males is mated to each member of another group of parents used as females. It is useful in estimating genetic variance and combining ability as well degree of dominance (Stuber, 1980). This method is more applicable to plants that produce multiple flowers and each plant can be used repeatedly both as a female and male (Stuber, 1980; Lynch and Walsh, 1998; Acquaah, 2009). Every male is mated to each female following a two-way analysis of variance, in which the variation can be partitioned into differences between males ( $\sigma^2_m$ ) and females ( $\sigma^2_f$ ) and the interaction between them ( $\sigma^2_{m \times f}$ ) (Hill et al., 1998; Acquaah, 2009).

**Table 1.1: ANOVA for the North Carolina II design repeated over environments**

Source	df	Mean squares	E(MS)
Environments	e-1		
Replications /E	e(r-1)		
Males (GCA)	(m-1)	M <sub>7</sub>	$\sigma^2 + r\sigma^2_{mfe} + rfo^2_{me} + re\sigma^2_{mf} + ref\sigma^2_m$
Females (GCA)	(f-1)	M <sub>6</sub>	$\sigma^2 + r\sigma^2_{mfe} + rmo^2_{fe} + re\sigma^2_{mf} + rem\sigma^2_f$
Males x females (SCA)	(m-1)(f-1)	M <sub>5</sub>	$\sigma^2 + r\sigma^2_{mfe} + re\sigma^2_{mf}$
Males x E	(m-1)(e-1)	M <sub>4</sub>	$\sigma^2 + r\sigma^2_{mfe} + rfo^2_{me}$
Females x E	(f-1)(e-1)	M <sub>3</sub>	$\sigma^2 + r\sigma^2_{mfe} + rmo^2_{fe}$
Males x females x E	(m-1)(f-1)(e-1)	M <sub>2</sub>	$\sigma^2 + r\sigma^2_{mfe}$
Pooled error	e(r-1)(mf-1)	M <sub>1</sub>	$\sigma^2$
Total	ermf-1		

Where:  $\sigma^2$  = Variance within full-sibs = environmental variance;  $\sigma^2_m$  = Variation between males = GCA<sub>m</sub> variance;  $\sigma^2_f$  = Variation between females = GCA<sub>f</sub> variance;  $\sigma^2_{mf}$  = Variation due to interaction between males and female = SCA variation;  $\sigma^2_{me}$  = Variation due to interaction between males and the environment;  $\sigma^2_{fe}$  = Variation due to interaction between females and the environment;  $\sigma^2_{mfe}$  = Variation due to SCA interaction with the environment.

**Source:** Hallauer and Miranda (1988)

In the North Carolina II design, the mean square (MS) for males and MS for females provide direct estimates of the GCA for males and GCA for females, respectively. The male x female interaction MS estimates the SCA (Hallauer and Miranda, 1988).

North Carolina III was developed by Comstock and Robinson (1948). In this design, two parents (s and m) are hybridised to produce the hybrids (sm) which becomes the reference population. Random selection from these hybrids is done and those that are selected are backcrossed to the two parents. At this level, the two parents become the females (seed parents) and the selected hybrids are the males (pollen parents). This generates a new population 2sm. The 2sm progeny families are divided into n sets for field planting. Each set comprises of p pairs of progeny families. In this design, members of each pair have the male parent in common but the female parents are different. The female parents are fixed while the male parents are randomly selected from the sm. Thus, the effects of the females are regarded as fixed (Dabholkar, 1992). The advantages of this design are that it estimates: the average level of dominance of genes affecting the evaluated traits; the additive and dominance variance for sm population assuming no linkage and epistasis; and heritability of the traits evaluated (Hallauer and Miranda, 1988).

North Carolina mating designs I, II and III provide plant breeders with information regarding the inheritance of traits being investigated for a reference population. This knowledge allows plant breeders to determine whether selection aimed at cultivar development will be feasible from this source population and what breeding method could be the best for such a goal (Ortiz and Golmirzaie, 2002).

### **1.9 Participatory selection in sweetpotato**

In most developing countries, relatively few farmers in marginal areas have adopted improved cultivars (Witcombe et al., 1996). The low adoption rate of new cultivars among the resource poor farmers is sometimes due to lack of exposure to acceptable cultivars that can fully replace their landraces even though cultivars with desired attributes may exist among the new releases (Joshi and Witcombe, 1996; Witcombe et al., 1996). Farmers prefer their landraces to the new cultivars even if the improved ones are higher yielding and more resistant to pests and diseases. This is because over the years, farmers have selected their landraces for specific attributes which may be lacking among the new introductions (Witcombe et al., 1996). In addition, some attributes that scientists consider important may not actually be what the farmers really want. There is therefore a need to shift from formal plant breeding (FPB) to Participatory Plant Breeding (PPB) (Sperling et al., 1993) or participatory cultivar/variety selection (PVS) (Witcombe et al., 1996; Almekinders and Elings, 2001). In PPB, the farmers influence the breeding objectives which in turn influences the choice of parents and mating designs and are involved in selection of genotypes from segregating populations, whereas in PVS, farmers evaluate advanced selections that are being considered for release (Witcombe et al., 1996).

Participatory breeding in sweetpotato has been extensively used by the North Carolina State University in USA since the early 1990s (Yencho et al., 2002). The involvement of farmers in

the evaluation of advanced sweetpotato lines has also been successfully done in Kenya (Ndolo et al., 2001), Uganda (Abidin et al., 2002; Abidin, 2004) and South Africa (Laurie and Magoro, 2008).

In Uganda, the National Sweetpotato Program in collaboration with the CIP initiated client-oriented breeding in 1995 with a survey of farmer needs (Bashaasha et al., 1995). The most important traits to the farmers were sweet taste, high dry mass and good yield, and based on the identified needs, six cultivars were bred on-station using some of the local germplasm with farmer desired attributes (Mwanga et al., 2007). Similarly, Gibson et al. (2008) worked with farmers and NGOs to develop new sweetpotato genotypes in three districts; Masaka, Luwero and Mpigi. The program was a success and led to the development and release of NASPOT 11 (Mwanga et al., 2011). Evidently, the involvement of farmers at crucial stages in a breeding program is important.

### **1.10 Selection Index**

A selection index (SI) can be used to integrate farmer identified traits and preferences with breeder objectives into an index of merit upon which superior genotypes are selected (Ceballos et al., 2004). Hazel (1943) introduced the aggregate genotype concept which is a linear combination of genetic values, each weighted by the relative economic value and designed to maximise the genetic-economic merit or aggregate breeding value for multiple traits among individuals in a population. Relative efficiency of the selection index depends upon the number of traits selected, relative economic values of traits, heritability, phenotypic and genotypic correlation between traits and selection intensity (Young and Tallis, 1961). The main purpose of the SI is that it can also be used as a performance index (Nordskog, 1978).

### **1.11 Genotype x environment interaction in sweetpotato**

A further challenge facing breeders is the interaction between genotypes and environments (GEI) which reduces the association between the genotype and phenotype. Sweetpotato is known to be very sensitive to environmental changes (Bacusmo et al., 1988). It is grown in diverse environments especially by small-scale resource poor farmers who use degraded soils with low use of agricultural inputs. Despite being grown in such diverse environments, it has been observed that the performance of different sweetpotato cultivars depends on the environment (Nasayao and Saladaga, 1988). This change in sweetpotato performance is a result of the complex phenomenon of GEI which may lead to a change in the relative ranking of the genotypes from one environment to another. The sensitivity of sweetpotato to environmental changes has been studied for several important traits (Collins et al., 1987; Bacusmo et al., 1988; Kanua and Floyd, 1988; Martin et al., 1988; Nasayao and Saladaga, 1988; Naskar and

Singh, 1992; Ngeve, 1993; Manrique and Hermann, 2000) and in all cases the GEI has been observed to complicate sweetpotato breeding and genotype selection.

Genotype x environment interaction has a significant effect on yield and yield components of sweetpotato (Bacusmo et al., 1988), thus it is important to determine the most suitable cultivar for a certain site (Caliskan et al., 2007a,b). Root mass, one of the most important traits, crude protein, and percentage dry mass exhibited significant variation under different environments (Collins et al., 1987). Studies by Osiru et al. (2009) in Uganda, Mbwaga et al. (2007) in Tanzania, Caliskan et al. (2007a) in Turkey and Moussa et al. (2011) in Egypt showed significant GEI among sweetpotato cultivars grown in different agro-ecological zones as well as over seasons. In a related study, Caliskan et al. (2007b) recorded significant differences in percentage dry mass (DM%) among cultivars across sites. Furthermore, Kanua and Floyd (1988) also reported significant GEI among sweetpotato cultivars in Papua New Guinea but in addition they observed that exotic cultivars had greater interaction with the environment than the local ones.

In a study to determine the GEI for a set of sweetpotato genotypes across several ecological conditions in Peru, Grüneberg et al. (2005) observed three categories of high yielding genotypes: those that were high yielding with wide adaptation; those that were high yielding with specific adaptation to medium and high yielding environments; and those that were high yielding with specific adaptation to low yielding environments. Therefore, it is possible to breed sweetpotato for high yield and wide adaptation.

A genotype is considered to be stable if it shows consistent performance across different sites or years (Fernandez, 1991). Several statistical methods have been used to determine stability in sweetpotato over a wide range of environments. Ngeve (1993) carried out studies to determine if there were significant differences in the yield potential, total yield, marketable yield, and number of storage roots in both the local and improved genotypes. He observed significant differences due to site and year. However, the regression methods of Eberhart and Russell (1966) and Shukla (1972) ranked the genotypes differently with some genotypes ranked as stable by the one method and as unstable by the other. Bacusmo et al. (1988) compared the effectiveness of different stability methods in determining the stability and adaptability of 14 sweetpotato genotypes. The results indicated that the Eberhart and Russell (1966) and Tai (1971) methods are related and did not effectively separate the genotypes according to their stability. Shukla's (1972) stability method had a good association with the Eberhart and Russell (1966) and Tai (1971) methods but Shukla's method provides a means of assigning a variance component due to individual genotypes and a test of significance of the variance components. It is the variance component and the trait mean of each genotype that are used for selecting superior and stable genotypes. These observed inconsistencies in identifying stable genotypes



by different methods show that choice of method is crucial in identifying stable genotype and more than one method should be used in determining the stability of genotypes.

All the above methods have been widely used in GEI studies. However, the Additive Main effects and Multiplicative Interaction (AMMI) analysis method has gained popularity and is now widely preferred for GEI studies in sweetpotato (Manrique and Hermann, 2000; Grüneberg et al., 2005; Mbwaga et al., 2007; Mwololo et al., 2009; Osiru et al., 2009). The AMMI analysis gives a more appropriate statistical analysis of trials that may exhibit GEI. It incorporates both additive and multiplicative components into an integrated, powerful, least squares analysis and is the most appropriate when both the main effects and interactions are important (Freeman, 1985).

For graphical examination of the relationship among genotypes, test environments and GEI, AMMI biplots for interaction principal component analysis 1 (IPCA1) scores (y-axis) versus the genotype and environmental means (x-axis) or IPCA2 (y-axis) versus IPCA1 (x-axis) (Zobel et al., 1988) and the GGE (genotype main effect plus genotype by environment interaction) biplots (Yan et al., 2000) can be used. These are effective tools for (i) mega-environment analysis (“which won where” pattern) whereby specific genotypes can be recommended for specific mega environments (Yan and Kang, 2003; Yan and Tinker, 2006), and (ii) genotype evaluation (the mean performance and stability) and environment evaluation (the power to discriminate among genotypes in the target environments) (Ding et al., 2007).

#### **1.11.1 AMMI stability value**

Since the AMMI model does not directly make provision for a quantitative stability measure, Purchase et al. (2000) developed the AMMI stability value (ASV) based on the IPCA1 and IPCA2 scores for each genotype. The ASV is the distance from zero to each co-ordinate point (i.e. the hypotenuse) in a two dimension scattergram of IPCA1 versus IPCA2 scores and is determined using the Pythagoras’ theorem. Due to the higher contribution of the IPCA1 axis to the GEI SS than the IPCA2 axis, the IPCA1 score is weighted by the ratio of IPCA1 SS to IPCA2 SS in the calculation of the ASV. The lower the ASV, the higher the stability ranking of the genotype. However, in selecting preferred cultivars, stability *per se* is not the only parameter considered since the most stable cultivars are not necessarily the best performers for the trait of interest. Therefore, the genotype selection index (GSI) was developed.

#### **1.11.2 Genotype selection index**

The genotype selection index (GSI) incorporates both the mean performance and stability of a cultivar for a particular trait into a single index (Farshadfar, 2008). The GSI combines the ASV rank for a particular genotype and the mean performance rank of the genotype in each

environment. For example, a genotype with the lowest ASV for a trait is ranked one and a genotype with the best mean performance for a trait (e.g. yield) is ranked one. The ranks for each genotype are added together providing a single selection index, the GSI, for trait performance and stability. The genotype with the smallest GSI is considered the most desirable combining stability and high mean performance for the trait.

### **1.12 Heterosis**

Heterosis has been recognized as a phenomenon in plant and animal breeding for more than a century. In plants, heterosis is evidenced by, for example, increased vigour, size, fruitfulness, speed of development, resistance to diseases and pests and climatic vigour (Shull, 1952). Heterosis may also manifest as enhanced hybrid performance (Hartl and Clark, 2007). Heterosis results from the combined action and interaction of allelic and non-allelic factors and is usually closely and positively correlated with heterozygosity (Burton, 1968). It is considered to be an outcome of genetic complementation between divergent parents and the quantitative genetic explanation for this phenomenon depends directly on the existence of dominance action at different loci in the hybrids (Prasad and Singh, 1986). Heterosis can be expressed as mid-parent heterosis, better parent heterosis and best parent heterosis (BPH). The latter, reflects superiority of the hybrids over the best parent (Islam et al., 2011).

### **1.13 Summary**

It is apparent from the literature that *Alternaria* blight of sweetpotato is a serious production constraint, which if not addressed may completely undermine sweetpotato production in the near future. Given that *Alternaria* blight thrives very well in low fertility soils, resource poor farmers who use marginal land with no inputs will be the most affected. Since sweetpotato is a low value crop, host plant resistance is the most appropriate option to control *Alternaria* blight. However, farmers desire genotypes that combine disease resistance with their preferred traits. This requires a well-designed breeding program to identify *Alternaria* blight resistant genotypes from the available germplasm and recommend them to farmers in areas with high incidence of the disease, while at the same time breeding new genotypes that combine disease resistance with farmer-preferred traits. The target farmers should also be involved at appropriate stages in the program to facilitate selection for their preferred traits.

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## Chapter 2

### **Farmers' awareness and perceptions of *Alternaria* leaf petiole and stem blight and their preferred sweetpotato traits in Uganda**

#### **Abstract**

A participatory rural appraisal was conducted in Kabale district in south-western Uganda and Luwero district in central Uganda in January, 2010 in order to establish farmers' awareness and perceptions of *Alternaria* leaf petiole and stem blight (commonly referred to as *Alternaria* blight) and their varietal preferences. The study revealed that the two regions had similar production constraints but the degree of importance of the constraints varies between each region. Diseases, pests and drought are the most important production constraints in both regions. Among the diseases, *Alternaria* blight is the most important disease constraint in Kabale whereas sweetpotato virus disease is the most important in Luwero. Among the pests, caterpillars (*Acraea acerata*) are a bigger problem in Luwero than in Kabale, while vermin, especially mole rats (*Tachyoryctes splendens*), are a bigger problem in Kabale than in Luwero. Drought is a serious constraint but mainly in Luwero. Furthermore, clean planting material availability and distribution are important constraints. Among the most desired sweetpotato attributes in both districts are high yield, early maturity, high dry mass, and storability in the soil after maturity to enable sequential harvesting. Most of the farmers consider *Alternaria* blight to be a serious production constraint and estimate the yield loss in severely infected fields to be above 50%. However, *Alternaria* blight incidence has seasonal variations with higher incidences in the wet and very wet seasons in Kabale. On the other hand, *Alternaria* blight is most severe during the dry season in Luwero. Most of the farmers are not aware of any control measures for these diseases. However, some of them use roguing as a control measure and others cultivate resistant genotypes like Rwabafuruki and Nyinakamanzi in Kabale, and Kakamega in Luwero. Since most of the existing genotypes are susceptible, breeding for *Alternaria* blight is a priority in both districts combined with an effective seed distribution system to increase utilization of the improved cultivars by the resource poor farmers.

## 2.1 Introduction

Sweetpotato (*Ipomoea batatas* (L.) Lam.) is a major food security crop in Uganda (Low, 2000). It is a staple for both the urban and rural-resource poor communities with a per capita consumption of 82.5 kg yr<sup>-1</sup> (FAOSTAT, 2010). The crop is mainly grown for its edible storage roots, but in isolated cases the leaves are eaten as vegetables (Bashaasha et al., 1995). Low productivity characterises sweetpotato production in the country and this has been attributed to several factors. These include susceptibility to diseases including sweetpotato virus disease (SPVD) and *Alternaria* leaf petiole and stem blight (commonly referred as *Alternaria* blight), use of marginal lands, low input use and use of low-yielding and narrowly adapted landraces (Bashaasha et al., 1995; Low, 2000). Some of these constraints can be overcome by the release of improved cultivars specifically bred to overcome those constraints. Between 1995 and 2011, the Uganda National Sweetpotato Program released a total of 20 cultivars (Mwanga et al., 2011). However, despite the abundance of new improved cultivars, the majority of the farmers still prefer their landraces which are lower yielding and more susceptible to diseases and pests (Abidin et al., 2002). Lack of an organised seed distribution system is one of the factors for low adoption of the new cultivar (Gibson et al., 2009). Another factor is the lack of farmer desired attributes. Cultivars NASPOT 2, NASPOT 5 and Sowola 6 from the National Sweetpotato Program were abandoned by farmers soon after their release because they lacked farmer preferred attributes (Abidin et al., 2002). The low adoption rate among the resource poor farmers is sometimes due to lack of exposure to acceptable new cultivars that can replace the landraces in use (Joshi and Witcombe, 1996; Derera et al., 2006).

Farmers have good knowledge of the traits they would like to have included in a new cultivar (Abidin et al., 2002; Were et al., 2012). Therefore a complementation between farmers' preferred traits and traits selected for by the breeder that the farmers may not understand due to the complexity thereof is the way forward. Farmer involvement has led to rapid selection and dissemination of new sweetpotato cultivars with desired traits in South Africa (Laurie and Magoro, 2008), in Kenya (Ndolo et al., 2001) and in some parts of Uganda (Gibson et al., 2008). In their selection criteria for sweetpotato, farmers take several factors into consideration which include the number and size of storage roots, the taste, skin and flesh colour, and culinary qualities (Abidin et al., 2002).

A farmer-oriented breeding process should start with a participatory rural appraisal (PRA) (Joshi and Witcombe, 1996). According to Chambers (1997), "PRA is a family of approaches and methods to enable local people to share, enhance, and analyse their knowledge of life and conditions, to plan and to act". It entails involving local people in the gathering of information so that the actual farmer conditions are understood and a dialogue between the scientists and

farmers is established (Odendo et al., 2002). In Uganda, the National Sweetpotato Program initiated client-oriented breeding in 1995 with a survey of farmer needs (Bashaasha et al., 1995) which became the basis for the development of several improved cultivars (Mwanga et al., 2007). Similarly, in a bid to improve adoption, Gibson et al. (2008) worked with farmers and non-governmental organisations (NGOs) to develop new sweetpotato genotypes in Mpigi, Luwero and Kiboga districts. This effort yielded results with the release of NASPOT 11, the first cultivar bred from segregating populations by participatory plant breeding (PPB) in Uganda (Mwanga et al., 2011). During the early stages of evaluating this cultivar, Gibson et al. (2008) reported a decline in farmer enthusiasm among the participating farmers. To maintain farmers' enthusiasm, it is better to involve them in evaluating materials grown on the research station and only let them grow advanced materials in their fields (Ceccarelli et al., 2000). In this process, traits are identified that breeders had not considered important or were not previously aware of. With careful consideration of farmers' concerns and production conditions, genotypes selected using this procedure are likely to become widely adapted and more productive (Odendo et al., 2002).

The present study was designed to obtain information from farmers to help understand their current farming conditions and problems. This information will help in supporting a sweetpotato breeding programme in Uganda for resistance to *Alternaria* blight. The PRA was carried out in January 2010 with the following objectives:

- i. identify farmers' preferred sweetpotato attributes;
- ii. determine farmers' perceptions of sweetpotato production constraints;
- iii. establish the sweetpotato production practices and the major genotypes grown in the study areas;
- iv. assess farmers' awareness of *Alternaria* blight incidence and severity;
- v. assess farmers' practices in combating *Alternaria* blight;
- vi. assess farmers' preferred sweetpotato genotypes; and
- vii. establish the sweetpotato attributes that farmers consider as priorities for breeders to work on.

## **2.2 Materials and methods**

### **2.2.1 Study area**

The study was carried out in two districts: Kabale district (1°45' S; 29°18' E) located in South-western Uganda 400 km from Kampala; and Luwero district (0°50' N; 32°28' E) located in central Uganda 40 km from Kampala. Both districts are major sweetpotato producing areas. Kabale is a "hotspot" for *Alternaria* blight while Luwero is a "hotspot" for SPVD with medium *Alternaria* blight

disease pressure (Osiru et al., 2007). In each district, one sub-county was selected. In each sub-county, two parishes were selected and in each parish two villages were purposively selected based on the production of sweetpotato. Selection of the sub-county was done in consultation with the district agricultural officers based on the sweetpotato production records. Selection of the parishes was done in consultation with the sub-county agricultural extension officers.

In Kabale, the study was carried out in Bubaare sub-county (1°15' S; 29°91' E), Bubaare and Nyamiyaga parishes. Bushura and Rwamutasya villages were selected from Bubaare parish, while Rwembugu and Hamurara were selected from Nyamiyaga parish. In Luwero district, Nakatonya and Sambwe parishes were selected in Nyimbwa sub-county (0°36' N; 32°48' E). In Nakatonya parish, Kikomeko and Mayirikiti villages were selected, while Kiyana village was selected in Sambwe parish.

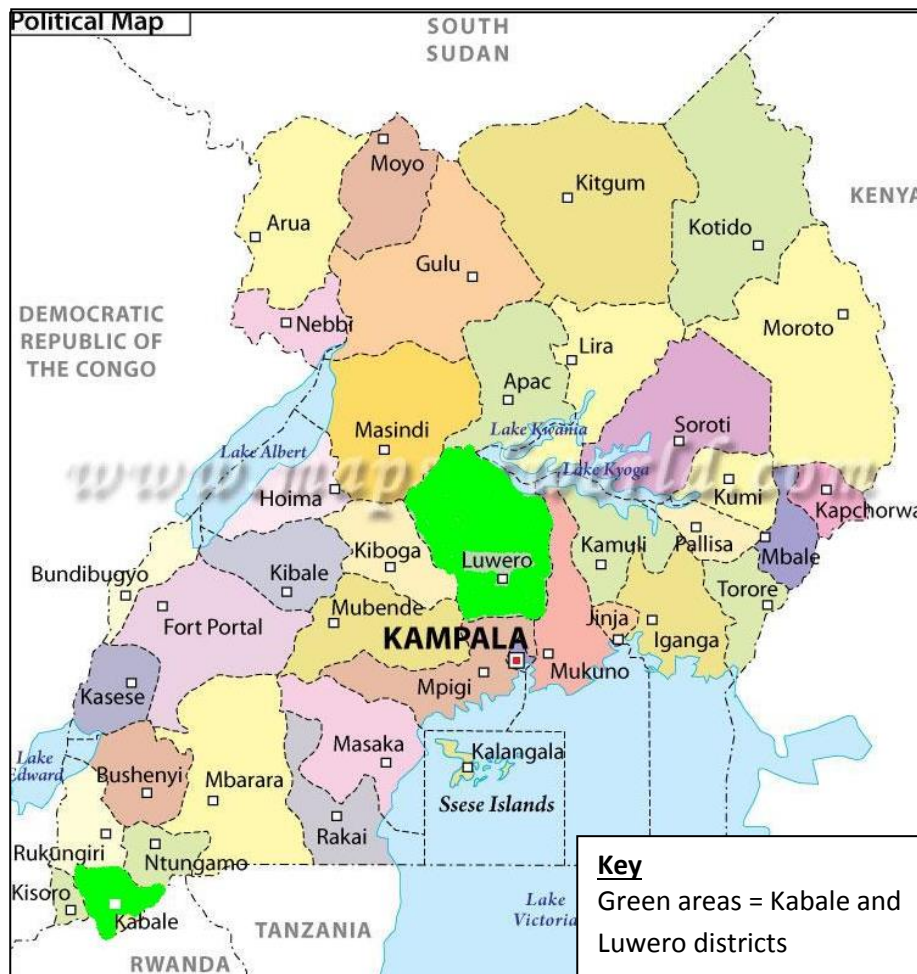
### **2.2.2 Description of the study districts**

Kabale district borders with Kisoro district in the west, Kanungu and Rukungiri districts in the north, Ntungamo district in the east, and the Republic of Rwanda in the south (Figure 2.1). Kabale district has a high population density of 317 people per km<sup>2</sup> in non-forested areas (Uganda Bureau of Statistics, 2002) and the residents are mainly from the Bakiga tribe and others are Banyarwanda and Bafumbira. It is characterised by small, highly fragmented landholdings and declining soil fertility and a high rate of male migration in search of employment (Low, 2000). The landscape in Kabale is very hilly, interlaced with narrow and broad valleys. Altitudes range from 1400 - 2500 m above sea level. Annual rainfall ranges from 1000 - 1500 mm and occurs in two seasons. The first season is from mid-February to May and is referred to as the short rains, while the second season is from September to December and is referred to as the long rains. The annual temperatures range between 11.6 and 24.1°C, and the mean annual temperature is 18°C.

Luwero district borders with Kiboga and Mubende districts in the west, Masindi and Nakasongola districts in the north, Kayunga and Mukono in the east, and Wakiso district in the south (Figure 2.1). The district has a population density of 90 persons per km<sup>2</sup> and the residents are of several ethnic backgrounds mainly the Baganda, who are the original inhabitants, Banyankole from western Uganda, Banyarwanda, Luo speakers and Nubians of Sudanese origin. Agriculture is the major economic activity employing over 85% of the workforce. Altitude ranges from 1050 - 1200 m above sea level. The climate can be described as modified equatorial climate with mean maximum diurnal temperature ranging between 18 and 35°C while the corresponding mean minimum diurnal temperature ranges between 8 and 25°C. Rainfall is



well distributed throughout the year and much of the area receives 1000 - 1250 mm per annum with two peaks in March - June, and October - November (NEMA, 2004).



Source: <http://www.mapsofworld.com/uganda/uganda-political-map.html#>

**Figure 2.1 The two study districts in Uganda**

The study was conducted in January 2010. In order to obtain qualitative and quantitative data; both an individual household questionnaire (Appendix 2.1) and focus group discussion (FGD) (semi-structured questionnaires) were used. Fifteen farm households were selected from each village. One FGD was conducted in each of the study parishes, thus a total of four FGD. Each focus group consisted of 15-20 people who included experienced sweetpotato farmers, opinion leaders/elders, local council or village leaders, a youth representative and a trader.

Prior to the study, the principal researcher together with a socio-economist carried out a reconnaissance study of the two districts to establish a rapport with the district agricultural officers (DAO) and the sub-county agricultural extension officers. During the visits, the production records were reviewed with the assistance of the DAO and a decision made on which sub-counties to conduct the study in. Each sub-county agricultural extension officer

assisted in selecting the parishes and villages. A questionnaire was developed, pre-tested in Mukono and corrections made before the study was carried out.

### **2.2.3 Household (individual) interviews**

The individual interviews (Figure 2.2) were carried out by the principal investigator and the socio-economist using a questionnaire (Appendix 2.1) to obtain the following information: the farmers' bio-data (background information e.g. sex, age, marital status, size of the family); size of the farm, crops grown; area under sweetpotato; why the farmer grows sweetpotato; yields per hectare; genotypes grown; seed supply system; attributes of sweetpotato genotypes and pairwise ranking of these attributes; criteria for selecting or rejecting genotypes; sweetpotato production constraints and pairwise ranking of these constraints; *Alternaria* blight awareness; incidence and severity; varietal susceptibility; seasonal variation; yield loss; *Alternaria* blight control measures; and market values for the different genotypes. The farmers compared the prevalence of the constraints over different seasons and years. Throughout an interview, open-ended questions were used so as to capture as much information as possible. A compass direction was randomly taken by the team and along that direction the fourth homestead, for example, would be randomly selected. For the owner of the homestead to be interviewed, he/she had to be a regular sweetpotato grower and have a field grown to sweetpotato during the season of the study. Sixty farmers were interviewed in each district providing a total of 120 farmers for the whole survey.



**Figure 2.2 Individual household interview in Bubaare sub-county, Kabale district (2010)**

### 2.2.4 Focus group discussions

The discussion (Figure 2.3) was assisted by a facilitator who was proficient in both the local language and English. A checklist of discussion topics/questions was developed (Appendix 2.2) and used to guide the discussion. Open-ended questions were asked to generate discussion and the facilitator made sure every person present contributed towards the discussion topic.

The information obtained in these focus group discussions included: sweetpotato production constraints (biotic and abiotic and their causes), genotypes grown and preferred sweetpotato attributes. All these were ranked using the pairwise ranking method (Narayanasamy, 2009) (Figure 2.4) so that the factor with the highest number of points is ranked as number one. Particular attention was given to *Alternaria* blight and the participants drew a seasonal calendar and indicated which time of the year the disease was more likely to occur.

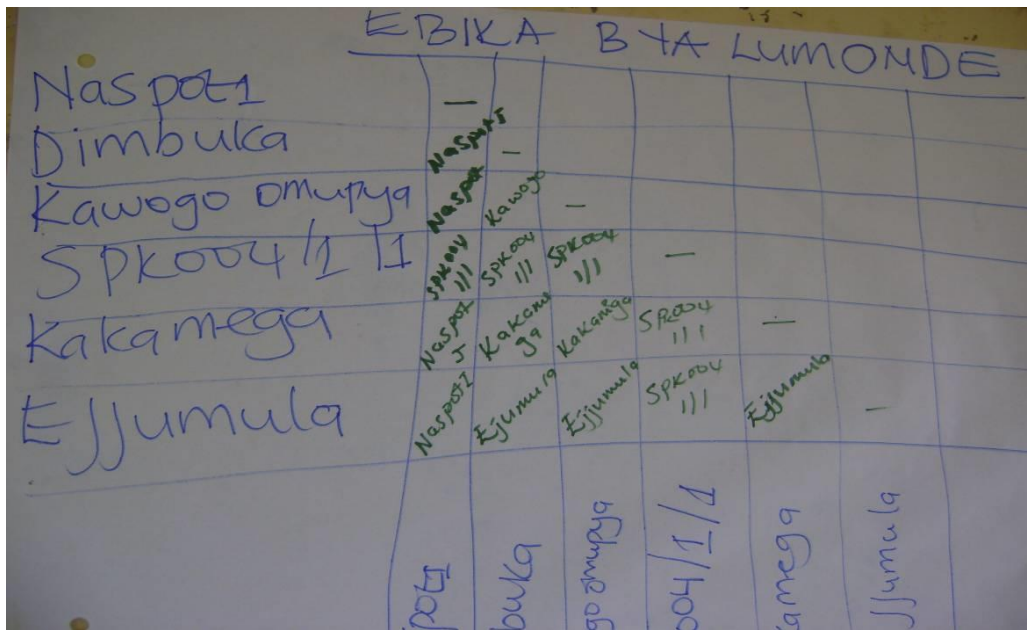


**Figure 2.3 Focus group discussion at Nyamiyaga parish, Bubaare sub-county, Kabale district (2010)**

Since one of the objectives of the PRA was to identify breeding priorities, the participants were asked what attributes they desired in new sweetpotato cultivars.

### 2.2.5 Secondary data

Details of the geographical location of each sub-county was obtained from the sub-county records including the neighbouring sub-counties, demographic information, major crops grown and sweetpotato production trends over the last five years. Meteorological information was also collected from each sub-county.



**Figure 2.4** Pairwise ranking for sweetpotato genotypes at Nakatonya, Luwero district (2010)

### 2.2.6 Data analysis

Data from the survey were analysed using the Statistical Package for Social Scientists Version 15.0 for Windows (SPSS, Inc. 2008).

### 2.3 Results

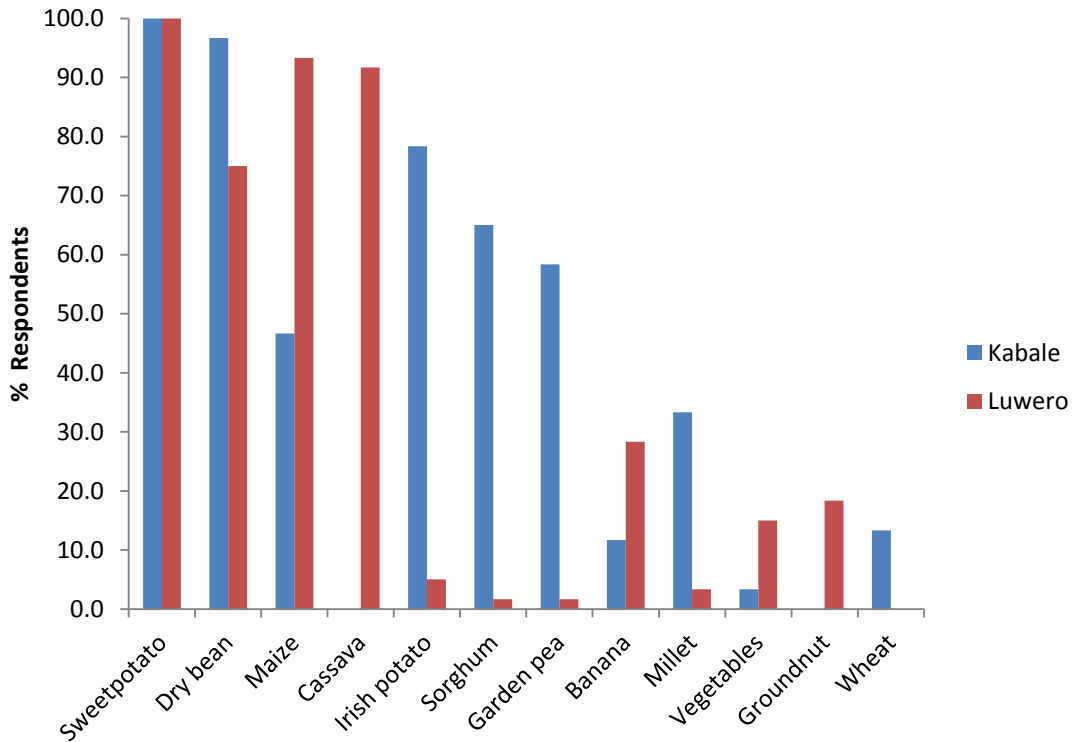
#### 2.3.1 Gender and ages of interviewed farmers

Most of the respondents in both districts were females (72.5%). The ages of the respondents varied greatly with the youngest being 19 and the oldest 81 years old. The farmers in Kabale have been growing sweetpotato for periods ranging from 2 to 65 years while those from Luwero for 3 to 7 years.

#### 2.3.2 Size of the land and crops grown

From the structured survey, the average size of farmland in the two districts was 1.1 ha with farmers in Luwero district owning an average of 1.2 ha while those in Kabale had an average of 0.9 ha. Of this farmland, the average area under crops was 0.9 and 0.7 ha in Luwero and Kabale, respectively. Farms in Luwero district had a larger area under sweetpotato production per season of 0.3 ha as compared to 0.2 ha in Kabale. Luwero district had higher average sweetpotato yields ( $6.9 \text{ t ha}^{-1}$ ) than Kabale ( $4.6 \text{ t ha}^{-1}$ ). Farmers in both districts grew a large number of crops and most of them were grown as intercrops. Other than sweetpotato, the most common crops in Kabale were dry bean (*Phaseolus vulgaris* L.) (96.7%), Irish potato (*Solanum tuberosum* L.) (78.3%) and sorghum (*Sorghum bicolor* L.) (65.0%), whereas in Luwero they

were maize (*Zea mays* L.) (93.3%), cassava (*Manihot esculenta* Crantz) (91.7%) and dry bean (75.0%). Cassava and groundnut (*Arachis hypogea* L.) were grown only in Luwero district whereas wheat (*Triticum aestivum* L.) was grown only in Kabale (Fig. 2.5).

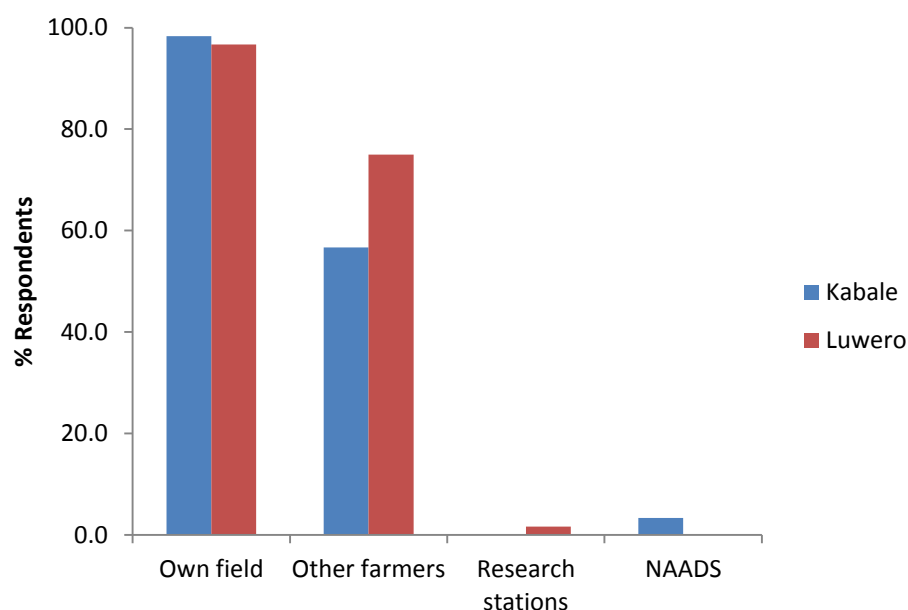


**Figure 2.5 Major crops grown in Kabale and Luwero districts of Uganda (2010)**

### 2.3.3 Source of planting materials

The principal source of sweetpotato planting materials (vines) in both districts was the farmers' own fields (Figure 2.6). Most farmers (97.5%) retained some vines from the previous season in the field as a source of planting material for the new season. Some farmers (65.8%) sourced their vines from other farmers. In Kabale, all vines were shared free of charge whereas in Luwero, the vines were occasionally sold. The other common sources of vines were research stations, especially in Luwero, and the National Agricultural Advisory Services (NAADS) in Kabale.

The majority of farmers (61.7%) in both districts had problems with planting materials. The problems included lack of access to good (healthy) vines and scarcity thereof, especially after a long dry spell. Infestation by caterpillars of vines was a problem in Luwero district (14.9%), usually after a long dry spell.



**Figure 2.6 Sources of sweetpotato vines in Kabale and Luwero districts of Uganda (2010)**

### 2.3.4 Sweetpotato cropping method

The majority of farmers in both districts (76.0%) planted sweetpotato in pure stands. In Kabale, some farmers intercropped, mainly with dry bean and garden pea (*Pisum sativum* L.) whereas in Luwero some farmers intercropped with dry bean, cassava or maize (Table 2.1). In Kabale, the farmers intercropped because of shortage of land whereas in Luwero for food security reasons.

**Table 2.1 Crops commonly intercropped with sweetpotato in Kabale and Luwero districts of Uganda (2010)**

Intercrop	% Kabale	% Luwero
Maize	0.0	16.7
Dry bean	61.5	16.7
Cassava	0.0	66.6
Garden pea	38.5	0.0

The majority of the farmers (83.0%) planted several sweetpotato genotypes in a single plot or garden. In Kabale, all the farmers planted mixed genotypes, whereas in Luwero only 16.7% planted a single genotype per field and these were mainly for the production of vines and roots for the market. All the farmers in Luwero planted sweetpotato on individual mounds whereas most of the farmers in Kabale (95.0%) planted on long, narrow ridges across the hill slope. In Kabale, some farmers planted sweetpotato in the wetlands during the dry season to provide planting materials for planting on the hillsides in the forthcoming rainy season.

### 2.3.5 Sweetpotato genotypes grown

In Kabale, 95.0% of the farmers grew only landraces while the rest grew both improved cultivars and landraces. In Luwero, 8.3% of the farmers grew improved cultivars only and 91.7% grew both improved cultivars and landraces. The farmers who planted only the improved cultivars were those involved in commercial vine production and some also produced orange fleshed sweetpotato (OFSP).

The most highly ranked attributes by farmers were high yield, early maturity and sweetness of the roots (Tables 2.2 and 2.3). The most commonly grown genotypes in Kabale were all landraces whereas in Luwero they were all improved cultivars.

**Table 2.2 Most commonly grown sweetpotato genotypes in Kabale district of Uganda and their attributes (2010)**

Genotype	Desirable attributes (ranked)			
	1	2	3	4
Nyinakamanzi	High yield	Early maturity	Good ground cover	Sweetness
Mukazi	High yield	Sweetness	Early maturity	High dry mass
Rwabafuruki	Early maturity	Sweetness	High yield	High dry mass
Mukono	High yield	Early maturity	Sweetness	Good ground cover
Kanyasi	Sweetness	High dry mass	High yield	Ground storability
Kidodo	High yield	Early maturity	Sweetness	Large roots

**Table 2.3 Most commonly grown sweetpotato genotypes in Luwero district of Uganda and their attributes (2010)**

Genotype	Desirable attributes (ranked)			
	1	2	3	4
NASPOT 1	High yield	Early maturity	Sweetness	High dry mass
Kakamega	High yield	Early maturity	Sweetness	Resistance to SPVD
Ejumula	Early Maturity	High yield	Sweetness	Vitamin A
NASPOT 10 O	Early maturity	High yield	Large roots	Sweetness
New Kawogo	High dry mass	High yield	Early maturity	Sweetness
NASPOT 9 O	Early maturity	High yield	Sweetness	High dry mass

### 2.3.6 Farmers' preferred genotype attributes

The farmers listed several desired sweetpotato attributes. The most important attributes ranked by the farmers in Luwero were high yield (96.7%) followed by early maturity (68.3%),

sweetness/taste (46.7%) and drought tolerance (25.0%) (Table 2.4). Ranking of attributes in Kabale was in the following order: sweetness/taste (95.0%); high yield (91.7%); early maturity (80.0%); and high dry mass (25.0%). Sweetness/taste of the sweetpotato root was ranked first in Kabale and third in Luwero and was one of the reasons that the farmers mentioned for not adopting recently introduced high yielding, disease resistant cultivars. Early maturity is ranked third in Kabale but second in Luwero. The genotypes grown varied greatly in the time required to reach harvest maturity. Some matured within three months and others within six months. Another related attribute that was only important in Luwero district (11.7%) was the ability to yield well in all types of soils especially infertile soils. Disease resistance was ranked the fourth most desired attribute in Luwero and sixth in Kabale. The major diseases were the SPVD and the Alternaria blight. Resistance to sweetpotato weevil was only important in Luwero (25%) where it was ranked sixth.

**Table 2.4 Percentage respondents and ranking of farmers' preferred sweetpotato attributes in Kabale and Luwero districts of Uganda (2010)**

Attribute	Kabale		Luwero	
	% Respondents	Rank	% Respondents	Rank
Sweetness	95.0	1	46.7	3
High yielding	91.7	2	96.7	1
Early maturity	80.0	3	68.3	2
High dry mass	25.0	4	18.3	10
Large roots	21.7	5	20.0	9
Disease resistance	20.0	6	46.7	4
Tolerance to drought	13.3	7	25.0	7
Good seed production	15.0	8	-	-
Soft roots (low dry mass)	8.3	10	-	-
Good in-field root storability	6.7	11	38.3	5
Good ground cover	6.7	12	3.3	14
Orange fleshed (Vitamin A)	3.3	13	5.0	13
Resistance to caterpillars	1.7	14	5.0	12
Resistance to weevils	0.0	-	25.0	6
Yields well in all soils	0.0	-	11.7	11
Red skin	0.0	-	3.3	15

Good groundcover was reported as a desired attribute by 6.7% of the farmers in Kabale and 3.3% of the farmers in Luwero. The farmers in Kabale wanted genotypes that covered the soil surface fast so that the speed of water runoff was reduced (because of the hilly nature of their terrain) and the requirement for weeding was less. According to the farmers in Luwero, such genotypes that cover the ground rapidly protect the roots from weevil damage and rotting during the dry season. This attribute goes hand in hand with good seed production which was ranked eighth (15.0%) in Kabale with a nil response for this attribute in Luwero. There was no



commercial vine production in Kabale and the farmers preferred genotypes that produce enough vines and are tolerant to dry conditions to provide planting materials at the beginning of the planting season. Orange flesh and red skin of the sweetpotato roots were lowly ranked in both districts. The reason the farmers gave for the low ranking of the OFSP was the unpleasant flavour and low dry mass. Of the farmers interviewed, only those who produced for the market were concerned about the skin colour where red was preferred.

### **2.3.7 Farmers perceptions of sweetpotato production constraints**

The most important constraint identified by most farmers in Luwero district was the caterpillars of sweetpotato butterfly (*Acraea* spp.), and in Kabale it was *Alternaria* blight (Table 2.5). Some of the most popular genotypes (Mukazi in Kabale and NASPOT 1 in Luwero) turned out to be the most susceptible to *Alternaria* blight and caterpillars. Caterpillars usually become a serious problem during the dry season. The SPVD was a more important constraint in Luwero (ranked second) than in Kabale (ranked eighth). Drought was ranked as the fourth most serious constraint in Luwero, but was ranked eleventh in Kabale. Low soil fertility, theft, stray animals and low yielding genotypes were the other serious constraints in Kabale. Vermin and weevils were important production constraints in the two districts. Vermin were considered a bigger problem in Kabale while weevils were a bigger problem in the Luwero. Weevil damage was considered to be highly linked to drought. Low yielding genotypes was a more important production constraint in Kabale (40.0%), where mostly unimproved genotypes are planted. This problem may be further compounded by the low soil fertility levels in the area. Scarcity of vines was reported in both districts but was considered a more serious problem in Luwero (28.3%) than in Kabale (15.0%). In addition, shortage of land and labour were important constraints in Kabale expressed by 23.3 and 31.7% of the respondents, respectively. The labour problem was exacerbated by the women having the sole responsibility for food production while the men are involved in cash crop production or marketing.

**Table 2.5 Percentage respondents and ranking of sweetpotato production constraints in Kabale and Luwero districts of Uganda (2010)**

Constraint	Kabale		Luwero	
	%Respondents	Rank	%Respondents	Rank
Alternaria blight	76.7	1	11.7	10
Vermin	60.0	2	13.3	6
Soil infertility	45.0	3	6.7	11
Theft	41.7	4	1.7	12
Caterpillars	38.3	5	76.7	1
Shortage of labour	31.7	6	11.7	9
Low yielding genotypes	40.0	7	1.7	13
Sweetpotato virus disease	28.3	8	61.7	2
Stray animals	25.0	9	1.7	14
Lack of planting materials	15.0	10	28.3	5
Shortage of land	23.3	10	11.7	8
Drought	15.0	11	61.7	3
Lack of market	6.7	12	11.7	7
Weevils	6.7	13	58.3	4
Rotting of roots	5.0	14	6.7	10
Delayed/late maturity	5.0	14	0.0	-
Poor quality roots	1.7	16	0.0	-
Price fluctuation	1.7	17	0.0	-
Fibrous roots	1.7	17	0.0	-

### 2.3.8 Farmer awareness of Alternaria blight of sweetpotato

Most of the farmers in both districts were aware of Alternaria blight. Only 1.7% of the farmers in Kabale and 13.8% of the farmers in Luwero did not know the disease. Of those who knew the disease, 94.8 and 89.5% considered it a major production constraint in Kabale and Luwero districts, respectively.

The most common local names for the disease in Kabale were “Okubabuka” (88.3%) and “Kusirira” (6.7%). Literal translation of these two names is “getting burnt”. In Luwero district, some of the farmers (21.7%) called it “Alternaria”, and these were the farmers who had interacted with NARO, NAADS and The Regional Network for Improvement of Potato and Sweetpotato in Eastern and Central Africa (PRAPACE); 13.3% called it “Okubabuka” and 1.7% called it “Kusirira” and the rest (58.3%) did not know the local name.

In Kabale, 44.1% of the farmers reported the disease to be more severe during the wet season and 37.3% during the dry season (Table 2.6). According to some farmers (16.9%), the disease becomes severe only when the rainfall is above average while others (1.7%) reported no seasonal variations in disease severity. However, in Luwero district 98.2% of the farmers reported the disease to be more severe during the dry season and only 1.8% in the wet season.

**Table 2.6 Farmers' perceptions of the season in which *Alternaria* blight caused the most severe damage in Kabale and Luwero districts of Uganda (2010)**

Season	Overall (%)	Kabale (%)	Luwero (%)
Dry season	66.9	37.3	98.2
Wet	23.5	44.1	1.8
Very wet season	8.7	16.9	0.0
All seasons	0.9	1.7	0.0

According to the farmers, disease symptoms become severe during the first two (35.1% of the respondents) to three (35.1%) months after planting (Table 2.7). In Luwero, 42.3 and 34.6% of the respondents reported the disease to become severe during the second and third month after planting, respectively. In Kabale, the disease becomes severe from the second month (28.8%), third month (35.6%) through to the fourth month (30.5%). Some farmers in Luwero reported higher incidences of the disease in older fields especially those used for sequential harvesting.

**Table 2.7 Farmers' record of the time in months after planting when *Alternaria* blight symptoms become severe in the two districts of Uganda (2010)**

Time after planting	Overall (%)	Kabale (%)	Luwero (%)
1 month	1.8	0.0	3.8
2 months	35.1	28.8	42.3
3 months	35.1	35.6	34.6
4 months	19.8	30.5	7.7
5 months	2.7	3.4	2.0
7 months	5.4	1.7	9.6

### **2.3.9 Information on control and management *Alternaria* of blight**

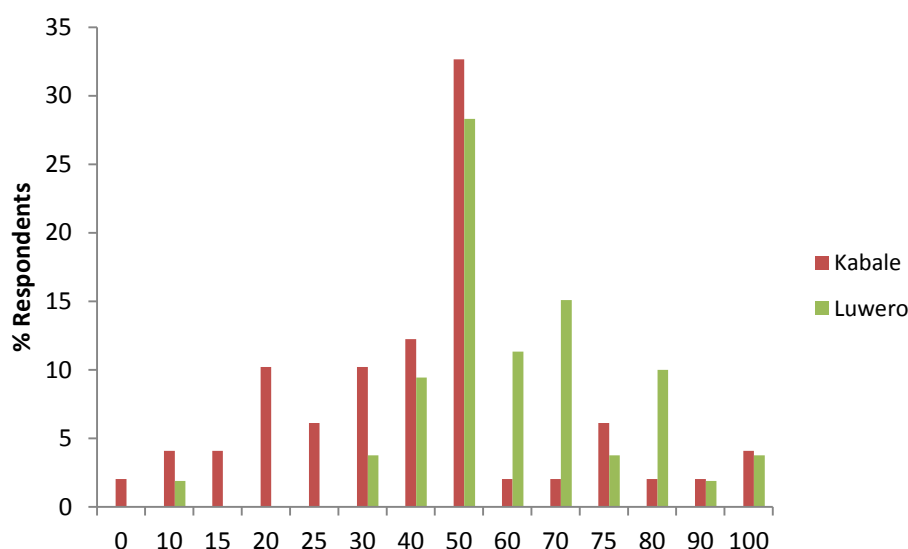
The sources of information about the control measures for the Luwero farmers were mainly NARO and PRAPACE. Only a few farmers (22%) made an effort to control *Alternaria* blight mainly by roguing infected plants, spraying with fungicides, use of healthy planting materials and use of resistant genotypes.

The control measures employed included roguing infected plants, spraying with fungicides, use of healthy planting materials and use of resistant genotypes. Some farmers did not rogue when infection was wide spread. Rather than pulling an infected plant out of the ground, they left it so as to at least obtain some small harvest.

Most farmers (73.0%) were aware of the differences in resistance between genotypes to *Alternaria* blight. The resistant genotypes identified in Kabale are Rwabaufuruki (14.1%), Nyinakamanzi (10.6%), and Kanyansi (10.6%); and in Luwero are Kakamega (27.1%), New Kawogo (16.5%) and Ejumula (12.9%).

### 2.3.10 Farmers' estimation of yield loss per hectare in a field severely infected by *Alternaria* blight

The farmers estimated the yield loss attributed to *Alternaria* blight in susceptible genotypes (Figure 2.7). The greater percentage of farmers in both districts indicated a 50.0% yield loss. However, others indicated higher yield losses especially when the environmental factors favour disease spread. For example in Luwero, according to 10.8% of the farmers, the yield loss can be as high as 80.0%. A small percentage, 4.1% in Kabale and 3.8% in Luwero, indicated that in some cases the yield loss can be 100%.



**Figure 2.7 Farmers' estimates of total sweetpotato yield loss due to *Alternaria* blight in Uganda (2010)**

## 2.4 Discussion

The PRA highlighted the farmers' production problems, their desired sweetpotato attributes and their knowledge about *Alternaria* blight. The study identified the actual production constraints, desired genotype attributes and the extent to which the farmers regard *Alternaria* blight as a serious production constraint. All these aspects will be important in designing future sweetpotato breeding programs.

### 2.4.1 Crop management and genotype mixes

The study revealed that a large number of crops are grown alongside sweetpotato and in some cases as intercrops. Kabale farmers intercrop legumes with sweetpotato unlike in Luwero where

the majority of the farmers intercrop with cassava. This indicates a lack of good extension advice in Luwero district, since both cassava and sweetpotato are root crops and will compete for the same nutrients and root space, and therefore neither crop will yield to its full potential. Farmers who do not intercrop, plant several sweetpotato genotypes on the same piece of land either as mixed genotypes or each genotype planted separately in a small portion of the land. The major reason cited for this practice is a lack of enough planting materials for one genotype to cover the available land especially after the dry season. In some cases the farmers plant several genotypes as a security measure in case one of the genotypes fails. Some farmers exploit the different maturation periods of the genotypes to meet their harvest requirements. Since some genotypes mature very early and others late, the farmers are able to sequentially harvest a crop over an extended period of time. This has been previously reported by Bashaasha et al. (1995). Low (2000) while working in Kabale reported that some farmers harvest roots from their land for a period of 3 months after planting up to 10 months after planting by planting genotypes with different maturation dates.

Access to disease free planting materials is also a problem in the area surveyed. There is no organised system of distribution of planting materials to the farmers. The major sources of planting materials are farmers replanting vines from their previous crop and others obtaining vines from neighbours. Vines from the neighbours are normally provided free of charge thus there is no incentive for commercial seed production (Gibson et al., 2009). This informal distribution system lacks any proper seed quality control mechanisms and is a major avenue for the spread of pests and diseases since no thorough inspection is done. However, according to Chiona (2009), the informal farmer to farmer seed supply system may be advantageous in that farmers are able to select genotypes with the desired attributes for their particular locality.

#### **2.4.2 Preferred attributes**

While high yield is the most important attribute to farmers in Luwero; taste (sweetness) is the most important in Kabale. This is indicative of the divergence in preferred traits and necessitates localised selection of genotypes. Before adoption, farmers evaluate a number of important traits often accepting genotypes of lower yield but with higher quality. Therefore, high yield is not always the most important determinant of the adoption of new cultivars. Some of the other quality attributes that farmers desire are high dry mass, and certain flesh and skin colours. This was also previously reported by Low (2000). The majority of the farmers prefer white-fleshed genotypes with high dry mass but for the traders, red skin colour is also important. That farmers normally reject OFSP because of their unpleasant flavour and low dry mass underlines the need to educate them about the health benefits of OFSP in terms of vitamin A. For the market oriented farmers and traders, genotypes with red skin are easier to market than the

other colours. However, farmers who don't produce for the market require a sweetpotato genotype with their preferred attributes such as high yield, taste and high dry mass while skin colour is not considered very important.

### **2.4.3 Production constraints**

The two districts have almost similar production constraints. However, the perceived seriousness of the constraints differs considerably. Constraints considered to be very important in Kabale are not necessarily important in Luwero. In Kabale, *Alternaria* blight and vermin, especially mole rats, are the most important constraints whereas in Luwero caterpillars, weevils, SPVD, and drought are important. These differences in constraints can be influenced by the prevailing weather conditions at the two locations whereby the colder and moister conditions in Kabale do not favour caterpillars but favour the development of *Alternaria* blight. Consideration of the different constraints and attributes for the two regions calls for different breeding strategies. If this is not done, then breeding cultivars with multiple complementary traits that can be released in both locations could be the answer (Mwanga et al., 2007).

Most farmers in both districts consider *Alternaria* blight a constraint to sweetpotato production but it is a more serious production constraint in Kabale. In Kabale the disease is most severe during the wet season, while in Luwero it is most severe during the dry season. This is an indication that the *Alternaria* pathogens do not only cause severe damage under high levels of moisture as earlier reported by Osiru et al. (2007), but also under dry conditions. It may be true that infection takes place during the wet season but due to the crop vigour at that time the disease is suppressed and the severe symptoms are more prominent during the dry season and when the crop is older (Ojiambo et al., 1999). The majority of the farmers in both locations reckon that the disease causes about 50% yield loss. Similarly, Osiru et al. (2007) reported yield losses of 27.3 to 54.3% among susceptible cultivars. There are several options in controlling the disease but given that sweetpotato is a low value crop and mainly grown by resource poor farmers who use marginal lands, the best control measure is use of host plant resistance (Hakiza et al., 2000). Thus breeding efforts should be geared towards the development of new *Alternaria* blight resistant genotypes.

Drought remains a major challenge in Uganda where sweetpotato is grown during dry seasons (Bashaasha et al., 1995). During prolonged dry spells most of the farmers who cannot afford supplemental irrigation lose most of the vines (Bashaasha et al., 1995; Yanggen and Nagujja, 2006). Therefore, if a formal seed system is to be established, there is a need to invest in irrigation equipment so that vines can be produced during the dry months under irrigation and supplied to farmers at the beginning of the rainy season. Farmers with access to wetlands produce vines during the dry season (Bashaasha et al., 1995; Gibson et

al., 2009) but some of these wetlands dry out during prolonged dry spells.

The overall sweetpotato yields are higher in Luwero than in Kabale. This situation may be attributed to highly degraded soils in Kabale due to overuse of the soil for crop production and subsequent loss of fertility, lack of manure to replenish nutrients, soil erosion especially on steep slopes (Bashaasha et al., 1995; Low, 2000), and use of landraces with lower yield potential.

## **2.5 Conclusion**

The study identified what the farmers considered to be their major production constraints, as well as the farmers' preferred sweetpotato attributes and their perceptions on *Alternaria* blight. Sweetpotato farmers in the different regions of Uganda face the same production constraints and have the same preferred attributes but the degree of importance of the constraints and ranking of the preferred attributes differ. Some farmers are aware of genotypes that are resistant to *Alternaria* blight. This is an indication that sources of resistance to the disease are available within the germplasm and therefore it is possible to breed for resistance to the disease. These findings will be important in designing future breeding programs as farmers' production constraints and preferred attributes have been identified. However, careful parental and progeny genotype selection and involvement of farmers at an appropriate stage of selection is essential to ensure that the traits identified as important by the farmers will be incorporated into the new genotypes. In turn, this will lead to an increase in the adoption rate of the new genotypes since they will meet the requirements of the farmers.

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## Appendices

### Appendix 2.1: Participatory rural appraisal for sweetpotato production in central and south-western Uganda (2010)

#### Individual household interview questionnaire

Name of interviewer..... Date.....

#### A. Location information

District ..... Sub-county.....

Parish..... Village.....

GPS reading.....

#### B. Respondent details

Name of household head .....

Name of respondent..... Sex..... (1=male and 2=female)

Age..... Marital status..... (1=single, 2=married, 3=widowed)

Education level..... (1=no formal education, 2=primary, 3=secondary, 4=tertiary)

#### C. Sweetpotato production information

1. Size of your farm land (hectares) ..... Area under crops.....

2. Crops grown.....

3. Average area under sweetpotato per season (hectare).....

4. Estimate of production per hectare ( $t\ ha^{-1}$ ).....

5. How long have you been growing sweetpotato? (Years).....

6. Main source of your planting materials..... (specify: 1=from own field, 2=fellow farmers, 3=research station, 4=other sources).....

Any problems with planting materials?..... (1=yes, 2=no)

If yes, specify.....

7. a) How do you plant your sweetpotato?

Monocrop.....

Intercrop.....

Rotation.....

If in intercrop, with which crops?.....

b) Do you grow sweetpotato as a single variety or a mixture of varieties? .....  
 (1=single, 2=mixture)

8. Do you grow local varieties? ..... (1=yes, 2=no)

If yes, list the varieties.....  
 .....

9. Do you grow improved varieties? ..... (1=yes, 2=no)

If yes, list the varieties.....  
 .....

Variety	Maturity period (Months)	Yield (t or kg ha <sup>-1</sup> )	Attributes of the variety

(a) 1. High yield, 2. Early maturing, 3. High dry mass, 4. Good groundcover, 5. Resistance to pests, 6. Resistance to diseases, 7. Others (specify) .....

**D. Sweetpotato preferred attributes**

	Attribute (Description of attribute)	Rank	Variety
1			
2			
3			
4			
5			

**E. Production constraints**

**Biotic and abiotic constraints**

Constraint	Rank	Approximate yield loss (t ha <sup>-1</sup> )	Coping mechanism	Variety (If applicable)

**F. Alternaria blight (Specimen samples to be carried)**

1. Have you ever seen this disease in your field? ..... (1=yes, 2=no)  
 If yes, what is its local name? .....  
 If no, have you ever seen it in another person's field? ..... (1=yes, 2=no)
2. a) Is it a major production constraint in this area? ..... (1=yes, 2=no)  
 b) Its effect on yield..... 1=No effect, 2=Reduced, 3=No yield at all,  
 4=Others
3. Estimation of yield loss per hectare (t ha<sup>-1</sup>) in a severely affected field .....
4. What are the major symptoms

Major symptoms on leaf	Major symptoms on stem	Major symptoms on root

**Yield loss**

Variety	Yield loss (t ha <sup>-1</sup> )

5. During what seasons is the disease more severe? ..... (1=dry, 2=wet, 3=very wet)  
 Months when most common (severe).....
6. At what growth stage (months after planting) do the disease symptoms become visible?  
 .....
7. Do you get any information on its control and management? ..... (1=yes, 2=no)  
 If yes, source of information and measures (practices).....
8. a) Are you aware of any resistant varieties? ..... (1=yes, 2=no)  
 b) If yes, list them.....  
 .....  
 c) How effective are the resistant varieties? ..... (1=very effective,  
 2=not effective, 3=not sure)  
 d) Rank the different varieties (local or improved) according to resistance levels  
 (1=resistant, 2=mild resistant, 3=susceptible)

Variety	Resistance level

## **Appendix 2.2: Focus group discussions (FGD)**

Overall goal of the FGD

Specific objectives

Program (activity and responsibility)

Check list

1. What are the major crops grown in this area?
2. How important is sweetpotato compared with other crops (ranking).
3. What are the most preferred sweetpotato attributes? (List and rank).
4. What varieties do you grow? (list and rank) Include desired and non-desired attributes of each variety.
5. What are the major production constraints? (list and rank) [Categorise as biotic and non-biotic, socio-economic (land, capital, social infrastructure)]. Rank according to category and overall rank.
6. What are the market requirements for sweetpotato?
7. Various uses of sweetpotato.
8. Average area and yield.
9. Main seed source by variety and yield potential.
10. Alternaria blight coverage (incidence, severity, spread) in the area. Opinion on cause, control and how the community is addressing it.
11. What opportunities do you think exist in the village for sweetpotato production?
12. Any sweetpotato breeding needs (requirements)?

## Chapter 3

### Evaluation of sweetpotato genotypes for resistance to *Alternaria* leaf petiole and stem blight, and stability of agronomic traits in Uganda

#### Abstract

*Alternaria* leaf petiole and stem blight (*Alternaria* spp.) is an important disease of sweetpotato (*Ipomoea batatas* (L.) Lam.) in Uganda. The severity of the disease varies with environment, with higher disease levels recorded under high moisture and humidity conditions. To breed for resistance to *Alternaria* leaf petiole and stem blight (commonly referred to as *Alternaria* blight), germplasm that is resistant and high yielding, combined with agronomic stability and adaptability must be identified through multi-locational trials. This study was conducted to evaluate selected sweetpotato genotypes for: stable resistance to *Alternaria* blight across sites and seasons; stability for storage root yield (TRY) and other important traits; and yield gain in response to fungicide treatment. To this effect, 30 sweetpotato genotypes from different agro-ecological zones of Uganda and the National Sweetpotato Program were evaluated for resistance to *Alternaria* blight, TRY and other traits at Namulonge and Kachwekano over three seasons. There were highly significant differences among the genotypes for *Alternaria* blight severity, measured by the area under disease progress curve (AUDPC), yield, harvest index, dry mass, weevil damage and sweetpotato virus disease. *Alternaria* blight severity was higher at Kachwekano than Namulonge. Genotypes Shock, Silk Luwero and the resistant check Tanzania had the lowest AUDPC values and were therefore the most resistant while NASPOT 1, NASPOT 7, New Kawogo and Dimbuka had the highest AUDPC values and were the most susceptible. Genotypes from the National Sweetpotato Program (improved cultivars) were more susceptible to *Alternaria* blight than the landraces. Genotypes Tanzania, Namusoga, BND145L, NASPOT 4, Sowola 6 and NASPOT 1, and environment Namulonge 2011B were the most stable for *Alternaria* blight. NASPOT 8 and NASPOT 11 had the highest yield over the three seasons, while Ejumula, NKA259L and Malagalya had the lowest yields. The highest yield gain in response to fungicide treatment relative to the *Alternaria* inoculum sprayed plots was 61.2% recorded by MBR 536. There was a negative but non-significant correlation between *Alternaria* blight severity and yield meaned over genotypes, seasons and sites for the *Alternaria* inoculated plots. Improved cultivars were generally more stable for yield than landraces with NASPOT 8, NASPOT 7, and NASPOT 11 the most stable, respectively. Among the environments, Kachwekano 2011B was the most stable for yield while Namulonge 2011A was the most high yielding but unstable. Those genotypes with acceptable performance for the desired traits may be used as parents in breeding new genotypes with improved performance.

### 3.1 Introduction

Sweetpotato (*Ipomoea batatas* (L.) Lam.) production in Uganda is constrained by several abiotic and biotic factors. Among the biotic factors are: sweetpotato weevil (*Cylas* spp.) (Stathers et al., 2003), sweetpotato virus disease (SPVD) (Mwanga et al., 2002) and *Alternaria* leaf petiole and stem blight (*Alternaria* spp.) commonly referred to as *Alternaria* blight (Skoglund et al., 1994; Anginyah et al., 2001; Osiru et al., 2007a; Osiru et al., 2007b). *Alternaria* blight is the most important sweetpotato fungal disease in Uganda (Mwanga et al., 2007b; Osiru et al., 2007a; Osiru et al., 2007b) especially in areas of mid to high altitude (Osiru et al., 2007a; Mwanga and Ssemakula, 2011). Both *A. bataticola* and *A. alternata* have been isolated from infected plants but *A. bataticola* is the more aggressive species (Anginyah et al., 2001; Osiru et al., 2007a; Osiru et al., 2007b). Previous studies have indicated high yield losses due to *Alternaria* blight ranging from 27.3 to 54.3% in susceptible genotypes (Osiru et al., 2007b). With such high losses, it is necessary to put control measures in place that can curb the losses. Several measures have been suggested to control *Alternaria* blight of sweetpotato. However, given that sweetpotato is a low value crop grown mainly by resource poor farmers, the most cost effective control method is the use of host plant resistance (HPR) (Ames et al., 1996).

In order to breed for HPR, there is a need to identify sources of resistance among the existing genotypes, which may be used as parents in an improvement program. Studies by Osiru et al. (2007b) in Uganda, van Bruggen (1984) in Ethiopia, Anginyah et al. (2001) in Kenya and Lopes and Boiteux (1994) in Brazil, indicated variation in resistance to *Alternaria* blight within the sweetpotato germplasm. This variation in resistance is an indication that it is possible to select desirable parents from within the existing germplasm and breed for resistance to *Alternaria* blight. To develop new resistant genotypes, the parental genotypes with appreciably higher levels of resistance can be selected for areas with high incidence of the *Alternaria* blight. This necessitates that potential parents be evaluated for stability in the expression of *Alternaria* blight resistance and agronomic performance across environments.

In their study to determine the reaction of elite genotypes to *Alternaria* blight and associated yield losses, Osiru et al. (2007b) depended on natural disease infection to identify resistant genotypes. However, natural infection may not always be very reliable given that the inoculum pressure may be too low to give good differentiation between resistant and susceptible genotypes with some even escaping disease infection. They highlighted the need to inoculate some plots with *Alternaria* blight inoculum in order to establish adequate disease pressure and also to spray other plots with a fungicide to reduce the disease level as much as possible. This would enable calculation of the yield gains in the fungicide treated plots relative to the inoculated ones.



Selection of superior genotypes across several environments is almost always complicated by genotype x environment interaction (GEI) (Eberhart and Russell, 1966). The effect of GEI in plant breeding programs is to reduce the correlation between the phenotype and the genotype potentially resulting in invalid or biased conclusions about genetic variance if the GEI effects are not taken into account (Collins et al., 1987). Many important traits in sweetpotato are sensitive to environmental change as evidenced in several studies (Naskar and Singh, 1992; Manrique and Hermann, 2000; Grüneberg et al., 2005; Osiru et al., 2009). It is therefore important to quantify the GEI and determine the stability of the different genotypes through the application of appropriate statistical analyses to multi-locational and multi-seasonal trials (Thomason and Philips, 2006).

Several methods for handling multi-environment data have been developed to study the patterns in GEI. These include the joint regression (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Perkins and Jinks, 1968), and the additive main effects and multiplicative interaction (AMMI) (Gauch, 2006) models. The AMMI model is the proposed model of choice when main effects and interactions are both important (Zobel et al., 1988). The AMMI model is a powerful multivariate tool which integrates analysis of variance and principal component analysis into one unified approach (Gauch and Zobel, 1996; Pourdad and Mohammadi, 2008; Sadeghi et al., 2011) and can be used to identify both superior and stable genotypes (Crossa, 1990).

This study was conducted to:

1. evaluate selected sweetpotato genotypes for resistance to *Alternaria* blight across two sites and three seasons;
2. determine the stability of the selected sweetpotato genotypes for *Alternaria* blight resistance, storage root yield, and other important traits; and
3. determine the yield gain after application of fungicide treatment to control *Alternaria* blight.

## **3.2 Materials and methods**

### **3.2.1 Germplasm collection**

Vines of genotypes grown by the farmers that were visually free of disease symptoms were collected from three different agro-ecological zones, namely: central, eastern and western Uganda and multiplied at Mukono Zonal Agricultural Research and Development Institute (Mukono) during the first planting season of 2010 (2010A). The improved cultivars and promising genotypes were obtained from the National Sweetpotato Program at Namulonge. A total of 30 genotypes were selected for the trials (Table 3.1) which included 13 farmer landraces

commonly grown in different regions of the country, two farmers' cultivars that were evaluated by the National Sweetpotato Program and released by the Variety Release Committee (VRC), 12 cultivars bred by the National Sweetpotato Program and released by the VRC, and three promising genotypes (pre-release) from the National Sweetpotato Program.

**Table 3.1 Sweetpotato genotypes evaluated at Namulonge and Kachwekano (2010-2012)**

<b>Genotype</b>	<b>District</b>	<b>Status</b>	<b>Genotype</b>	<b>Status</b>
Semanda	Mpigi	Landrace	New Kawogo	Landrace (Released)
Silk Luwero	Luwero	Landrace	NASPOT 1	Released cultivar
Kidodo	Kabale	Landrace	NASPOT 2	Released cultivar
Dimbuka	Rakai	Landrace	NASPOT 3	Released cultivar
Araka Red	Soroti	Landrace	NASPOT 4	Released cultivar
MBL 170	Mpigi	Landrace	NASPOT 7	Released cultivar
Shock	Mbale	Landrace	NASPOT 8	Released cultivar
Magabali	Kabale	Landrace	NASPOT 10 O	Released cultivar
Budde	Masaka	Landrace	NASPOT 11	Released cultivar
Kigaire	Soroti	Landrace	Ejumula	Landrace (Released)
MBR 536	Mbarara	Landrace	SPK004	Landrace (Released)
Namusoga	Kamuli	Landrace	NKA259L	Pre-released cultivar
Otada	Lira	Landrace	BND145L	Pre-release cultivar
Tanzania	-	Landrace (Released)	NKA318L	Pre-release cultivar
Bwanjule	-	Landrace (Released)	NKA103M	Pre-release cultivar

**Sources:** Mwanga et al. (2001a); Mwanga et al. (2003b); Mwanga et al. (2007a); Mwanga et al. (2011); [www.viazivitamu.org/ugasp\\_db/index.php](http://www.viazivitamu.org/ugasp_db/index.php)

### 3.2.2 Trial site description

The trials were established at two sites. The first site was at the National Crops Resources Research Institute (NaCRRI) at Namulonge (27 km from Kampala) at 0°32' N, 32°35' E; 1150 metres above sea level (masl) in Wakiso district, central Uganda. It has a bimodal rainfall pattern with annual rainfall range of 1000-1200 mm and annual mean temperature of 21°C. The second site was at Kachwekano Zonal Agricultural Research and Development Institute (KAZARDI) (400 km from Kampala) at 01°16' S, 29°57' E; 2200 masl in Kabale district in south-western Uganda. It has a bimodal rainfall pattern with annual rainfall ranging between 1200-1500 mm and annual mean temperature of 18°C. These sites are located in two of the main sweetpotato production regions of the country and *Alternaria* blight disease is common at both sites (Osiru et al., 2007a). Kachwekano is a "hotspot" for the *Alternaria* blight, and Namulonge is a medium disease pressure zone but a "hotspot" for SPVD (Mwanga et al., 2007b).

### 3.2.3 Trial establishment and field layout

The trials were planted in a 5 x 6 row-column design replicated three times (Appendix 3.1). The planting and harvest dates are provided in Appendix 3.2. Seventeen vine-tip cuttings, each

0.30 m in length, were planted 0.30 m apart in each of four, 5 m long ridged rows spaced 1 m apart per plot. The two left rows of the plot were sprayed once with a spore suspension of *Alternaria* inoculum (concentration  $5.0 \times 10^4$  conidia  $\text{ml}^{-1}$ ) one month after planting (MAP) and the two right rows were sprayed with a fungicide, Indofil M-45 (Mancozeb, 80%) according to the manufacturer's instructions at two-week intervals. No fertilizers or irrigation was applied and the plots were weeded manually. This trial was repeated at the same site using the same layout and genotypes for three seasons. The seasons were: second planting season of 2010 (2010B) from September 2010 to January 2011; first planting season of 2011 (2011A) from April to August; and second planting season of 2011 (2011B) from September 2011 to January 2012. The crop at Namulonge was harvested at 5 MAP. However, due to the lower temperatures at Kachwekano (Appendix 3.3), the crop was harvested at 7 MAP. Cultivars Tanzania and NASPOT 1 were included as resistant and susceptible checks, respectively (Osiru et al., 2007b).

#### **3.2.4 Inoculum preparation and inoculation**

Leaves and petioles with *Alternaria* blight symptoms (infection sites) were selected from the field. Infected leaves and petioles were detached and washed under running water to remove any contaminants. Tissue sections were excised from around the leading edge of the lesions. These sections were surface sterilised in a one part NaOCl to nine parts water solution for two minutes, washed three times by transferring briefly to sterile distilled water and then dried on sterile paper under filtrated air on a laminar flow bench. From these sections, smaller sections (approx. 2 x 2 mm) were then excised and plated on Potato Dextrose Agar. The isolation plates were incubated at 25°C in an inverted position to prevent condensation of water vapour on the agar surface. Re-isolation was done on  $\text{CaCO}_3$  sporulation media (30 g  $\text{CaCO}_3$ , 20 g Agar and 20 g sucrose in 1000 ml of distilled water) to speed up the sporulation. The plates were left to sporulate for 15 days. A suspension of conidia was prepared by flooding the culture with sterile water and gently dislodging the conidia with a glass plate. The mycelial and conidial suspension was filtered through two layers of cheesecloth. The spore density was determined using a haemocytometer and adjusted to an approximate concentration of  $5.0 \times 10^4$  spores  $\text{ml}^{-1}$  (Lopes and Boiteux, 1994). The designated rows in each plot were sprayed with the spore suspension late in the evening to avoid the process of spore germination being affected by heat and UV radiation.

#### **3.2.5 Data collection**

##### ***Alternaria* leaf petiole and stem blight rating**

Disease severity was scored starting at three weeks after inoculation and continued at three-week intervals such that four data sets were collected. The disease severity rating scoring was

done by inspection of individual plants for symptoms and rating was done using a subjective visual scale of 0 to 5 modified after van Bruggen (1984), where: 0 = no disease; 1 = <1%; 2 = 1 to 10%; 3 = 11 to 25%; 4 = 26 to 50%; and 5 = > 50% foliar infection. The disease severity scores were expressed on a plot mean basis. The rows sprayed with *Alternaria* inoculum and those sprayed with the fungicide were scored separately. Disease severity data for each cropping season and site was used to calculate the AUDPC according to Shaner and Finney (1977).

$$\text{AUDPC} = \sum_{i=1}^n [(X_{i+1} + X_i)/2][t_{i+1} - t_i]$$

Where:

$X_i$  = infected leaf area (%) at the  $i^{\text{th}}$  observation

$t_i$  = time (days) at the  $i^{\text{th}}$  observation

$n$  = total number of observations

In addition to rating for *Alternaria* blight, rating for SPVD was also done using the subjective 1 to 9 severity rating scale of Grüneberg et al. (2010), where: where 1 indicated no virus symptoms; 2 = unclear virus symptoms; 3 = clear virus symptoms at < 5% of plants per plot; 4 = clear virus symptoms at 6 to 15% of plants per plot; 5 = clear virus symptoms at 16 to 33% of plants per plot; 6 = clear virus symptoms at 34 to 66% of plants per plot (more than 1/3, less than 2/3); 7 = clear virus symptoms at 67 to 99% of plants per plot (2/3 to almost all); 8 = clear virus symptoms at all plants per plot (not stunted); 9 = severe virus symptoms in all plants per plot (stunted).

### **Storage root yield**

At harvest the total number of storage roots (TRN), total storage root fresh mass (TRY) (kg), number of marketable storage roots (MRN), mass of marketable storage roots (MRY) (kg), number of unmarketable roots (UMRN), mass of unmarketable storage roots (kg), shoot mass and total fresh biomass (kg) were recorded on a per plot basis then the mass per plot was converted to  $\text{t ha}^{-1}$  for analysis. Rating for weevil damage was done using a damage scale of 1-5: where 1 = 0% weevil damage; 2 = 1-25%; 3 = 26-50%; 4 = 51-75%; and 5 = 76-100% (Stathers et al., 2003). For percentage dry mass composition (DM%), two medium size fresh storage roots were randomly selected from each genotype and spray treatment, sliced into small chips and a 200 g sub-sample was placed in a paper bag. The sub-samples were oven dried at 72°C until constant mass was attained. The dry mass was expressed as a percentage of the fresh mass (Islam et al., 2002):

$$\text{Dry mass (\%)} = \frac{\text{Dry mass}}{\text{Fresh mass}} \times 100$$

The harvest index (HI) was calculated as the proportion of the TRY to the total fresh biomass (total of the vine mass and root mass).

The percentage yield gain in the fungicide treated plots relative to the *Alternaria* inoculated plots was calculated as:

$$\text{Yield gain (\%)} = \frac{\text{Mean yield (Fungicide spray)} - \text{Mean yield (Alternaria spray)}}{\text{Mean yield (Alternaria spray)}} \times 100$$

The percentage disease reduction was calculated as:

$$\text{Disease reduction (\%)} = \frac{\text{Mean AUDPC (Fungicide spray)} - \text{Mean AUDPC (Alternaria spray)}}{\text{Mean AUDPC (Alternaria spray)}} \times 100$$

### 3.2.6 Data analysis

The analysis of variance (ANOVA) was conducted using the generalised linear model of SAS version 9.3 (SAS Institute, 2010). Data were first analysed for each site separately and then homogeneity of the error variances for the environments was tested using Hartley's  $F_{\max}$  test (Hartley, 1950); the differences were not significant ( $P \leq 0.05$ ). The combined ANOVA was generated using the generalised linear model of SAS version 9.3 (SAS Institute, 2010).

Each combination of site and season was considered to be a different environment, thus two sites over three seasons equal six environments. To determine the effects of GEI, the data were subjected to AMMI analysis by GENSTAT 14<sup>th</sup> Edition (Payne et al., 2011) using the following model:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^N \lambda_n \gamma_{gn} \eta_{en} + \theta_{ge} + \xi_{ij}$$

Where:  $Y_{ge}$  is the yield (or other traits) of genotype  $g$  in environment,  $e$ ;  $\mu$  is the grand mean;  $\alpha_g$  is the genotype mean deviation;  $\beta_e$  is the environment mean deviation;  $N$  is the number of interaction principal component analysis (IPCA) axes retained in the model;  $\lambda_n$  is the eigenvalue of the interaction principal component analysis axis (IPCA)  $n$ ;  $\gamma_{gn}$  and  $\eta_{en}$  are genotype and environment IPCA scores for the  $n^{\text{th}}$  IPCA axis;  $\theta_{ge}$  is the residual of the GEI unaccounted for by the IPCA axes; and  $\xi_{ij}$  is the experimental error.

Since each genotype was inoculated with *Alternaria* inoculum and also treated with a fungicide, these two treatments did not represent the infection levels that would occur naturally under field conditions. Therefore, as an estimate of the natural field infection, the average of the two spray

treatments per genotype was computed and subjected to AMMI analysis to determine stability for resistance to the disease.

For this study two stability indices, namely the AMMI Stability Value (ASV) (Purchase et al., 2000) and the Genotype Selection Index (GSI) (Farshadfar, 2008) were used to identify stable genotypes. The interaction patterns of the genotypes and the environments were graphically represented in a biplot of the respective IPCA1 scores (y-axis) versus the genotype and environmental means (x-axis) for the two main traits considered in this study, namely *Alternaria* blight AUDPC and TRY. Since distribution of the AUDPC values within the range was uneven, the data were standardised before being graphed. In the biplot, displacement in the horizontal plane reflects differences in the mean performance, while displacement in the vertical plane reflects differences in interaction effects (Zobel et al., 1988).

The ASV is calculated using Pythagoras' theorem as the distance (hypotenuse) from the coordinate point to the origin in a two-dimensional biplot of IPCA1 scores versus IPCA2 scores. Since the IPCA1 axis contributes more to the GEI sum of squares (SS) than the IPCA2 axis, the IPCA1 score is weighted in the calculation of the ASV by the ratio of the IPCA1 SS to the IPCA2 SS as follows:

$$ASV_i = \sqrt{\left[ \frac{IPCA1\ SS}{IPCA2\ SS} (IPCA1\ score) \right]^2 + (IPCA2\ score)^2}$$

The larger the IPCA score for a genotype either negative or positive, the greater the interaction of a genotype with certain environments. Consequently, the genotype with the lowest ASV is the most stable and that with the highest ASV the least stable. In selecting for superior genotypes across environments, stability *per se* is not the only parameter for selection since the most stable genotypes would not necessarily give the best performance for the trait of interest. In this regard, the GSI, which combines agronomic performance across environments and stability, was used to select the most desirable genotypes. The GSI for each genotype was calculated as the sum of the ranks for mean performance for each of the traits (AUDPC, TRY, etc.) across environments ( $RY_i$ ) and the rank for ASV ( $RASV_i$ ):

$$GSI_i = RY_i + RASV_i$$

The genotype with lowest GSI was considered to be the most stable and highest performing for that particular trait. To determine the best genotype that combined stability with good performance, the sum of GSI ranks across three selected traits: AUDPC, TRY and HI was obtained. The genotype with the lowest rank sum was the best in terms of these three traits.

### 3.3 Results

The genotypes were significantly ( $P < 0.05$ ) different for the traits considered (Table 3.2). The spray treatments were highly significantly different ( $P < 0.001$ ) for AUDPC, TRY and HI. Site effects were significant ( $P < 0.05$ ) for all the traits considered except SPVD ( $P < 0.05$ ). Similarly, seasonal effects were also highly significant ( $P < 0.001$ ) for all the traits except DM%. Genotype x spray treatment interaction was not significant ( $P > 0.05$ ) for all traits. The genotype x site interaction was highly significant ( $P < 0.001$ ) for all traits except DM% and SPVD. Genotype x season interaction was significant ( $P < 0.05$ ) for all traits except for HI and DM%. Site x spray treatment interaction was not significant for all the traits. Site x season interaction was significant for all traits except DM% and SPVD. Genotype x site x treatment interaction was not significant ( $P > 0.05$ ) for all the traits. Genotype x site x season interaction was significant ( $P < 0.05$ ) for all traits except HI, DM% and SPVD. Genotype x season x spray treatment and spray treatment x site x season interactions were not significant ( $P > 0.05$ ) for all traits evaluated. Furthermore, genotype x spray treatment x site x season interaction was not significant ( $P > 0.05$ ) for any of the traits. Significant differences between means are only discussed for the significant three way interaction (genotype x site x season), two way interactions (genotype x site, site x season, genotype x season) and main effects.

**Table 3.2 Analysis of variance mean squares for six sweetpotato traits evaluated at Namulonge and Kachwekano during seasons 2010B, 2011A and 2011B**

Source	DF	AUDPC	TRY	HI	DM%	Weevil damage	SPVD
Site (Rep)	4	1464.57**	668.42***	0.387***	94.11	2.76**	8.56***
Genotype	29	5093.92***	221.879***	0.159***	226.97*	2.37***	4.61***
Spray treatment	1	82311.49***	3248.06***	1.050***	200.64	0.01	7.47
Site	1	22002.21***	4425.11***	2.026***	798.79*	278.50***	0.64
Season	2	18104.11***	1767.96***	0.762***	3.61	105.11***	698.02***
Genotype x Spray treatment	29	387.06	10.41	0.004	135.54	0.25	0.51**
Genotype x Site	29	1336.66***	228.89***	0.101***	139.84	1.94***	7.95
Genotype x Season	58	677.19**	62.63**	0.025	151.42	0.97*	3.67**
Site x Spray treatment	1	229.25	5.079	0.064	63.77	0.05	3.57
Site x Season	2	9126.89***	3617.20***	1.411***	94.44	166.78***	6.50
Genotype x Spray treatment x Site	29	249.92	10.91	0.006	175.55	0.34	0.25
Genotype x Site x Season	58	949.85***	91.98***	0.032	146.24	0.91*	0.50
Genotype x Season x Spray treatment	58	309.60	9.16	0.005	121.60	0.38	0.51
Spray treatment x Site x Season	2	319.90	110.30	0.015	75.80	0.32	0.30
Genotype x Spray treatment x Site x Season	58	256.33	12.38	0.006	117.88	0.30	0.82
<b>R<sup>2</sup></b>		<b>0.62</b>	<b>0.65</b>	<b>0.54</b>	<b>0.34</b>	<b>0.78</b>	<b>0.75</b>
<b>CV%</b>		<b>22.90</b>	<b>50.20</b>	<b>21.38</b>	<b>38.40</b>	<b>37.80</b>	<b>41.80</b>

\*\*\* = significant at  $P \leq 0.001$ ; \*\* = significant at  $P \leq 0.01$ ; \* = significant at  $P \leq 0.05$ ; AUDPC = area under disease progress curve for *Alternaria* blight severity; TRY = total storage root yield ( $t\ ha^{-1}$ ); HI = harvest index; DM% = percentage dry mass; SPVD = sweetpotato virus disease (score 1-9: 1 = no SPVD, and 9 = SPVD causing stunted growth); Spray treatment = *Alternaria* inoculum or fungicide treatment; 2010B = second season of 2010 (September 2010 to January 2011); 2011A = first season of 2011 (April to August 2011); 2011B = second season of 2011 (September 2011 to January 2012)



### 3.3.1 Variation in traits in response to site, season, genotype and spray treatment

The effects of genotype x site were highly significant ( $P < 0.001$ ) for most traits (Table 3.2). The AUDPC increased across the seasons at Kachwekano (Figure 3.1a), while the AUDPC peaked in 2011B at Namulonge. As expected, the trend for yield was the reverse to that of AUDPC (Figure 3.1b). At Namulonge and Kachwekano, the yield was lowest in 2010B which coincided with the highest AUDPC. Generally, the HI was low when the disease severity was high (Figure 3.1c). Weevil damage was highest at Namulonge for all the seasons, and was lowest during season 2011B at both sites (Figure 3.1d).

As the four way interaction of genotype x spray treatment x site x season was not significant ( $P > 0.05$ ) for the traits considered (Table 3.2), the trends rather than significant differences between means thereof are discussed for AUDPC and TRY only. These two traits were the main focus of this study and are therefore discussed in detail. The AUDPC values for the genotypes were higher at Kachwekano than at Namulonge for both spray treatments and in all seasons (Table 3.3). At both sites, the highest disease severity for the genotypes was recorded in season 2011B. Across seasons and sites, Shock had lower AUDPC values of 95.3 and 43.0 with the *Alternaria* inoculation and fungicide treatments, respectively than the resistant check, Tanzania. NASPOT 11 was the third most resistant genotype with a mean AUDPC value of 104.6 when inoculated but with higher AUDPC values at Namulonge than at Kachwekano. NASPOT 1, the susceptible check, had the highest mean AUDPC values of 162.3 and 96.1 with inoculation and fungicide treatment, respectively. In addition to NASPOT 1, New Kawogo (145.4), Dimbuka (137.8) and NASPOT 7 (136.6) were the most susceptible when inoculation with the disease. Correspondingly, they had higher AUDPC values when sprayed with fungicide.

Fungicide treated plots recorded higher TRY than the inoculated plots (Table 3.4). NASPOT 8 was the highest yielder with means of 17.1 and 21.9 t ha<sup>-1</sup> under *Alternaria* inoculation and fungicide treatments, respectively. NASPOT 11 was the second highest yielder with mean yield of 14.2 and 19.2 t ha<sup>-1</sup> under *Alternaria* inoculum and fungicide treatments, respectively. NASPOT 7 was the third highest yielder with mean TRY of 12.7 and 17.2 t ha<sup>-1</sup>, for the same respective treatments. At Namulonge, the highest mean TRY of 14.5 and 20.1 t ha<sup>-1</sup> were obtained during season 2011A for the inoculation and fungicide treatments, respectively, while the lowest mean TRY were recorded during season 2010B for both spray treatments. At Kachwekano, the highest mean TRY of 11.7 and 16.6 t ha<sup>-1</sup> for inoculum and fungicide treatments, respectively were obtained during season 2010A, and the lowest mean TRY for both spray treatments were recorded in season 2011B. Generally, genotypes at Namulonge had better yields than Kachwekano.

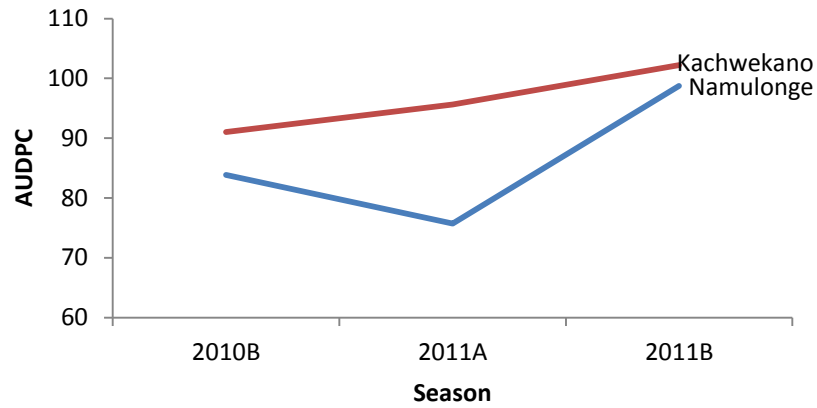


Figure 3.1 a Site x season interaction for area under disease progress curve (AUDPC)

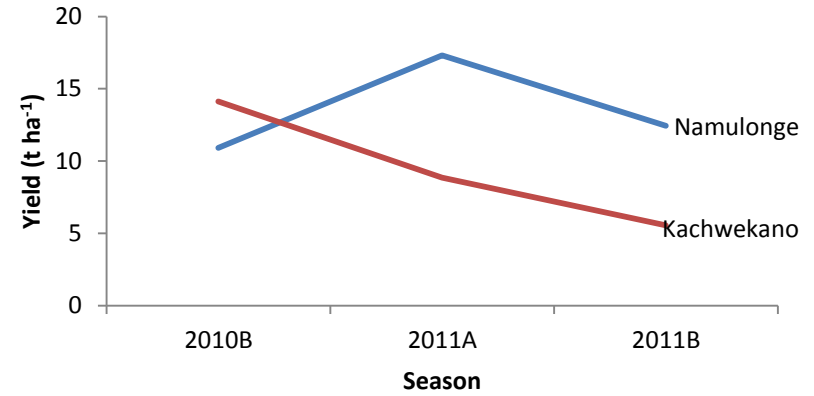


Figure 3.1 b Site x season interaction for total storage root yield

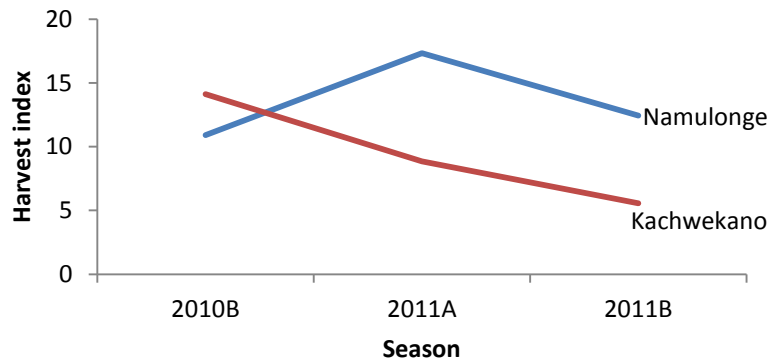


Figure 3.1 c Site x season interaction for harvest index

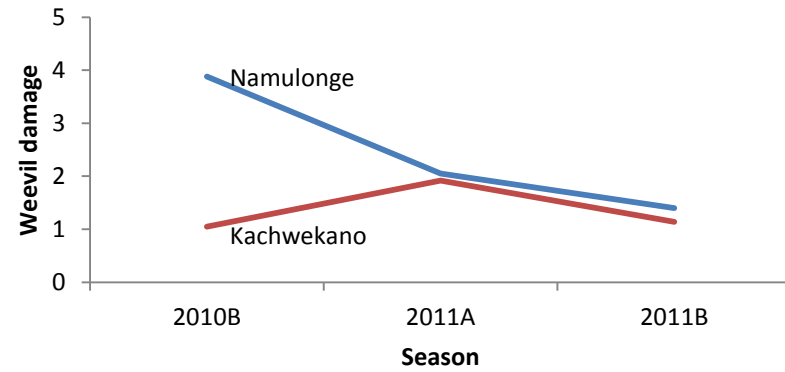


Figure 3.1 d Site x season interaction for weevil damage

Figure 3.1 Variation of traits with site and season meaned across genotypes and two spray treatments (inoculated with *Alternaria* versus sprayed with a fungicide)

**Table 3.3 Genotype means for Alternaria blight AUDPC values with *Alternaria* inoculum and fungicide spray treatments at Namulonge and Kachwekano during the 2010B, 2011A and 2011B seasons**

Genotype	Namulonge			Kachwekano			Namulonge			Kachwekano			Mean	Rank	%DR		
	2010B	2011A	2011B	2010B	2011A	2011B	2010B	2011A	2011B	2010B	2011A	2011B					
	ASP	ASP	ASP	ASP	ASP	ASP	FSP	FSP	FSP	FSP	FSP	FSP					
Araka Red	135.5	114.5	139.0	128.5	142.5	125.0	<b>130.8</b>	24	71.0	60.5	57.0	57.0	67.5	88.5	<b>66.9</b>	22	-48.9
BND145L	121.5	97.0	135.5	107.5	128.5	128.5	<b>119.8</b>	18	57.0	29.0	53.5	46.5	78.0	64.0	<b>54.7</b>	10	-54.3
Bwanjule	114.5	90.0	121.5	97.0	107.5	86.5	<b>102.8</b>	3	53.5	32.5	22.0	36.0	46.5	60.5	<b>41.8</b>	2	-59.3
Dimbuka	146.0	125.0	149.5	128.5	125.0	152.5	<b>137.8</b>	28	78.0	71.0	92.0	60.5	67.5	85.0	<b>75.7</b>	27	-45.1
Ejumula	125.0	107.5	121.5	114.5	107.5	126.5	<b>117.1</b>	15	60.5	50.0	57.0	57.0	50.0	67.5	<b>57.0</b>	11	-51.3
Kigaire	100.5	104.0	114.5	97.0	111.0	104.0	<b>105.2</b>	5	46.5	36.0	32.3	22.0	32.5	60.5	<b>38.3</b>	1	-63.6
Magabali	111.0	97.0	132.0	104.0	118.0	132.0	<b>115.7</b>	11	57.0	46.5	71.0	60.5	64.0	74.5	<b>62.3</b>	18	-46.2
Malagalya	121.5	128.5	125.0	100.5	97.0	111.0	<b>113.9</b>	10	67.5	71.0	50.0	67.5	43.0	53.5	<b>58.8</b>	13	-48.4
MBL 170	97.0	93.5	121.5	118.0	132.0	146.0	<b>118.0</b>	16	29.0	36.0	92.0	57.0	64.0	71.0	<b>58.2</b>	12	-50.7
MBR 536	114.5	79.5	111.0	107.5	118.0	114.5	<b>107.5</b>	6	67.5	29.0	53.5	64.0	50.0	50.0	<b>52.3</b>	8	-51.3
Namusoga	100.5	93.5	132.0	111.0	111.0	111.0	<b>109.8</b>	8	46.5	43.0	53.5	53.5	60.5	67.5	<b>54.1</b>	9	-50.7
New Kawogo	121.5	125.0	135.5	167.0	149.5	174.0	<b>145.4</b>	30	64.0	64.0	113.0	102.5	78.0	78.0	<b>83.3</b>	30	-42.7
NKA103M	100.5	90.0	118.0	139.0	107.5	140.5	<b>115.9</b>	20	36.0	32.5	81.5	78.0	57.0	71.0	<b>59.3</b>	21	-48.8
NKA259L	97.0	100.5	128.5	139.0	114.5	139.0	<b>119.8</b>	4	50.0	39.5	67.5	78.0	57.0	64.0	<b>59.3</b>	5	-50.5
NKA318L	93.5	97.0	135.5	128.5	146.0	146.0	<b>124.4</b>	22	32.5	43.0	95.5	60.5	88.5	67.5	<b>64.6</b>	23	-48.1
NASPOT 1	135.5	149.5	177.5	146.0	170.5	194.5	<b>162.3</b>	8	74.5	85.0	127.0	78.0	106.0	106.0	<b>96.1</b>	7	-40.8

**Table 3.3 continued**

Genotype	Namulonge			Kachwekano			Namulonge			Kachwekano			Mean	Rank	%DR		
	2010B	2011A	2011B	2010B	2011A	2011B	2010B	2011A	2011B	2010B	2011A	2011B					
	ASP	ASP	ASP	ASP	ASP	ASP	FSP	FSP	FSP	FSP	FSP	FSP					
NASPOT 10 O	132.0	107.5	132.0	121.5	132.0	121.5	<b>124.4</b>	26	64.0	43.0	60.5	67.5	74.5	85.0	<b>65.8</b>	27	-47.1
NASPOT 11	107.5	100.5	132.0	93.5	86.5	107.5	<b>104.6</b>	27	50.0	39.5	36.0	39.5	39.5	78.0	<b>47.1</b>	26	-55.0
NASPOT 2	93.5	104.0	128.5	139.0	139.0	160.0	<b>127.3</b>	14	36.0	43.0	99.0	74.5	81.5	74.5	<b>68.1</b>	19	-46.5
NASPOT 3	135.5	90.0	121.5	93.5	111.0	107.5	<b>109.8</b>	29	64.0	39.5	50.0	29.0	60.5	67.5	<b>51.8</b>	29	-52.8
NASPOT 4	121.5	125.0	142.5	132.0	132.0	156.5	<b>134.9</b>	12	64.0	67.5	95.5	81.5	71.0	74.5	<b>75.7</b>	15	-43.9
NASPOT 7	156.5	125.0	146.0	121.5	121.5	148.8	<b>136.6</b>	18	88.5	60.5	74.5	67.5	64.0	88.5	<b>73.9</b>	15	-45.9
NASPOT 8	100.5	111.0	121.5	121.5	118.0	128.2	<b>116.8</b>	20	78.0	53.5	60.5	67.5	64.0	64.0	<b>64.6</b>	19	-44.7
OTADA	114.5	86.5	118.0	123.5	121.5	135.5	<b>116.6</b>	13	46.5	32.5	81.5	60.5	74.5	67.5	<b>60.5</b>	17	-48.1
Semanda	97.0	97.0	121.5	139.0	118.0	142.5	<b>119.2</b>	17	39.5	29.0	81.5	78.0	67.5	57.0	<b>58.8</b>	13	-50.7
Shock	58.5	76.0	97.0	104.0	125.0	111.0	<b>95.3</b>	1	25.5	32.5	50.0	46.5	60.5	43.0	<b>43.0</b>	3	-54.9
Sowola 6	128.5	118.0	128.5	128.5	149.5	133.5	<b>131.1</b>	25	67.5	57.0	81.5	64.0	88.5	71.0	<b>71.6</b>	25	-45.4
SPK004	132.0	114.5	128.5	132.0	111.0	149.5	<b>127.9</b>	23	71.0	60.5	88.5	74.5	57.0	67.5	<b>69.8</b>	24	-45.4
Tanzania	97.0	97.0	107.5	111.0	90.0	86.5	<b>98.2</b>	2	32.5	36.0	25.5	57.0	64.0	50.0	<b>44.2</b>	4	-55.0
Silk Luwero	76.0	104.0	121.5	118.0	111.0	121.5	<b>108.7</b>	7	29.0	32.5	52.7	67.5	53.5	64.0	<b>49.9</b>	6	-54.1
<b>Mean</b>	<b>112.9</b>	<b>104.9</b>	<b>128.2</b>	<b>120.4</b>	<b>121.7</b>	<b>131.4</b>			<b>54.9</b>	<b>46.5</b>	<b>68.5</b>	<b>61.8</b>	<b>64.4</b>	<b>69.4</b>			
<b>SE</b>	<b>11.3</b>	<b>9.1</b>	<b>8.4</b>	<b>18.7</b>	<b>14.5</b>	<b>15.0</b>			<b>8.0</b>	<b>5.1</b>	<b>5.1</b>	<b>9.9</b>	<b>21.8</b>	<b>10.5</b>			
<b>LSD<sub>(0.05)</sub></b>	<b>32.1</b>	<b>25.8</b>	<b>23.7</b>	<b>51.8</b>	<b>41.1</b>	<b>42.5</b>			<b>22.7</b>	<b>14.4</b>	<b>14.6</b>	<b>27.9</b>	<b>61.7</b>	<b>29.7</b>			

Seasons 2010B, 2011A, 2011B = the second season of 2010 (September 2010 to January 2011), first season of 2011 (April to August 2011), and second season of 2011 (September 2011 to January 2012), respectively; ASP = inoculated with *Alternaria* inoculum; FSP = fungicide sprayed; %DR = percentage disease reduction by the fungicide and is the difference between mean AUDPC for fungicide spray and mean AUDPC for *Alternaria* inoculum spray treatment expressed as a percentage of mean AUDPC for *Alternaria* inoculum spray treatment

**Table 3.4 Genotype means for total storage root yield (t ha<sup>-1</sup>) with *Alternaria* inoculum and fungicide spray treatments at Namulonge and Kachwekano during the 2010B, 2011A and 2011B seasons**

Genotype	Namulonge			Kachwekano			Namulonge			Kachwekano			Mean	Rank	%Yield gain		
	2010B	2011A	2011B	2010B	2011A	2011B	2010B	2011A	2011B	2010B	2011A	2011B					
	ASP	ASP	ASP	ASP	ASP	ASP	FSP	FSP	FSP	FSP	FSP	FSP					
Araka red	17.0	14.0	11.9	4.8	8.3	5.9	<b>10.3</b>	11	19.1	15.5	15.3	6.6	10.2	7.7	<b>12.4</b>	20	20.4
BND145L	14.1	21.8	12.2	14.6	7.2	4.5	<b>12.4</b>	4	16.7	27.5	12.0	18.0	9.2	8.1	<b>15.2</b>	5	22.6
Bwanjule	12.2	16.9	9.5	13.3	5.2	3.6	<b>10.1</b>	12	13.5	26.8	12.4	19.3	6.5	4.2	<b>13.8</b>	12	36.6
Dimbuka	4.5	21.8	6.4	11.6	7.9	5.3	<b>9.6</b>	17	8.2	28.0	6.5	16.1	10.6	10.4	<b>13.3</b>	16	38.5
Ejumula	2.4	10.5	8.2	11.7	6.0	3.5	<b>7.0</b>	29	3.2	12.4	10.2	15.4	7.9	4.1	<b>8.9</b>	30	27.1
Kigaire	10.8	18.8	13.0	1.1	3.8	0.8	<b>8.1</b>	23	17.7	21.0	14.0	2.6	4.3	1.6	<b>10.2</b>	26	25.9
Magabali	9.8	8.7	13.6	6.2	5.5	1.7	<b>7.6</b>	26	15.8	17.3	16.3	9.8	8.2	3.2	<b>11.8</b>	22	55.3
Malagalya	4.2	9.3	6.9	10.8	9.7	4.4	<b>7.6</b>	27	5.7	11.3	8.2	14.6	13.8	5.5	<b>9.9</b>	28	30.3
MBL 170	3.8	10.6	10.2	12.8	7.9	6.9	<b>8.7</b>	20	10.1	13.2	11.9	20.2	12.2	8.4	<b>12.7</b>	19	46.0
MBR 536	8.7	10.4	5.4	6.1	5.9	3.6	<b>6.7</b>	30	11.8	20.9	6.8	10.1	9.9	5.4	<b>10.8</b>	23	61.2
Namusoga	9.2	11.5	7.9	10.8	5.1	6.9	<b>8.5</b>	21	14.2	16.5	11.9	20.2	9.2	9.0	<b>13.5</b>	14	58.8
New Kawogo	8.2	6.4	12.0	18.8	10.3	3.2	<b>9.8</b>	6	11.2	9.3	16.8	24.4	12.6	4.3	<b>13.1</b>	17	33.7
NKA103M	11.0	20.7	14.1	9.5	9.0	3.7	<b>11.3</b>	10	13.3	23.1	16.8	14.4	10.1	6.2	<b>14.0</b>	10	23.9
NKA259L	5.4	3.7	4.5	17.0	8.3	7.3	<b>7.7</b>	2	5.8	9.4	6.3	18.9	12.0	6.8	<b>9.9</b>	29	28.6
NKA318L	8.3	5.7	11.2	22.3	12.7	3.1	<b>10.5</b>	18	8.2	11.4	11.7	26.3	10.3	4.4	<b>12.1</b>	21	15.2
NASPOT 1	10.6	12.8	12.6	20.4	8.6	2.9	<b>11.3</b>	15	11.1	22.0	16.7	26.8	11.9	6.4	<b>15.8</b>	4	39.8

**Table 3.4 continued**

Genotype	Namulonge			Kachwekano			Namulonge			Kachwekano			%Yield gain				
	2010B	2011A	2011B	2010B	2011A	2011B	2010B	2011A	2011B	2010B	2011A	2011B					
	ASP	ASP	ASP	ASP	ASP	ASP	FSP	FSP	FSP	FSP	FSP	FSP		Mean	Rank		
NASPOT 10 O	7.1	18.6	11.0	17.4	5.3	3.6	<b>10.5</b>	22	12.4	28.7	14.0	20.0	8.0	4.3	<b>14.6</b>	6	39.0
NASPOT 11	13.0	14.7	18.7	18.2	13.1	7.5	<b>14.2</b>	3	17.0	23.9	24.4	23.9	17.8	8.0	<b>19.2</b>	2	35.2
NASPOT 2	13.0	13.8	17.0	4.2	6.8	2.9	<b>9.6</b>	1	16.9	24.5	20.5	7.4	9.8	4.2	<b>13.9</b>	11	44.8
NASPOT 3	4.2	18.1	8.8	11.4	10.5	7.0	<b>10.0</b>	16	8.7	21.6	10.8	17.6	12.7	9.6	<b>13.5</b>	15	35.0
NASPOT 4	16.3	7.8	11.8	4.5	3.7	5.2	<b>8.2</b>	5	18.0	14.1	12.9	7.5	5.1	5.5	<b>10.5</b>	25	28.0
NASPOT 7	9.2	18.7	18.6	13.2	6.4	9.9	<b>12.7</b>	25	12.7	25.9	21.6	23.2	9.2	10.4	<b>17.2</b>	3	35.4
NASPOT 8	24.1	23.5	18.2	20.9	8.7	7.3	<b>17.1</b>	9	25.2	30.7	22.7	32.5	11.2	9.5	<b>21.9</b>	1	28.1
OTADA	9.4	7.0	6.1	11.9	5.8	4.8	<b>7.5</b>	28	10.1	12.1	7.2	16.2	8.5	6.5	<b>10.1</b>	27	34.7
Semanda	11.7	23.3	18.8	5.0	3.8	3.7	<b>11.1</b>	7	17.6	26.2	23.0	8.9	5.1	3.7	<b>14.1</b>	8	27.0
Shock	9.3	20.4	8.3	7.8	<b>7.2</b>	7.8	<b>10.1</b>	13	12.2	23.6	8.8	14.3	9.5	9.8	<b>13.1</b>	18	29.7
Sowola 6	3.7	18.8	11.5	11.2	8.5	4.0	<b>9.6</b>	19	5.9	26.5	12.6	15.8	15.7	5.2	<b>13.6</b>	13	41.7
SPK004	4.7	13.7	8.8	12.4	5.7	2.5	<b>8.0</b>	24	6.6	18.1	10.3	16.2	9.9	3.2	<b>10.7</b>	24	33.8
Tanzania	9.3	11.2	10.6	12.6	15.2	4.5	<b>10.6</b>	8	7.7	16.0	13.2	15.4	26.3	6.2	<b>14.1</b>	9	33.0
Silk Luwero	11.3	22.3	10.1	7.7	5.0	4.4	<b>10.1</b>	14	12.3	26.3	13.6	14.4	7.5	11.7	<b>14.3</b>	7	41.6
<b>Mean</b>	<b>9.5</b>	<b>14.5</b>	<b>11.2</b>	<b>11.7</b>	<b>7.2</b>	<b>4.7</b>			<b>12.3</b>	<b>20.1</b>	<b>13.6</b>	<b>16.6</b>	<b>10.5</b>	<b>6.5</b>			
<b>SE</b>	<b>2.9</b>	<b>3.6</b>	<b>2.1</b>	<b>3.6</b>	<b>1.5</b>	<b>1.6</b>			<b>3.5</b>	<b>4.6</b>	<b>2.7</b>	<b>4.1</b>	<b>1.7</b>	<b>2.1</b>			
<b>LSD<sub>(0.05)</sub></b>	<b>8.2**</b>	<b>10.1**</b>	<b>5.9**</b>	<b>10.2**</b>	<b>4.1**</b>	<b>4.6*</b>			<b>9.9**</b>	<b>13.2**</b>	<b>7.5**</b>	<b>11.6**</b>	<b>4.7</b>	<b>5.9</b>			

\* = significant at P<0.05; \*\* = significant P<0.01; Seasons 2010B, 2011A; 2011B = the second season of 2010 (September 2010 to January 2011), first season of 2011 (April to August 2011), and second season of 2011 (September 2011 to January 2012), respectively; ASP = Inoculated with *Alternaria* inoculum; FSP = fungicide sprayed; %Yield gain is the difference between the yield from the *Alternaria* inoculum spray and the yield from the fungicide treatment for each genotype expressed as a percentage of the yield from the *Alternaria* inoculum spray treatment

The highest average yield gains of 61.2, 58.8 and 55.3% in response to fungicide treatment were recorded by MBR 536, Namusoga, and Magabali, respectively (Table 3.4). The lowest yield gains of 15.2, 20.4 and 22.6% were recorded by NKA318L, Araka Red and BND145L, respectively. With respect to *Alternaria* blight severity, treatment with fungicide resulted in variable reductions in severity among genotypes across seasons and sites (Table 3.3). NASPOT 1 recorded the lowest percentage reduction in disease severity of 40.8% between the *Alternaria* inoculated and fungicide treated plants. Kigaire recorded the highest percentage disease reduction of 63.6%.

Correlations between *Alternaria* blight severity and TRY were calculated using the AUDPC values and yield of the *Alternaria* inoculated plants. Both the AUDPC values and the TRY were meaned over the genotypes and seasons. There were negative but non-significant correlations between *Alternaria* blight severity and mean TRY across the genotypes during seasons 2010B and 2011A at Namulonge and 2011A and 2011B at Kachwekano (Table 3.5).

### **3.3.2 Stability of genotypes for *Alternaria* blight severity, total storage root fresh mass and harvest index across six environments**

The AMMI analysis was conducted for AUDPC, TRY, HI, DM%, weevil damage and SPVD (Tables 3.6 and 3.7); however, since no artificial infestation was done for weevils and SPVD at all experimental sites (since the insect pest and disease were not the focus of this study), it is likely that there was uneven distribution of weevils and SPVD increasing the probability of escapes. Therefore, results for these traits are not discussed in detail and only AUDPC, TRY and HI are fully discussed.

#### **3.3.2.1 Stability for *Alternaria* blight reaction**

The genotypes, environments and GEI effects were highly significant for AUDPC ( $P < 0.001$ ) (Table 3.6). The genotypes, environments and GEI accounted for 18.8, 8.1 and 16.8%, respectively of the total SS for AUDPC (expressed as a mean of the *Alternaria* inoculation and fungicide spray treatments for each genotype). Only IPCA1 and IPCA2 were significant ( $P < 0.0001$ ) and accounted for 47.3 and 30.2%, respectively of the GEI SS.

**Table 3.5 Correlation between Alternaria blight severity scores (expressed as area under the disease progress curve values) of inoculated plants and yield meaned over genotypes and seasons**

NAM1	-			
NAM2	0.595	-		
NAMY1	<b>-0.206</b>	0.003		
NAMY2	-0.017	<b>-0.054</b>		
KACY2	-0.029	0.047	<b>-0.091</b>	-0.092
KACY3	0.019	-0.090	-0.178	<b>-0.128</b>
	NAM1	NAM2	KAC2	KAC3

NAM1 = area under disease progress curve (AUDPC) at Namulonge 2010B; NAM2 = AUDPC at Namulonge 2011A; NAMY1 = Yield at Namulonge 2010B; NAMY2 = Yield at Namulonge 2011A; KAC2 = AUDPC at Kachwekano 2011A; KAC3 = AUDPC at Kachwekano 2011B; KACY2 = Yield at Kachwekano 2011A; KACY3 = Yield at Kachwekano 2011B

The rank order of the performance of the genotypes changed across the six environments (Appendix 3.4). However, some genotypes were consistently ranked as resistant and others were consistently ranked as susceptible. A genotype with the highest AUDPC mean AMMI estimate was considered to be the most susceptible and was ranked last (30<sup>th</sup>) while the genotype with the lowest AUDPC was the most resistant and was ranked first. NASPOT 1 was the most susceptible genotype in four of the six environments and ranked second most susceptible in the other two environments. New Kawogo and MBR 536 were the most susceptible genotypes at Namulonge 2010B and Namulonge 2011A, respectively. NASPOT 7 was the second most susceptible genotype in four of the environments. Shock was the most resistant genotype in four of the environments and NASPOT 3 the most resistant in the other two environments. Kigaire exhibited consistency in resistance to the disease and was second most resistant in two environments and third most resistant in three of the environments.

In the AMMI biplot (Figure 3.2), susceptible genotypes were scattered in quadrants I and II while resistant genotypes were scattered in quadrants III and IV. Genotypes close to the horizontal line have low interaction with the environments and are therefore stable whereas the further away genotypes are from the horizontal line the more unstable they are. The most stable genotypes for Alternaria blight with above average mean AUDPC values and susceptibility were NASPOT 1, Sowola 6, NASPOT 4 and NASPOT 10 O. The most stable genotypes with below average mean values and thus resistant were Magabali, BND145L, NASPOT 8, Namusoga, Tanzania and NKA259L. Genotypes MBR 536, NASPOT 2, NKA318L, Malagalya and NASPOT 7 were the furthest away from the horizontal line and therefore the least stable for Alternaria



blight severity. BND145L and NASPOT 10 O were in opposite quadrants to each other thus their contributions to the interaction SS were in opposing directions.

Genotypes Bwanjule, NASPOT 11, NASPOT 3 were specifically adapted to environment Namulonge 2011B. Dimbuka, Araka Red, NASPOT 7 were relatively stable and adapted to environment Namulonge 2011B. NKA318L, NASPOT 2 and MBR 536 were relatively unstable with specific adaptation to Kachwekano 2010B and Kachwekano 2011B, respectively. New Kawogo was relatively unstable with above average AUDPC value with low interaction with Kachwekano 2010B and Kachwekano 2011A. None of the environments was stable for *Alternaria* blight; however, Namulonge 2011A, Namulonge 2011B, Kachwekano 2010B, Kachwekano 2011B were relatively more stable than Namulonge 2010B and Kachwekano 2011B.

**Table 3.6 AMMI analysis for Alternaria blight severity, total storage root fresh mass and harvest index for 30 sweetpotato genotypes evaluated in six environments**

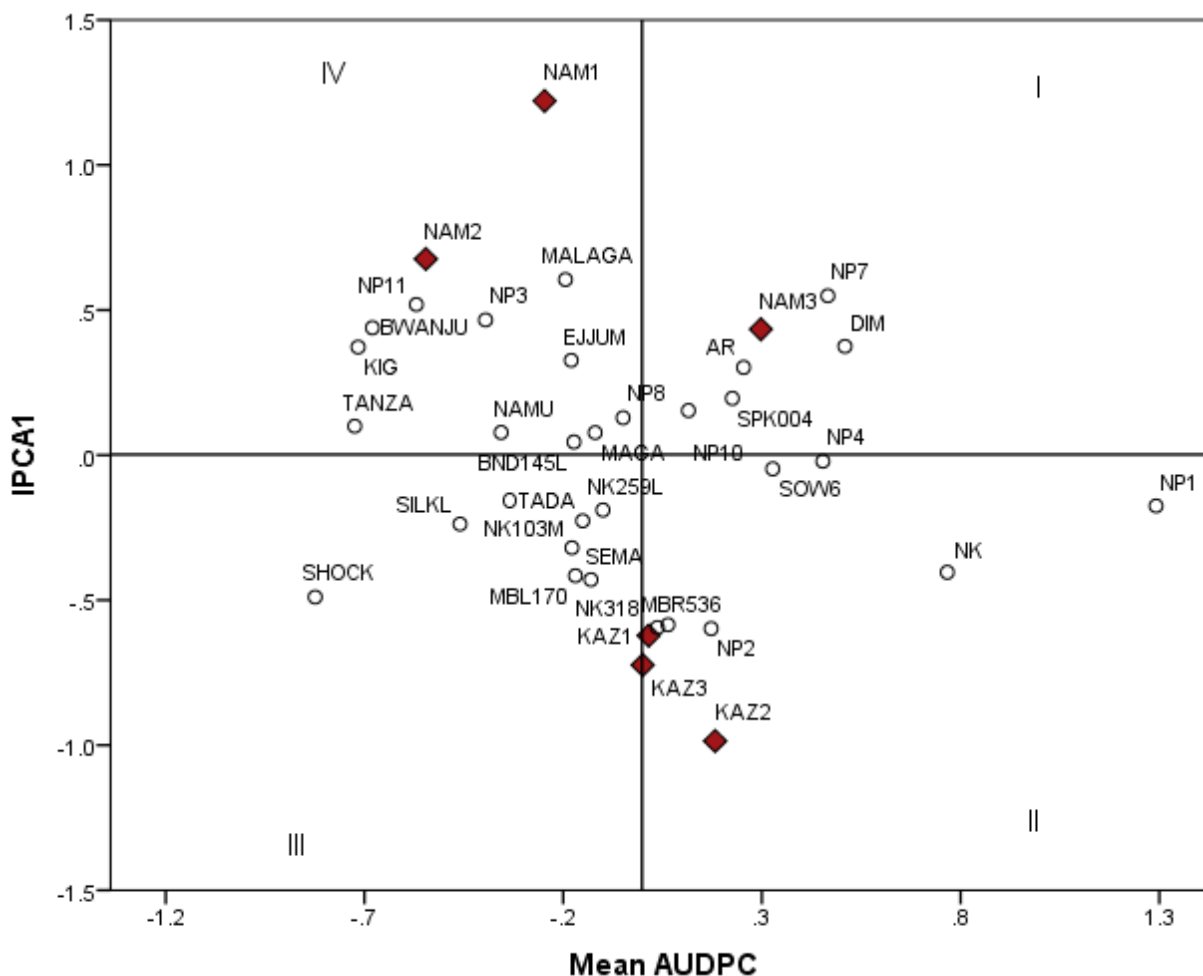
Source of variation	df	AUDPC				TRY				HI			
		SS	MS	%Total SS	%GEI SS	SS	MS	%Total SS	%GEI SS	SS	MS	%Total SS	%GEI SS
Total	1079	994490	866			69244	64.2			39.03	0.0362		
Treatments	179	433694	2428***	43.6		37235	208.0***	53.8		17.62	0.0984***	45.1	
Genotypes (G)	29	187073	6451***	18.8		6434	221.9***	9.3		4.65	0.1604***	11.9	
Environments (E)	5	80204	16041***	8.1		15195	3039.1***	21.9		6.65	1.3303***	17.0	
Interaction (G x E)	145	167417	1512***	16.8		15605	107.6***	22.5		6.31	0.0435***	16.2	
IPCA1	33	79163	2399***		47.3	7874	238.6***		50.5	3.26	0.0989***		51.7
IPCA2	31	50614	1633***		30.2	3522	113.6***		22.6	1.42	0.0458***		22.5
Residuals	81	37639	463		22.5	4209	52.0		27.0	1.63	0.0201		25.8
Error	887	481654	543			26834	30.2			17.74	0.0201		

\*\*\* = significant at  $P < 0.0001$ ; AUDPC = area under disease progress curve for Alternaria blight severity; TRY = total storage root fresh mass ( $t\ ha^{-1}$ ); HI = harvest index; df = degrees of freedom; SS = sum of squares; MS = mean square; %Total SS = percentage of total sum of squares; %GEI SS = percentage of genotype x environment interaction sum of squares; IPCA = interaction principal component analysis

**Table 3.7 AMMI analysis for percentage dry mass composition, weevil damage and sweetpotato virus disease severity for 30 genotypes evaluated in six environments**

Source of variation		DM%				Weevil damage				SPVD			
Source	df	SS	MS	%Total SS	%GEI SS	SS	MS	%Total SS	%GEI SS	SS	MS	%Total SS	%GEI SS
Total	1079	153562	142.3			1654.8	1.53			2884.3	2.67		
Treatments	179	29014	162.1	18.9		1238.8	6.92***	74.9		2087.0	11.66***	72.4	
Genotypes (G)	29	6644	229.1*	4.3		76.7	2.64***	4.6		242.3	8.36***	8.4	
Environments (E)	5	1001	200.1	0.7		977.7	195.54***	59.1		1455.6	485.19***	50.5	
Interaction (G x E)	145	21369	147.4	13.9		184.4	1.27***	11.1		389.1	4.47***	13.5	
IPCA1	33	15212	461.0***		71.2	83.8	2.54***		45.4	249.4	7.56***		64.0
IPCA2	31	4244	136.9		19.9	57.4	1.85***		31.1	101.5	3.27***		26.0
Residuals	81	1913	23.6		9.0	43.2	0.53		23.4	38.1	1.66		
Error	887	118702	136.8			389.4	0.48			623.2	1.08		

\*\*\* = significant at P<0.0001; \* = significant at P<0.05; DM% = percentage dry mass composition; SPVD = sweetpotato virus disease; df = degrees of freedom; SS = sum of squares; MS = mean square; %Total SS = percentage of total sum of squares; %GEI SS = percentage of genotype x environment interaction sum of squares; IPCA = interaction principal component analysis



**Figure 3.2 Biplot of mean area under disease progress curve (AUDPC) for Alternaria blight severity and the first interaction principal component axis (IPCA1) scores for 30 sweetpotato genotypes evaluated in six environments**

### Key

#### **Genotypes**

TANZA = Tanzania; NAMU = Namusoga; SILKL = Silk Luwero; SEMA = Semanda; NP2 = NASPOT 2; SOW6 = Sowola 6; NK = New Kawogo; NP1 = NASPOT1; NP4 = NASPOT4; NP10 = NASPOT 10 O; MAGA = Magabali; NP8 = NASPOT 8; KIG = Kigaire; BWANJU = Bwanjule; NP11 = NASPOT 11; NP3 = NASPOT3; MALAGA = Malagalya; AR = Araka Red; NP7 = NASPOT7; DIM = Dimbuka O

#### **Environments**

NAM1 = Namulonge 2010B; NAM2 = Namulonge 2011A; NAM3 = Namulonge 2011B; KAZ1 = Kachwekano 2010B; KAZ2 = Kachwekano 2011A; and KAZ3 = Kachwekano 2011B ◆

The biplot provides a useful diagrammatic overview of the interaction patterns of the genotypes and environments and their relative stability levels. However, for ranking purposes the AMMI model does not provide an integrated measure of stability based on scores for the first two important IPCAs. To rank the genotypes more holistically in terms of stability and performance the ASV and GSI for each genotype were calculated.

The ASV ranked NASPOT 1, Namusoga and NASPOT 8 with values of 0.63, 0.75 and 0.81 as the most stable and MBR 536, NASPOT 11 and Malagalya with values of 11.09, 5.29 and 5.14 as the least stable for Alternaria blight (Table 3.8). The GSI ranked Tanzania and Namusoga as the best genotypes combining stability and resistance to Alternaria blight.

**Table 3.8 Mean stability rankings of 30 sweetpotato genotypes for Alternaria blight severity (expressed as AUDPC values) for ASV and GSI indices across six environments meaned for spray treatments**

<b>Genotype</b>	<b>Mean AUDPC</b>	<b>Rank</b>	<b>ASV</b>	<b>Rank</b>	<b>GSI</b>	<b>Rank</b>
Araka Red	98.9	24	1.91	9	35	19
BND145L	87.2	11	2.10	10	24	8
Bwanjule	72.3	4	2.86	16	20	6
Dimbuka	106.7	28	4.07	22	49	28
Ejumula	87.0	10	3.01	18	33	17
Kigaire	71.7	3	3.18	19	21	7
Magabali	89.0	16	1.25	7	25	10
Malagalya	86.3	9	5.14	28	47	27
Mbl 170	88.1	13	2.39	12	19	4
MBR 536	92.8	19	11.09	30	36	21
Namusoga	82.0	8	0.75	2	11	2
New Kawogo	114.3	29	3.56	21	50	29
NKA103M	87.6	12	2.91	17	30	14
NKA259L	89.5	17	2.46	13	29	12
NKA318	94.5	20	4.63	25	42	25
NASPOT 1	129.2	30	0.63	1	31	16
NASPOT 10 O	95.1	21	0.93	4	27	11
NASPOT 11	75.8	5	5.29	29	37	23
NASPOT 2	97.7	22	4.34	23	43	26
NASPOT 3	80.8	7	4.37	24	36	22
NASPOT 4	105.3	27	1.15	6	33	18
NASPOT 7	105.2	26	5.11	27	52	30
NASPOT 8	90.7	18	0.81	3	24	9
OTADA	88.3	14	1.76	8	18	3
Semanda	89.0	15	3.54	20	30	15
Shock	69.1	1	4.68	26	29	13
Sowola 6	101.3	25	2.16	11	35	20
SPK004	98.9	23	2.79	15	37	24
Tanzania	71.2	2	1.14	5	6	1
Silk Luwero	79.3	6	2.76	14	19	5
<b>Mean</b>	<b>90.8</b>					

ASV = AMMI stability value, GSI = Genotype selection index

The environments were also ranked by the ASV and the GSI. The ASV ranked Namulonge 2011B as the most stable environment for *Alternaria* blight and Namulonge 2010B as the least stable. The GSI ranked Namulonge 2011A and Kachwekano 2010B as the most stable with low disease pressure and Kachwekano 2011A and Kachwekano 2011B as the least stable with high disease pressure (Table 3.9).

**Table 3.9 Mean stability ranking of the six test environments for *Alternaria* blight severity**

<b>Environment</b>	<b>Mean AUDPC</b>	<b>Rank</b>	<b>ASV</b>	<b>Rank</b>	<b>GSI</b>	<b>Rank</b>
Kachwekano 1	91.04	3	6.0647	2	4	1
Kachwekano 2	95.61	4	10.1770	5	9	5
Kachwekano 3	99.95	6	10.5150	4	10	6
Namulonge 1	83.88	2	11.9200	6	8	4
Namulonge 2	75.72	1	6.3888	3	4	1
Namulonge 3	98.76	5	4.1676	1	6	3

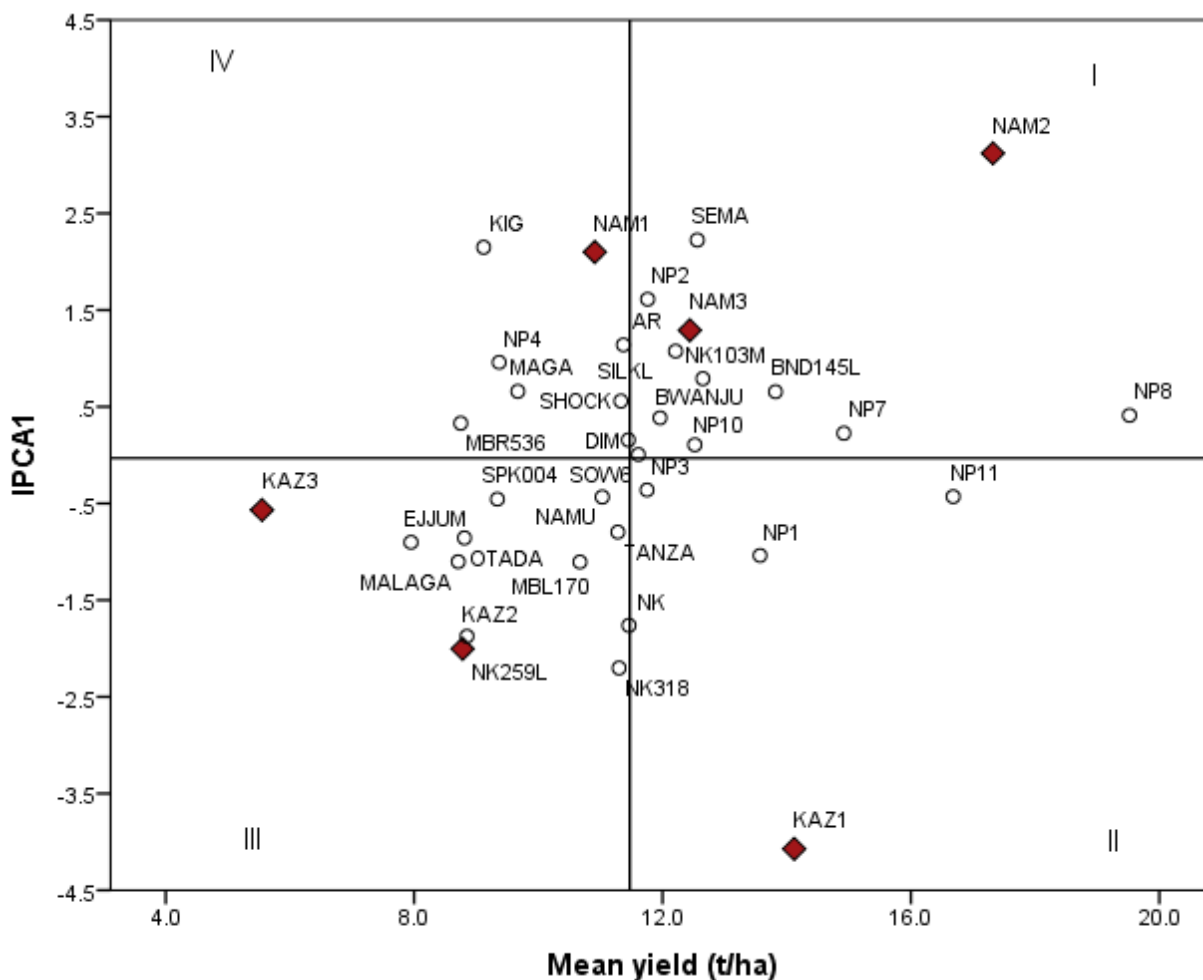
ASV = AMMI stability value; smallest ASV is the most stable and given rank 1; largest ASV is the most unstable and given rank 6; Kachwekano1 = 2010B; Kachwekano 2 = 2011A; Kachwekano 3 = 2011B; Namulonge 1 = 2010B; Namulonge 2 = 2011A; Namulonge 3 = 2011B

### 3.3.2.2 Stability for total storage root yield

The genotypes, environments and GEI effects for TRY were highly significant ( $P < 0.001$ ) (Table 3.6). The genotypes, environments and GEI SS accounted for 9.3, 21.9 and 22.5%, respectively of the total SS. The IPCA1 and IPCA2 were significant ( $P < 0.001$ ) and accounted for 50.5 and 22.5% of the GEI SS, respectively.

The highly significant ( $P < 0.001$ ) GEI effects indicate differential performance of the genotypes in terms of yield across the environments. NASPOT 8 was the best yielder in five of the six environments (Appendix 3.5). NKA318L was the best yielder at Namulonge 2010B. NASPOT 11 was the second best yielder in three of the six environments. Despite its susceptibility to *Alternaria* blight, NASPOT 1 was the second best yielder at Namulonge 2010B and was the fourth best yielder at Namulonge 2011A and Namulonge 2011B.

Many genotypes were relatively stable for TRY (Figure 3.3). Genotypes in quadrants I and II yielded above average (11.53) and those in quadrants III and IV yielded below average. The most yield stable genotypes with above average performance were NASPOT 8, NASPOT 7, NASPOT 11, NASPOT 10 O, NASPOT 3 and Sowola 6. Genotypes SPK004 and Namusoga were yield stable but with below average performance. Genotypes Dimbuka, Shock, Araka Red, Tanzania, New Kawogo and NKA318L lying on the vertical line produced average yields. Genotypes NASPOT 2, Araka Red and NKA103M performed best at Namulonge 2011B.



**Figure 3.3 Biplot of mean total storage root yield and the first interaction principal component axis (IPCA1) scores for 30 sweetpotato genotypes evaluated in six environments**

**Key**

**Genotypes**

TANZA = Tanzania; NAMU = Namusoga; SILKL = Silk Luwero; SEMA = Semanda; NP2 = NASPOT 2; SOW6 = Sowola 6; NK = New Kawogo; NP1 = NASPOT 1; NP4 = NASPOT 4; NP10 = NASPOT 10 O; MAGA = Magabali; NP8 = NASPOT 8; KIG = Kigaire; BWANJU = Bwanjule; NP11 = NASPOT 11; NP3 = NASPOT 3; MALAGA = Malagalya; AR = Araka Red; NP7 = NASPOT 7; DIM = Dimbuka O

**Environments**

NAM1 = Namulonge 2010B; NAM2 = Namulonge 2011A; NAM3 = Namulonge 2011B; KAZ1 = Kachwekano 2010B; KAZ2 = Kachwekano 2011A; KAZ3 = Kachwekano 2011B ◆

To investigate the stability of the genotypes for TRY, the ASV and GSI were used. The ASV ranked NASPOT 7, MBR 536 and NASPOT 8 as the most stable and Semanda, NKA318L and Kigaire were ranked as the least stable (Table 3.10). The GSI ranked NASPOT 8 and NASPOT 7 as the most stable and high yielding genotypes and NKA259L, Kigaire and NASPOT 4 as the least stable and low yielding.

**Table 3.10 Mean stability rankings of 30 sweetpotato genotypes for total storage root yield for ASV and GSI indices across six environments meaned for spray treatments**

<b>Genotype</b>	<b>Mean TRY</b>	<b>Rank</b>	<b>ASV</b>	<b>Rank</b>	<b>GSI</b>	<b>Rank</b>
Araka Red	11.37	16	2.99	24	40	23
BND145L	13.82	4	1.64	12	17	5
Bwanjule	11.96	10	1.11	5	19	6
Dimbuka	11.45	15	2.11	18	38	19
Ejumula	7.95	30	2.03	17	47	26
Kigaire	9.12	25	4.83	28	51	29
Magabali	9.67	22	1.96	15	37	18
Malagalya	8.71	29	2.47	20	47	26
Mbl 170	10.67	21	2.48	21	38	19
MBR 536	8.75	28	0.74	2	31	13
Namusoga	11.03	20	1.01	4	23	9
New Kawogo	11.46	14	4.11	26	34	16
NKA103M	12.65	6	1.78	13	19	6
NKA259L	8.78	27	4.49	27	52	30
NKA318L	11.30	18	4.96	29	39	21
NASPOT 1	13.57	5	2.33	19	23	9
NASPOT 10 O	12.52	8	1.28	8	15	4
NASPOT 11	16.68	2	1.16	6	8	3
NASPOT 2	11.76	11	3.74	25	40	23
NASPOT 3	11.75	12	1.33	9	21	8
NASPOT 4	9.37	23	2.84	23	47	28
NASPOT 7	14.92	3	0.62	1	4	1
NASPOT 8	19.52	1	0.93	3	4	1
OTADA	8.81	26	1.99	16	44	25
Semanda	12.56	7	4.98	30	39	21
Shock	11.33	17	1.62	11	32	14
Sowola 6	11.61	13	1.39	10	28	12
SPK004	9.34	24	1.16	7	33	15
Tanzania	11.28	19	1.82	14	25	11
Silk Luwero	12.21	9	2.58	22	35	17
<b>Mean</b>	<b>11.53</b>					

TRY = Total storage root fresh mass (t ha<sup>-1</sup>); ASV = AMMI stability value; GSI = Genotype selection index

Environment Kachwekano 2011B was the most stable but low yielding while Namulonge 2010A was the highest yielding but not very stable as per ASV (Table 3.11). However, in terms of combining both good yield and stability, GSI ranked Namulonge 2 the second best performing environment. Kachwekano 2010A was a high yielding but an unstable environment and Namulonge 2011B was a stable and relatively high yielding environment and was ranked the best by GSI.



**Table 3.11 Mean stability ranking of the six test environments for total storage root yield**

<b>Environment</b>	<b>Mean TRY</b>	<b>Rank</b>	<b>ASV</b>	<b>Rank</b>	<b>GSI</b>	<b>Rank</b>
Kachwekano1	14.12	2	7.27	6	8	4
Kachwekano 2	8.85	5	3.33	3	8	4
Kachwekano 3	5.55	6	1.03	1	7	3
Namulonge 1	10.91	4	4.51	4	8	4
Namulonge 2	17.32	1	6.59	5	6	2
Namulonge 3	12.44	3	2.96	2	5	1

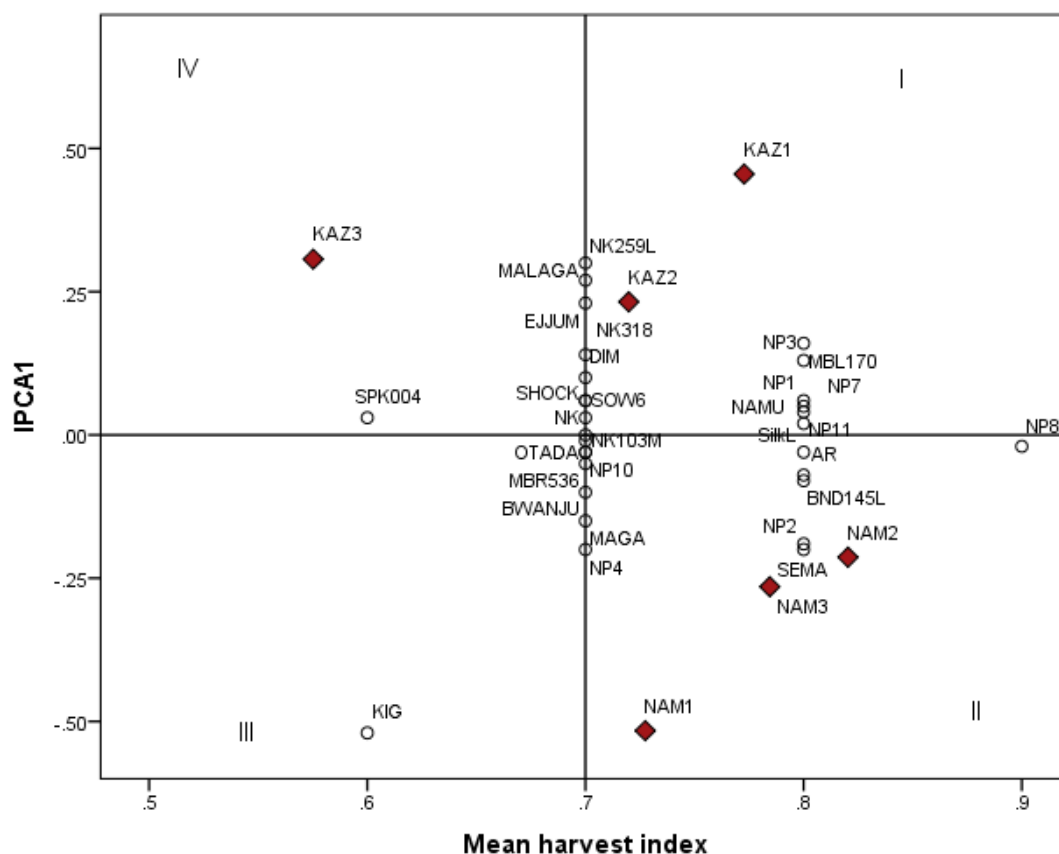
TRY = total storage root fresh mass (t ha<sup>-1</sup>); ASV = AMMI stability value; GSI = genotype selection index; Kachwekano1 = 2010B; Kachwekano 2 = 2011A; Kachwekano 3 = 2011B; Namulonge 1 = 2010B; Namulonge 2 = 2011A; Namulonge 3 = 2011B

### 3.3.2.3 Stability of harvest index across six environments

The genotypes, environments and GEI effects for HI were highly significant ( $P < 0.001$ ) (Table 3.6). The genotypes, environments and GEI accounted for 11.9, 17.0 and 16.2%, respectively of the total SS. The IPCA1 and IPCA2 were highly significant ( $P < 0.001$ ) contributing 51.7 and 22.5% of GEI SS, respectively. NASPOT 8 had the highest HI in four of the six environments (Appendix 3.6).

Few genotypes were stable for HI (Figure 3.4). Genotypes in quadrants I and II had above average (0.73) HI, while those in quadrants III and IV had below average HI. The most HI stable genotypes with above average performance were NASPOT 8, NASPOT 11, Silk Luwero and Araka Red. Genotype SPK004 was the only stable genotype with below average HI. Genotypes NKA259L, Malagalya, Ejumula, Dimbuka, Shock, Sowola 6, New Kawogo, NK 130M, Otada, NASPOT 10 O, MBR 536, Bwanjule, Magabali lying on the vertical line had average HI. NASPOT 8 had the highest mean HI (0.87) and was also very stable. Environments Kachwekano 2011A, Namulonge 2011A and Namulonge 2011B were relatively stable for HI with high interaction with several genotypes. Environments Namulonge 2010B, Kachwekano 2010B and Kachwekano 2011B were relatively unstable with very low interaction with the genotypes.

The ASV ranked NKA103M, Otada, NASPOT 8 and MBR 536 as the most stable genotypes for HI while Kigaire, NKA259L and Malagalya were ranked as the least stable genotypes for this trait (Table 3.12). The GSI ranked NASPOT 8, NASPOT 11 and NASPOT 1 as the best performing genotypes and Kigaire, Ejumula and NKA259L as the worst performing for HI.



**Figure 3.4 Biplot of mean harvest index and the first interaction principal component axis (IPCA1) scores for 30 sweetpotato genotypes evaluated in six environments**

**Key**

**Genotypes**

TANZA = Tanzania; NAMU = Namusoga; SilkL = Silk Luwero; SEMA = Semanda; NP2 = NASPOT 2; SOW6 = Sowola 6; NK = New Kawogo; NP1 = NASPOT 1; NP4 = NASPOT 4; NP10 = NASPOT 10 O; MAGA = Magabali; NP8 = NASPOT 8; KIG = Kigaire; BWANJU = Bwanjule; NP11 = NASPOT 11; NP3 = NASPOT 3; MALAGA = Malagalya; AR = Araka Red; NP7 = NASPOT 7; DIM = Dimbuka O

**Environments**

NAM1 = Namulonge 2010B; NAM2 = Namulonge 2011A; NAM3 = Namulonge 2011B; KAZ1 = Kachwekano 2010B; KAZ2 = Kachwekano 2011A; KAZ3 = Kachwekano 2011B ◆

**Table 3.12 Mean stability rankings of 30 sweetpotato genotypes for harvest index for ASV and GSI indices across six environments meaned for spray treatments**

<b>Genotype</b>	<b>Mean HI</b>	<b>Rank</b>	<b>ASV</b>	<b>Rank</b>	<b>GSI</b>	<b>Rank</b>
Araka Red	0.78	9	0.22	16	27	12
BND145L	0.79	6	0.23	17	21	9
Bwanjule	0.67	25	0.31	19	43	23
Dimbuka	0.71	19	0.24	18	39	21
Ejumula	0.65	28	0.53	27	55	29
Kigaire	0.55	30	1.20	30	57	30
Magabali	0.69	23	0.36	22	44	25
Malagalya	0.72	18	0.62	28	45	26
MBL 170	0.78	9	0.38	23	32	16
MBR 536	0.73	15	0.11	4	20	8
Namusoga	0.80	3	0.15	8	14	4
New Kawogo	0.68	24	0.20	12	38	19
NKA103M	0.75	12	0.05	1	15	5
NKA259L	0.73	15	0.69	29	47	28
NKA318L	0.67	25	0.36	21	46	27
NASPOT 1	0.80	3	0.15	9	12	3
NASPOT 10 O	0.71	19	0.13	6	26	11
NASPOT 11	0.85	2	0.13	5	7	2
NASPOT 2	0.76	11	0.45	24	34	17
NASPOT 3	0.79	6	0.33	20	27	13
NASPOT 4	0.73	15	0.51	26	41	22
NASPOT 7	0.80	3	0.20	13	18	6
NASPOT 8	0.87	1	0.08	3	4	1
OTADA	0.70	22	0.05	2	25	10
Semanda	0.75	12	0.46	25	38	20
Shock	0.67	25	0.21	14	43	24
Sowola 6	0.71	19	0.19	11	30	15
SPK004	0.64	29	0.15	7	37	18
Tanzania	0.75	12	0.21	15	27	14
Silk Luwero	0.79	6	0.15	10	18	7
<b>Mean</b>	<b>0.73</b>					

ASV = AMMI stability value, GSI = genotype selection index, HI = harvest index

The ASV ranked Kachwekano 2011A, Kachwekano 2011B and Namulonge 2011B as the first, second and third most stable environments for HI (Table 3.13). However, the GSI ranked Namulonge 2011B as the best environment in terms of combining good HI and stability. Environments Kachwekano 2011A and Namulonge 2011A were both ranked second.

**Table 3.13 Mean stability ranking of the six test environments for harvest index**

<b>Environment</b>	<b>Mean HI</b>	<b>Rank</b>	<b>ASV</b>	<b>Rank</b>	<b>GSI</b>	<b>Rank</b>
Kachwekano1	0.7727	3	0.67825	4	7	4
Kachwekano 2	0.7198	5	0.55331	1	6	2
Kachwekano 3	0.5752	6	0.59517	2	8	5
Namulonge 1	0.7274	4	4.59982	6	10	6
Namulonge 2	0.8203	1	0.77618	5	6	2
Namulonge 3	0.7845	2	0.64279	3	5	1

HI = harvest index; ASV = AMMI stability value; GSI = genotype stability index; Kachwekano1 = 2010B; Kachwekano 2 = 2011A; Kachwekano 3 = 2011B; Namulonge 1 = 2010B; Namulonge 2 = 2011A; Namulonge 3 = 2011B

#### **3.3.2.4 Overall stability and performance**

The genotype with the smallest GSI rank sum across AUDPC, TRY and HI was the best in terms of stability and performance across the three traits (Table 3.14). Genotype NASPOT 8 was the best genotype for the three traits under consideration. Genotypes Namusoga, BND145L, NKA103M and Tanzania were second, third, fourth and fifth, respectively. The least desirable genotypes were NKA259L, Ejumula, NKA318L and Malagalya.

**Table 3.14 Genotype selection index rank sum for Alternaria blight severity, total storage root yield and harvest index**

Genotype	AUDPC rank	TRY rank	HI rank	GSI rank sum	Overall rank
Araka Red	19	23	12	54	19
BND145L	8	5	9	22	3
Bwanjule	6	6	23	35	10
Dimbuka	28	19	21	68	25
Ejumula	17	26	29	72	28
Kigaire	7	29	30	66	23
Magabali	10	18	25	53	18
Malagalya	27	26	26	79	30
MBL 170	4	19	16	39	13
MBR 536	21	13	8	42	14
Namusoga	2	9	4	15	2
NASPOT 1	16	9	3	28	7
NASPOT 10 O	11	4	11	26	5
NASPOT 11	23	3	2	28	7
NASPOT 2	26	23	17	66	24
NASPOT 3	22	8	13	43	15
NASPOT 4	18	28	22	68	25
NASPOT 7	30	1	6	37	11
NASPOT 8	9	1	1	11	1
New Kawogo	29	16	19	64	22
NKA103M	14	6	5	25	4
NKA259L	12	30	28	70	27
NKA318L	25	21	27	73	29
OTADA	3	25	10	38	12
Semanda	15	21	20	56	20
Shock	13	14	24	51	17
Sowola 6	20	12	15	47	16
SPK004	24	15	18	57	21
Tanzania	1	11	14	26	5
Silk Luwero	5	17	7	29	9

AUDPC = area under disease progress curve for Alternaria blight severity; TRY = total storage root fresh mass ( $t\ ha^{-1}$ ); HI = harvest index; GSI = genotype stability index

### 3.4 Discussion

The severity of Alternaria blight, like many other diseases, varies with site and season. In this study, selected sweetpotato genotypes were evaluated for: resistance to Alternaria blight across seasons and sites; the stability of the genotypes for Alternaria blight resistance, yield and HI; and the yield gain obtained from using fungicide treatment to control Alternaria blight. The resistant genotypes identified in this study can be used as sources of resistance in breeding for Alternaria blight resistance or can be recommended to farmers for cultivation in Alternaria blight affected areas.

The study indicated that the site and spray treatments main effects for AUDPC, TRY and HI were highly significant ( $P < 0.001$ ). Non-significance of the first order interactions for genotype x spray treatment and site x spray treatment indicated that the effects of the two spray treatments (*Alternaria* inoculum and fungicide spray) were consistent over genotypes and over environments. Consistent with previous reports (Osiru et al, 2007a, b), *Alternaria* blight severity was higher at Kachwekano over the three seasons than Namulonge. This is likely to be due to differences in the environmental factors that prevailed at the two sites during the three seasons. In the development of *Alternaria* blight, it is not always the amount of rainfall that is as important as are high humidity and duration of leaf wetness (dew) in the presence of the inoculum (Shrestha et al., 2005). Vloutoglou and Kalogerakis (2000) reported an increase from 2 to 88% leaf area infection by *A. solani* on tomato (*Solanum lycopersicum* L.) when the duration of leaf wetness was increased from 4 to 24 hours and no symptoms when wetness was less than 4 hours. Kachwekano had lower daily temperatures and higher relative humidity than Namulonge, consequently the residual moisture on the plants took longer to evaporate thereby facilitating the infection process.

Equally important is the age of the plants. *Alternaria* blight is more severe in older than in young, vigorous plants and even favourable conditions may not induce a disease outbreak in young plants but susceptibility does increase with age (Rotem, 1994; Ojiambo et al., 1999; Vloutoglou and Kalogerakis, 2000). Since the crop was harvested at 7 MAP at Kachwekano compared to 5 MAP at Namulonge, the longer period in the field at Kachwekano could have increased the vulnerability of the crop. However, the importance of the age of the plants in relation to *Alternaria* blight severity does not exclude the fact that some genotypes like NASPOT 1 are inherently more susceptible and can succumb to the disease at an early age as long as conditions favourable for the development of the disease are present.

Some genotypes exhibited consistent performance across seasons. The resistant genotypes exhibited lower AUDPC levels across seasons and sites and, similarly, the susceptible ones had higher AUDPC values across seasons and sites. The genotypes with the lowest AUDPC were landraces and these included Shock, Tanzania, Silk Luwero. The most susceptible genotypes, NASPOT 1, NASPOT 7 and New Kawogo (released landrace), were from the National Sweetpotato Program. These findings are in agreement with those of Osiru et al. (2007b) and Anginyah et al. (2001) who reported landraces to have lower *Alternaria* blight severity than improved genotypes. They attributed this to landraces having a broader genetic base than the improved genotypes. These resistant genotypes can be used as sources of resistance in breeding for *Alternaria* blight resistance.

Application of the fungicide led to a remarkable reduction in *Alternaria* blight severity in some genotypes; for example, Kigaire with a 63.0% reduction. Concomitantly, high yield gain was

attained with fungicide application. In the absence of resistant genotypes, application of fungicides could help sweetpotato farmers in central Uganda where it is becoming unviable to grow their most popular cultivar NASPOT 1, which was released by the National Sweetpotato Program in 1999. It is early maturing, produces large roots, has high DM%, good taste and has good underground keeping qualities, which make it ideal for sequential harvesting. However, it is very susceptible to *Alternaria* blight, underscored by the 40.8% reduction in disease and 39.8% yield gain recorded in this study. In order to extend the production life of a popular cultivar such as NASPOT 1, it would therefore be necessary to use fungicides for controlling the disease with all the attendant management and economic considerations, of course.

The AMMI analysis revealed that the development of *Alternaria* blight is more influenced by genotype effects than by the GEI effects and to an even lesser extent by environment effects. This study has shown that some genotypes were resistant to *Alternaria* blight and others susceptible regardless of which of the six environments they were grown in. For example, Shock was the most resistant in most of the environments and NASPOT 1 the most susceptible. This may be an indication of stable genotypic effects whereby some genotypes are inherently more resistant even in high disease pressure areas.

The magnitude of the IPCA1 and IPCA2 from the AMMI analysis provided an indication of the stability of each genotype. The ASV ranked their stability according to a weighted combination of IPCA1 and IPCA2 scores, and the GSI combined their ASV stability ranking and their integrated performance ranking across environments. NASPOT 1 was ranked the most stable genotype by ASV but was poorly ranked by GSI due to its susceptibility to *Alternaria* blight. Tanzania and Namusoga were the best genotypes in terms of *Alternaria* blight resistance and stability. Worth noting was Shock with the lowest AUDPC but ranked sixth by GSI. In the AMMI biplot, Magabali, BND145L, NASPOT4, Sowola 6, NASPOT 1, NASPOT 8, Tanzania and Namusoga were positioned close to the horizontal line and were therefore stable for the degree of resistance to *Alternaria* blight. However, NASPOT 1, Sowola 6, NASPOT 4, NASPOT 10 O were stable for susceptibility to *Alternaria* blight and should therefore be planted in areas with low *Alternaria* blight pressure or protected with fungicides when planted in high pressure areas. Tanzania, Namusoga, BND145L, NASPOT 8 and Magabali were stable for *Alternaria* blight resistance and may be considered to be widely adapted to all of the test environments. Genotypes MBR 536, Malagalya and NASPOT 7, which were furthest from the horizontal line, have large GEI effects and are unstable for *Alternaria* blight expression i.e. the severity of the disease they express changes with the environment. These genotypes may be planted in the environments to which they are well adapted but they may perform poorly when environmental conditions change and in such cases *Alternaria* blight control methods such as roguing of infected plants and spraying plants with fungicides may be used.

On the other hand, such genotypes may be too expensive to breed since every agro-ecological zone may require a different genotype and given the poor seed distribution system in Uganda, they may never reach the target farmers. However, in terms of agronomic considerations only, for some environments specifically adapted genotypes may be the best option.

Stability of the environments is also very important. A stable and preferably top performing environment can support stable performance of preferably the top performing test genotypes and an unstable environment can only support those that are specifically adapted to it. In this study, no environment was very stable for *Alternaria* blight but Namulonge 2011B and Namulonge 2011A exhibited relatively good stability with several genotypes adapted to them. Kachwekano 2011A and Namulonge 2010B were the least stable environments with no genotype specifically adapted to either of them.

As would be expected, there was an inverse relationship between *Alternaria* blight severity and yield as indicated by the negative correlation between the AUDPC values and TRY. At Namulonge, the highest yield was recorded during season 2011A and this coincided with the lowest AUDPC values. At Kachwekano, the highest yield was recorded during season 2010B which also coincided with the lowest AUDPC values. The lowest yield was recorded at Kachwekano during 2011B, also coincident with the highest AUDPC values.

In the AMMI analysis the environments and GEI effects were highly significant ( $P < 0.0001$ ) for TRY and they each accounted for a sizable component of the total SS, almost 2.5 times that of the genotypes. The high significance of these effects implies that there were strong differential genotypic responses across the environments and the yield attained was greatly dependant on the genotypes and the environments in which they grew. Environmental factors influencing yield could be the moisture levels and nutrient status of the soils. NASPOT 8 and NASPOT 11 were the best yielders with good stability across environments as revealed by the AMMI biplot, ASV and GSI. These genotypes can be grown widely or used as parents to improve the yields of the stable but low yielding genotypes. This is in contrast to the findings of Manrique and Hermann (2000), and Mwangi et al. (2007b) who indicated that high yielding genotypes rarely showed acceptable level of stability.

The nine best performing and therefore most desirable genotypes (in terms of yield stability and high yield) were NASPOT 7, NASPOT 8, NASPOT 11, NASPOT 10 O, BND145L, Bwanjule, NKA103M, NASPOT 3 and NASPOT 1. All these are from the National Sweetpotato Program with BND145L and NKA103M being promising pre-release cultivars and the rest released cultivars. Bwanjule is a landrace but was also evaluated and released by the National Sweetpotato Program. This indicates that all these genotypes were selected for wide adaptation and high yield through multi-locational testing. They should, therefore, give stable yields in a



diverse range of environments unlike the landraces that were selected by farmers within particular environments and exhibit specific adaptation to those environments. The nine least stable genotypes for yield were NKA318L, Semanda, NASPOT 2, Araka Red, Otada, Malagalya, Kigaire, NASPOT4 and NKA259L. Of these, only NASPOT 2 and NASPOT 4 have been released from the National Sweetpotato Program; NKA318L and BND 259L are still undergoing evaluation at the National Sweetpotato Program; and the rest (five) are landraces. The landraces have specific adaptation and may perform poorly outside their adaptation zones. Therefore, they should be preferably planted in areas of their specific adaptation.

The best genotype combining stability, resistance to *Alternaria* blight, good TRY and good HI was NASPOT 8. It is an orange fleshed genotype bred by the National Sweetpotato Program and released by the National Variety Release Committee in 2007. It has dry mass of 32.0%, moderate resistance to SPVD and *Alternaria* blight, and a  $\beta$ -carotene content of  $143.6 \mu\text{g}^{-1}$  DM (dry mass basis) (Mwanga et al., 2009). Given that most Ugandans reject OFSP genotypes due to their generally low dry mass, this genotype which combines high dry mass content with other good attributes can be used to change people's perceptions of OFSP.

In the AMMI biplot for TRY the genotypes and environments were widely dispersed over the four quadrants indicating the existence of a large amount of variability in the stability and performance of the genotypes and environments. Wide variability among environments indicates that the environments were diverse and differences among environmental means caused most of the variation in TRY. Kachwekano 2011B was a stable but low yielding environment indicating that the environment causes stable but low yields to be achieved. Namulonge 2011B was a relatively stable and high yielding environment to which most of the high yielding genotypes were adapted. The ASV ranked the lowest yielding environment, Kachwekano 2011B, as the most stable. Ranking of these environments in this manner is important in that it acts as a guide when selecting appropriate genotypes for these environments. Selective release of genotypes can be based on this statistical information pertaining to the stability and mean performance of the genotypes and the target environments. This should contribute towards improving the productivity of sweetpotato in Uganda and elsewhere.

An important consideration in wide yield stability is the stability of the HI (Grüneberg et al., 2005). Harvest index is a significant criterion in improving the economic yield of sweetpotato. Significant differences in genotypes, environments and GEI effects indicated that all these components influence the expression of HI and they play a role in determining its stability. However, much of the variation observed in HI could be attributed to environmental effects. All the genotypes had HI above 50% indicating that the photosynthate was predominantly partitioned to the storage roots rather than the foliage (Bhagsari and Ashley, 1990).

### **3.5 Conclusions**

The study revealed that there are differences in the reaction of different sweetpotato genotypes to *Alternaria* blight under Ugandan conditions with the landraces proving to be more resistant than the improved genotypes. Site and season were very important determinants of the severity of *Alternaria* blight on each genotype. The severity of *Alternaria* blight was higher at Kachwekano than at Namulonge indicative of the more favourable conditions for the development of the disease at this site. Genotypes NASPOT 8, Namusoga, NASPOT 10 O, Otada and NASPOT 1 were the most stable genotypes with the lowest AMMI ASV rank sum across AUDPC, TRY and HI (Appendix 3.7). Furthermore, NASPOT 8, Namusoga, BND145L, NKA103M and Tanzania had the lowest GSI rank sums across AUDPC, TRY and HI and were the most desirable in terms of stability and performance for these three traits. Tanzania and Namusoga were the most stable low *Alternaria* blight severity and can therefore be planted in environments with high *Alternaria* blight disease pressure or used as sources of resistance in breeding for resistance to *Alternaria* blight. Environmental stability for *Alternaria* blight is important in that environments that are stable for high disease pressure can be used for evaluating germplasm for *Alternaria* blight resistance while environments with stability for low disease pressure are suitable for seed multiplication. The GSI identified NASPOT 8, NASPOT 7 and NASPOT 11 as the most stable, high yielding genotypes, therefore, these genotypes can be widely grown in any of the test environments and will give good yields, and they can be used to breed for high yield.

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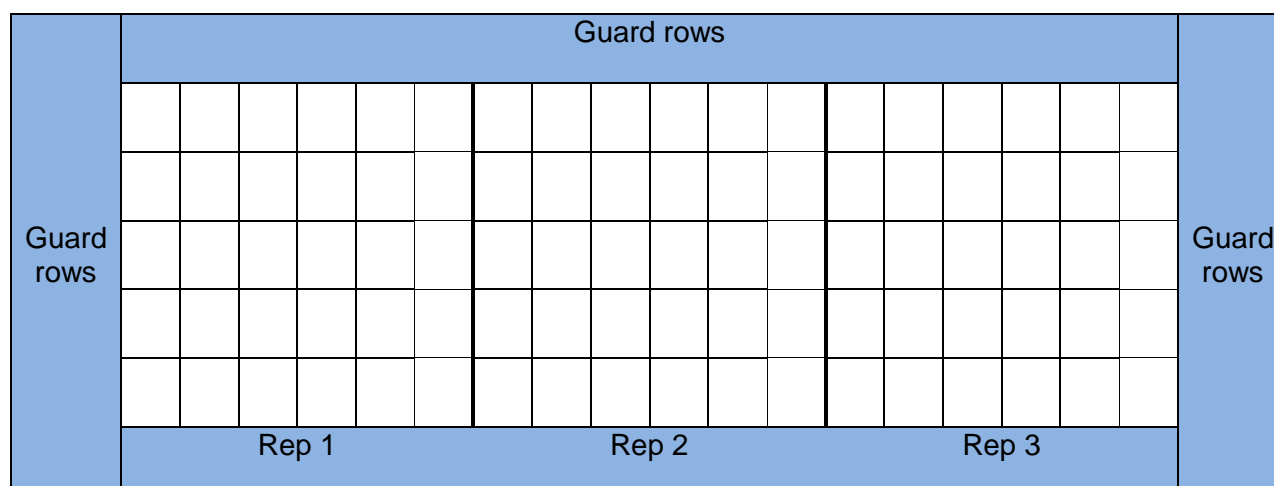
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## Appendices

### Appendix 3.1 Row x column (5 x 6) design for the field trial of 30 sweetpotato in six environments in Uganda



There were four rows per plot at 1 m apart; each plot was 4 x 5m

### Appendix 3.2 Planting and harvest dates

Season	Planting date	Harvesting date
Namulonge 2010B	10 October 2010	13 March 2011
Namulonge 2011A	15 April 2011	21 September 2011
Namulonge 2011B	20 October 2011	02 April 2012
Kachwekano 2010B	18 October 2010	12 May 2011
Kachwekano 2011A	25 April 2011	03 December 2011
Kachwekano 2011B	26 October 2011	20 May 2012

### Appendix 3.3 Weather data for Namulonge and Kachwekano 2010 to 2012

Season	Rainfall total (mm)		Temperature range (°C)				Average Relative Humidity (%)	
	Namulonge	Kachwekano	Namulonge		Kachwekano		Namulonge	Kachwekano
			Max	Min	Max	Min		
2010B (Sep 2010-Jan 2011)	264.6	490.3	28.7-30.0	16.1-16.8	23.7-25.0	11.4-12.5	70.3	77.3
2011A (Apr-Aug 2011)	566.9	367.7	27.5-28.4	16.3-16.9	24.0-26.4	10.5-13.5	75.6	77.8
2011B (Aug 2011-Jan 2012)	560.8	367.7	28.3-30.1	16.1-16.9	24.4-24.7	11.3-12.3	75.6	80.5

**Appendix 3.4 Mean AMMI performance estimates and ranking of the genotypes for Alternaria blight AUDPC in six environments of Uganda from 2010 to 2012**

Genotype	NAM1		NAM2		NAM3		KAC1		KAC2		KAC3	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
Araka Red	92.9	17	104.9	24	92.3	14	105.6	27	87.9	24	109.6	24
BND145L	75.1	5	104.4	22	91.3	12	87.7	19	68.4	10	96.4	15
Bwanjule	65.7	3	77.5	5	56.0	1	86.0	17	64.6	7	84.2	4
Dimbuka	94.3	18	96.4	18	120.7	25	109.3	28	97.6	28	122.1	29
Ejumula	85.1	10	79.2	6	90.0	10	89.3	20	79.5	19	99.2	19
Kigaire	62.5	2	69.9	3	70.1	3	79.8	12	63.1	4	85.1	5
Magabali	81.7	7	91.4	15	102.4	16	84.8	13	74.0	17	99.6	20
Malagalya	88.3	14	67.4	2	78.7	6	96.2	24	86.7	23	100.7	21
Mbale 170	87.9	13	97.7	19	120.1	24	65.2	5	64.3	5	93.3	11
MBR536	84.8	9	161.6	30	81.0	7	85.2	14	54.8	2	89.1	6
Namusoga	82.7	8	85.5	10	85.3	9	78.8	11	69.1	11	90.5	7
New Kawogo	133.5	30	114.6	26	140.1	29	85.9	15	95.8	27	116.1	30
NKA103M	104.7	24	84.6	8	110.6	21	63.4	4	71.5	14	91.1	22
NKA259L	106.4	26	87.0	12	103.2	17	71.2	9	75.8	18	93.6	10
NKA318L	96.5	21	116.0	27	123.1	26	68.9	7	66.2	8	96.4	18
NASPOT 1	116.4	29	135.5	29	163.3	30	113.9	29	106.7	30	139.2	14
NASPOT 10 O	92.4	16	104.6	23	91.6	13	96.7	26	81.6	21	103.7	26
NASPOT 11	66.9	4	62.7	1	76.0	4	85.9	16	71.8	15	91.7	28
NASPOT 2	107.5	27	109.8	25	130.5	28	67.2	6	72.2	16	99.1	17
NASPOT 3	59.2	1	87.0	11	77.4	5	95.4	23	69.4	13	96.3	27
NASPOT 4	108.3	28	100.6	21	124.9	27	92.7	22	91.4	26	113.9	9
NASPOT 7	91.6	15	94.6	17	109.1	20	115.2	30	99.2	29	121.8	12
NASPOT 8	95.1	19	90.7	14	92.7	15	87.1	18	79.6	20	98.9	16
OTADA	87.2	12	100.0	20	106.7	19	74.1	10	67.4	9	94.3	13
Semanda	105.9	25	94.4	16	110.6	22	63.1	3	69.4	12	90.5	8
Shock	79.0	6	90.5	13	82.1	8	48.6	1	45.0	1	69.6	1
Sowola 6	97.7	22	118.2	28	105.6	18	96.4	25	82.3	22	107.9	23
SPK004	101.2	23	85.3	9	114.5	23	92.0	21	90.2	25	110.2	25
Tanzania	86.0	11	75.8	4	57.6	2	69.6	8	62.1	3	76.0	2
Silk Luwero	95.2	20	80.7	7	91.1	11	61.6	2	64.3	6	82.8	3

NAM1 = Namulonge 2010B; NAM2 = Namulonge 2011A; NAM3 = Namulonge 2011B; KAC1 = Kachwekano 2010B; KAC2 = Kachwekano 2011A; KAC3 = Kachwekano 2011B; Lowest AUDPC value = Rank 1 (most resistant); Highest AUDPC value = Rank 30 (most susceptible)



**Appendix 3.5 Mean AMMI performance estimates and ranking of the genotypes for total storage root yield in six environments from 2010 to 2012**

Genotype	NAM1		NAM2		NAM3		KAC1		KAC2		KAC3	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
Araka Red	7.8	26	7.1	23	4.4	21	17.1	2	15.1	19	16.7	4
BND145L	14.5	16	9.6	10	7.7	5	12.7	11	24.3	5	14.2	9
Bwanjule	13.7	20	8.3	16	5.9	12	10.4	13	21.5	11	12.0	15
Dimbuka	15.4	14	7.7	19	5.9	13	5.8	28	25.2	2	8.6	26
Ejumula	14.4	17	6.9	24	2.5	28	4.9	29	11.7	24	7.3	30
Kigaire	2.5	30	2.6	30	1.8	30	14.3	7	19.8	13	13.8	11
Magabali	8.3	25	6.2	26	3.0	26	13.7	9	12.9	22	13.9	10
Malagalya	15.7	12	8.1	17	3.3	24	6.1	27	10.6	26	8.5	28
MBL 170	17.6	7	10.1	8	5.3	17	8.2	21	12.4	23	10.5	20
MBR 536	10.1	24	5.4	29	2.6	27	8.6	20	15.9	17	9.9	23
Namusoga	15.1	15	9.3	12	5.2	19	10.2	15	14.5	20	11.9	17
New Kawogo	20.1	5	12.5	5	6.2	10	10.2	16	7.5	29	12.3	14
NKA103M	12.2	22	8.4	14	6.3	8	13.2	10	21.7	10	14.2	8
NKA259L	19.2	6	10.0	9	3.9	22	4.8	30	7.1	30	7.7	29
NKA318L	22.3	1	13.0	3	6.4	7	7.6	24	8.1	28	10.5	21
NASPOT 1	20.6	2	12.8	4	8.2	4	10.3	14	16.9	16	12.8	12
NASPOT 10 O	15.9	11	9.2	13	6.8	6	8.9	19	23.2	6	11.2	18
NASPOT 11	20.4	3	15.0	2	10.8	2	16.8	5	18.8	15	18.3	2
NASPOT 2	6.8	27	6.4	25	4.6	20	17.1	4	19.0	14	16.6	5
NASPOT 3	16.8	9	9.3	11	6.2	9	7.7	23	20.2	12	10.2	22
NASPOT 4	6.2	28	5.6	28	2.4	29	15.5	6	11.5	25	15.0	7
NASPOT 7	17.0	8	11.7	6	8.9	3	13.9	8	22.7	7	15.4	6
NASPOT 8	20.3	4	16.1	1	13.3	1	20.0	1	26.2	1	21.2	1
OTADA	14.3	19	7.9	18	3.2	25	7.8	22	9.9	27	9.7	25
Semanda	5.9	29	5.8	27	5.3	18	17.1	3	24.6	4	16.7	3
Shock	12.7	21	7.2	21	5.3	16	9.2	18	22.6	8	11.0	19
Sowola 6	15.5	13	8.4	15	6.0	11	7.5	25	22.4	9	9.9	24
SPK004	14.3	18	7.3	20	3.8	23	6.3	26	15.7	18	8.6	27
Tanzania	11.9	16	10.2	7	5.7	15	10.0	17	13.19	21	11.9	16
Silk Luwero	12.8	13	7.2	22	5.9	14	11.5	12	24.71	3	12.8	13

NAM1 = Namulonge 2010B; NAM2 = Namulonge 2011A; NAM3 = Namulonge 2011B; KAC1 = Kachwekano 2010B; KAC2 = Kachwekano 2011A; KAC3 = Kachwekano 2011B

**Appendix 3.6 Mean AMMI performance estimates and ranking of the genotypes for harvest index in six environments from 2010 to 2012**

Genotypes	NAM1		NAM2		NAM3		KAC1		KAC2		KAC3	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
Araka Red	0.81	8	0.87	9	0.83	10	0.73	23	0.73	14	0.69	9
BND145L	0.82	6	0.91	3	0.88	2	0.84	9	0.77	8	0.54	20
Bwanjule	0.70	19	0.79	20	0.77	19	0.75	21	0.66	25	0.36	29
Dimbuka	0.65	24	0.78	22	0.74	23	0.81	13	0.72	16	0.56	16
Ejumula	0.52	30	0.70	30	0.65	30	0.83	11	0.70	20	0.50	21
Kigaire	0.82	7	0.75	24	0.75	21	0.36	30	0.42	30	0.22	30
Magabali	0.75	13	0.81	17	0.79	16	0.71	25	0.65	26	0.41	27
Malagalya	0.58	28	0.75	25	0.70	26	0.88	3	0.77	10	0.65	10
MBL 170	0.70	21	0.83	16	0.78	18	0.86	6	0.79	5	0.72	6
MBR 536	0.75	14	0.83	15	0.80	14	0.76	20	0.71	17	0.55	18
Namusoga	0.79	10	0.87	8	0.83	9	0.80	15	0.77	7	0.72	5
New Kawogo	0.63	25	0.76	23	0.72	24	0.79	17	0.69	23	0.46	25
NKA103M	0.74	16	0.84	14	0.81	12	0.80	16	0.74	13	0.56	17
NKA259L	0.57	29	0.74	26	0.69	29	0.86	5	0.77	9	0.71	7
NKA318L	0.58	27	0.74	28	0.70	25	0.83	10	0.70	18	0.45	26
NASPOT 1	0.76	12	0.88	5	0.85	6	0.89	1	0.81	3	0.63	13
NASPOT 10 O	0.71	18	0.81	18	0.78	17	0.78	18	0.70	19	0.47	23
NASPOT 11	0.82	5	0.92	2	0.88	3	0.88	2	0.84	2	0.75	2
NASPOT 2	0.86	2	0.89	4	0.85	5	0.68	27	0.70	21	0.60	14
NASPOT 3	0.72	17	0.85	12	0.80	15	0.85	7	0.80	4	0.74	4
NASPOT 4	0.84	4	0.84	13	0.80	13	0.59	29	0.64	28	0.65	11
NASPOT 7	0.78	11	0.87	10	0.82	11	0.80	14	0.78	6	0.75	1
NASPOT 8	0.87	1	0.95	1	0.91	1	0.87	4	0.84	1	0.75	3
OTADA	0.70	20	0.78	21	0.74	22	0.72	24	0.68	24	0.57	15
Semanda	0.85	3	0.88	6	0.86	4	0.70	26	0.69	22	0.54	19
Shock	0.66	23	0.74	27	0.69	28	0.65	28	0.64	27	0.63	12
Sowola 6	0.67	22	0.8	19	0.76	20	0.83	12	0.73	15	0.50	22
SPK004	0.61	26	0.72	29	0.69	27	0.73	22	0.64	29	0.41	28
Tanzania	0.75	15	0.85	11	0.83	8	0.84	8	0.74	12	0.46	24
Silk Luwero	0.81	9	0.88	7	0.84	7	0.77	19	0.76	11	0.70	8

NAM1 = Namulonge 2010B; NAM2 = Namulonge 2011A; NAM3 = Namulonge 2011B; KAC1 = Kachwekano 2010B; KAC2 = Kachwekano 2011A; KAC3 = Kachwekano 2011B

**Appendix 3.7 AMMI stability value rank sum for Alternaria blight severity, total storage root yield and harvest index**

<b>Genotype</b>	<b>AUDPC rank</b>	<b>TRY rank</b>	<b>HI rank</b>	<b>Rank sum</b>	<b>Overall rank</b>
Araka Red	9	24	16	49	17
BND145L	10	12	17	39	11
Bwanjule	16	5	19	40	12
Dimbuka	22	18	18	58	22
Ejumula	18	17	27	62	24
Kigaire	19	28	30	77	30
Magabali	7	15	22	44	15
Malagalya	28	20	28	76	29
MBL 170	12	21	23	56	21
MBR 536	30	2	4	36	10
Namusoga	2	4	8	14	2
NASPOT 1	1	19	9	29	5
NASPOT 10 O	4	8	6	18	3
NASPOT 11	29	6	5	40	13
NASPOT 2	23	25	24	72	26
NASPOT 3	24	9	20	53	19
NASPOT 4	6	23	26	55	20
NASPOT 7	27	1	13	41	14
NASPOT 8	3	3	3	9	1
New Kawogo	21	26	12	59	23
NKA103M	17	13	1	31	7
NKA259L	13	27	29	69	25
NKA318L	25	29	21	75	27
OTADA	8	16	2	26	4
Semanda	20	30	25	75	28
Shock	26	11	14	51	18
Sowola 6	11	10	11	32	8
SPK004	15	7	7	29	6
Tanzania	5	14	15	34	9
Silk Luwero	14	22	10	46	16

AUDPC = area under disease progress curve for Alternaria blight severity; TRY = total storage root fresh mass (t ha<sup>-1</sup>); HI = harvest index

## Chapter 4

### Genetic analysis of resistance to *Alternaria* leaf petiole and stem blight, and inheritance of yield traits

#### Abstract

*Alternaria* leaf petiole and stem blight (*Alternaria* spp.) (commonly referred to as *Alternaria* blight) is an important sweetpotato disease in Uganda causing yield losses of over 50% in susceptible genotypes. The most prudent control measure for this disease is the use of resistant genotypes. Therefore, understanding the mode of inheritance of resistance to the disease and general combining abilities of the available germplasm is crucial in the development of genotypes with resistance to this disease. The objective of this study was to understand the mode of inheritance of *Alternaria* blight resistance and root yield components in sweetpotato. Thirty two  $F_1$  families were generated from two sets of parents in a North Carolina II mating scheme. The families were evaluated at two sites using a 5 x 7 row-column design with two replications. The site main effects were highly significant ( $P < 0.001$ ) for all eight traits evaluated. There were significant differences among the families in *Alternaria* blight severity. Both general combining ability (GCA) and specific combining ability (SCA) mean squares (MS) were highly significant ( $P < 0.001$ ) but the predominance of GCA sum of squares (SS) for *Alternaria* blight at 67.4% of treatment SS indicated that additive effects were more important in controlling this trait. However, some parents that had high, negative GCA effects produced families with undesirable SCA effects and the reverse was also true. This implies that the best parents should not be chosen on GCA alone but also on SCA of their best crosses. The wide range in the area under the disease progress curve (AUDPC) for the families indicated that it was possible to select for highly resistant genotypes. For the yield components, the GCA MS were significant ( $P < 0.05$ ) and the GCA SS accounted for more than 60% of the treatment SS except for percentage dry mass where SCA was predominant at 53.0%. The selection index used to identify superior progeny selected progeny mostly from three female parents, Shock, Bwanjule and Mbale. Best parent heterosis (heterosis relative to the best performing parent of all the parents) in the desired direction was achieved for all the traits considered. The family Bwanjule x NASPOT 4 recorded consistently good performance for most of the traits and was therefore the best family overall.

#### 4.1 Introduction

*Alternaria* leaf petiole and stem blight (*Alternaria* spp.) is an important sweetpotato disease. It is a minor disease in many parts of the world where sweetpotato is grown (Clark et al., 2009). However, in East Africa, it is a serious production constraint due to the presence of aggressive *Alternaria* spp. (Lenné, 1991b). The major *Alternaria* species are *Alternaria bataticola* and *A. alternata* but *A. bataticola* is the more aggressive species (Anginyah et al., 2001; Osiru et al., 2007b; Osiru et al., 2008). In Uganda, *Alternaria* leaf petiole and stem blight (commonly referred to as *Alternaria* blight) has gained importance in the last few years with resultant yield losses ranging from 25 to 54% in different parts of the country (Osiru et al., 2007b). Several control measures can be employed against *Alternaria* blight. However, given the fact that sweetpotato is a low value crop and mostly grown by resource poor farmers in marginal areas, the most economic control measure is the use of resistant genotypes (Osiru et al., 2007b). Anginyah et al. (2001) and van Bruggen, (1984) reported differences in resistance levels among genotypes in Kenya and Ethiopia. Similarly, in Uganda, Osiru et al. (2007b) identified *Alternaria* resistant and susceptible genotypes and attributed the differences in disease levels among these genotypes to inherent differences in susceptibility or resistance of the genotypes. In order to breed for resistance to the disease, whether durable or non-durable, is essential to understand the mode of inheritance of resistance; however, there is currently scant information about the inheritance of resistance to *Alternaria* blight in sweetpotato.

The mode of inheritance for resistance to several production constraints in sweetpotato, and for yield components has been studied by several workers. For example, Mihovilovich et al. (2000), Mwanga et al. (2002) and Okada et al. (2002) studied the mode of inheritance of sweetpotato virus disease (SPVD) and stability of the virus-resistant genes, and Collins (1977) investigated the inheritance of resistance to *Fusarium* wilt. Jones and Dukes (1980) estimated heritability of resistance to root knot nematodes (*Meloidogyne* spp.), and heritability for resistance to soil insect pests was estimated by Jones et al. (1979). The application of 10 heritability estimates for different traits in sweetpotato breeding was reviewed by Jones (1986). Courtney et al. (2008) determined heritability estimates for micronutrient composition of sweetpotato storage roots while Gasura et al. (2008) analysed the genetic variance of root yield and quality, and severity of various virus diseases in sweetpotato germplasm in Uganda. However, no such studies have been carried out for *Alternaria* blight of sweetpotato and thus the need for this study.

In studying the mode of inheritance of various traits, it is very important to select an appropriate mating design. Different mating designs have been used to study the genetic determination of various traits of sweetpotato. For example: Mwanga et al. (2002) used a diallel mating design to study inheritance of resistance to SPVD; Mihovilovich et al. (2000) also used a diallel to study the combining ability for resistance to feathery mottle virus; and Chiona (2009) used a diallel to study the inheritance of  $\beta$ -carotene content and yield components in sweetpotato. North Carolina II or factorial designs have also been used by several breeders in different crops. For example: Derera et al. (2008) in maize (*Zea mays* L.); Ortiz and Golmirzaie (2002) in potato (*Solanum tuberosum* L.); Kamau et al. (2010) in cassava (*Manihot esculenta* Crantz); and Gasura et al. (2008) in sweetpotato. The factorial mating design provides the plant breeder with genetic information on the reference population for the trait(s) being investigated (Ortiz and Golmirzaie, 2002), and also provides a good measure of the average degree of dominance involved in the action of genes governing quantitative traits (Hallauer and Miranda, 1988). An advantage of factorial designs is that additional parents can be included without a significant increase in resource requirements (Hallauer and Miranda, 1988). Given the level of self- and cross-incompatibility in the sweetpotato germplasm (Wilson et al., 1989), a factorial design was selected in this study so as to accommodate more parents without the attendant increase in the number of families that occurs with a diallel design.

The study was carried out to determine the mode of inheritance of *Alternaria* blight resistance, and root yield components of sweetpotato.

## **4.2 Materials and methods**

### **4.2.1 Germplasm source**

Parental genotypes for this study comprised of six cultivars released by the National Sweetpotato Program at the National Crops Resources Research Institute (NaCRRI) and 10 landraces commonly grown in different parts of Uganda. The released cultivars were NASPOT 1, NASPOT 2, NASPOT 4, Bwanjule, Tanzania, New Kawogo, and the landraces were Silk Omupya, Semanda, Kidodo, Araka Red, Dimbuka, Shock, Mbale, Budde, Magabali, and Silk Luwero. The best performing genotypes from Chapter 3 were among this list of genotypes to be used as parents in the crossing block but some had to be excluded as they proved to be shy in flowering (Namusoga, NASPOT 8, NASPOT 10, NASPOT 11, BND145L, NKA103M). The levels of resistance of these parents to *Alternaria* blight were already known (Table 4.1). The resistant parents were used as female (seed) parents, while the moderately resistant and susceptible were used as male (pollen) parents.

**Table 4.1 Selected parents**

Name	District	Status	Alternaria blight	Root yield (t ha <sup>-1</sup> )	Reference
Semanda	Mpigi	Landrace	Resistant	20.8	Mwanga et al. (2009)
Silk Omupya	Palisa	Landrace	Resistant	20.7	USD
Silk Luwero	Luwero	Landrace	Moderate	7.7	Osiru et al. (2009a)
Kidodo	Kabale	Landrace	Resistant	17.5	USD
Dimbuka	Rakai	Landrace	Susceptible	20.0	Mwanga et al. (2007c)
Araka Red	Soroti	Landrace	Moderate	9.0	USD
Mbale	Mpigi	Landrace	Resistant	17.1	USD
Shock	Mbale	Landrace	Resistant	12.0	USD
Magabali	Kabale	Landrace	Susceptible	10.0	USD
Budde	Masaka	Landrace	Susceptible	7.5	USD
Bwanjule		Released	Resistant	17.0	Mwanga et al. (2001)
New Kawogo		Released	Susceptible	17.0	Mwanga et al. (2001)
NASPOT1		Released	Susceptible	20.0	Gibson (2006); Mwanga et al. (2003)
NASPOT2		Released	Susceptible	18.0	Mwanga et al. (2003)
NASPOT4		Released	Moderate	18.0	Mwanga et al. (2003)
Tanzania		Released	Resistant	21.0	Osiru et al. (2009b)

USD = Uganda Sweetpotato Database; The National Sweetpotato Program collected sweetpotato landraces from all regions of Uganda in 2005 and evaluated them for SPVD, *Alternaria* blight and total storage root yield. The details are posted on the Uganda Sweetpotato Database ([www.viazivitu.org/ugasp\\_db/index.php](http://www.viazivitu.org/ugasp_db/index.php)).

#### 4.2.2 Crossing block

The selected parents were planted in a crossing block at Mukono Zonal Agricultural Research and Development Institute (MUZARDI) in June 2009 and hand crosses were made using a 7 x 9 North Carolina mating II design (Comstock and Robinson, 1948). However, as some parents were not cross-compatible (Table 4.2), they were divided into two compatibility groups or sets (Table 4.3). Set 1 comprised the following females: Bwanjule, Silk Omupya, Semanda, Kidodo; and males: Araka Red, NASPOT 2, NASPOT 4, Dimbuka and NASPOT 1. Set 2 comprised the following females: Shock, Mbale, Tanzania; and males: Budde, Magabali, New Kawogo and Silk Luwero. A total of 32 families were generated from the crosses, viz. 20 families (4 x 5) from Set 1, and 12 families (3 x 4) from Set 2.

**Table 4.2 Cross-compatibility of sweetpotato genotypes selected as female and male parents**

♀/♂	Budde	Araka Red	Magabali	New Kawogo	NASPOT 4	Dimbuka	NASPOT 2	NASPOT 1	Silk Luwero
Shock	✓	x	✓	✓	x	x	x	x	✓
Bwanjule	✓	✓	✓	x	✓	✓	✓	✓	x
Silk Omupya	x	✓	x	✓	✓	✓	✓	✓	✓
Mbale	✓	✓	✓	✓	x	x	x	x	✓
Tanzania	✓	x	✓	✓	x	x	✓	x	✓
Semanda	x	✓	x	✓	✓	✓	✓	✓	✓
Kidodo	✓	✓	✓	✓	✓	✓	✓	✓	x

✓ = *Compatible*    x = *Incompatible*

**Table 4.3 Cross-compatible sweetpotato genotypes within each of two sets**

Set 1		Set 2	
Females	Males	Females	Males
Semanda	Dimbuka	Tanzania	New Kawogo
Silk Omupya	NASPOT 2	Mbale	Silk Luwero
Kidodo	NASPOT 1	Shock	Magabali
Bwanjule	NASPOT 4		Budde
	Araka Red		

#### 4.2.3 Hand pollination

Hand pollination was carried out using a modification of the method described by Wilson et al. (1989). The flower buds of the female parents to be hand pollinated the following morning were selected late in the evening, gently opened, emasculated and the corolla was then held closed at the tip with a finely coiled length of aluminium foil (Figure 4.1). Similarly, unopened flowers of the male parents were held closed until the following morning. Hand pollination was carried out in the morning between 06h00 and 09h00 (Figure 4.2). Each flower to be used as the source of pollen was removed from the male parent plant, the corolla opened and the anthers rubbed gently on the stigma of the reopened flower of the female parent plant. The corolla of the female flower was then fastened closed again to prevent contamination by pollen carried by insects. The crossed female flowers were inspected five to seven days later and those that had been successfully pollinated as evidenced by swollen ovaries were counted and recorded (Figure 4.3).





**Figure 4.1 Fastened female and male parent flowers**



**Figure 4.2 Performing controlled pollinations**



**Figure 4.3 Inspecting crosses**



**Figure 4.4 Germinating the seeds**



**Figure 4.5 Seedlings in trays**



**Figure 4.6 Transplanted seedlings growing out in polyethene bags**

#### 4.2.4 Seedling generation

A wire file was used to mechanically scarify the seeds. The seeds were then immersed in water for 30 minutes and placed on moistened blotting paper overnight to allow the radical to emerge (Figure 4.4). The germinated seeds were then individually planted in the cells of plastic seedling trays containing heat sterilised soil and grouped according to family (Figure 4.5). When the seedlings were 6-10 cm in height they were transplanted to polyethylene bags, containing sterilised soil, for further growth (Figure 4.6). Foliar fertilizer was applied once a week to speed up growth. Thirty seedlings from each family that had good growth and attained a vine length of 30-40 cm were selected for further multiplication. Side shoots were also cut and planted. In order to produce enough vine cuttings for a replicated trial at two sites, the rapid multiplication technique was used. Each vine was cut into short lengths of three nodes each to give 5-6 cuttings per  $F_1$  genotype. Each cutting was planted in a polyethylene bag filled with sterilised soil, and watered twice daily. Foliar fertilizer was applied once a week after the cuttings had set roots. After 4 months the plants had produced several vines from which 30 cm long cuttings were taken for planting in the trial.

#### 4.2.5 Field evaluation of $F_1$ Families

The  $F_1$  genotypes were evaluated at two sites during the first rains<sup>1</sup> of 2011 (2011A): National Crops Resources Research Institute (NaCRRI), located at Namulonge, 28 km from Kampala in central Uganda (0°32' N, 32°35' E; 1150 metres above seas level (masl); and Kachwekano Zonal Agricultural Research and Development Institute (KAZARDI) located 400 km from Kampala in south western Uganda (01°16'S, 29°57'E; 2200 masl). Kachwekano is a "hotspot" for *Alternaria* blight (Mwanga et al., 2007b; Osiru et al., 2007a), while Namulonge is located in an area of medium disease incidence (Mwanga et al., 2007b). The two trials were established in April 2011 (when the first rains had commenced) using a 5 x 7 row-column design (Patterson and Williams, 1976) with two replications at each site (Appendix 4.1). All 32 families from the two sets (without considering the sets) were randomly allocated to the plots within the design. The extra three plots at the bottom, right of each replication were planted to the 16 parents but no data was taken from the last two of these plots. Five cuttings from each of 30 genetically unique siblings (that produced the best cuttings in the nursery) per family were planted 0.3 m apart on six ridges, each 7.5 m in length and spaced 1 m apart, per plot i.e. 150 cuttings were planted per plot. Ten cuttings of each parent were similarly spaced on six ridges per plot i.e. 160 cuttings per plot. Data for each sibling were collected from the middle three plants of each single, five plant row.

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<sup>1</sup>First rains start at the end of March up to end of June

Likewise data for each parent were collected from the middle three plants of each single, 10 plant row of the harvested plot. NASPOT 1, which was previously tested to be the most susceptible of the parents to *Alternaria* blight (Mwanga et al., 2003a; Gibson, 2006; Osiru et al., 2009b) was planted as a border row around the perimeter of the trial to act as a spreader of the disease. Inoculation of the NASPOT 1 border rows with the *Alternaria* pathogen was carried out as previously described (Chapter 3, section 3.1.4) at one month after planting. Data for each genotype were collected from the middle three plants of each single, five plant row.

#### 4.2.6 Data collection

Plants were scored for *Alternaria* blight severity as previously described (Chapter 3, section 3.2.5), starting three weeks after inoculation and then at three-week intervals until four data sets were obtained. The *Alternaria* blight scores were used to calculate the area under disease progress curve (AUDPC). Plants were simultaneously scored for sweetpotato virus disease (SPVD) severity according to Grüneberg et al. (2010) using a scale of 1-9, where: 1 = disease free; and 9 = whole plot infected and plants showing stunted growth. While the AUDPC was calculated for *Alternaria* blight severity scores, the severity of SPVD was presented as scores throughout this chapter. The trials were harvested five months after planting, and the following data were collected for each genotype on a per plot basis: total number of storage roots (TRN); total storage root fresh mass (TRY (kg)); number of marketable storage roots per plant (MRN); marketable storage roots (kg); number of unmarketable storage roots per plant (UMRN); unmarketable storage roots (kg); and shoot mass (kg). Marketable storage roots weighed at least 200 g. Fresh mass (kg) for each trait was converted to  $t\ ha^{-1}$  for statistical analysis.



**Figure 4.7 Marketable and unmarketable roots of two genotypes harvested at Namulonge (2011B)**

### **Dry mass composition determination**

Root dry mass composition per genotype was determined according to Islam et al. (2002). Two roots were randomly selected from each genotype and chopped into slices of which a 200 g sample was dried in a forced draught oven at 72°C until constant mass was attained. Percentage dry mass composition (DM%) was calculated as:

$$\text{Dry mass (\%)} = \frac{\text{Dry mass}}{\text{Fresh mass}} \times 100$$

### **Harvest index**

The harvest index (HI) for each genotype was calculated as:

$$\text{Harvest index} = \frac{\text{Total storage root fresh mass}}{\text{Total biomass (roots + vines)}} \times 100$$

### **Selection index**

A selection index (SI) was used for discriminating between genotypes with a good aggregate of farmer desired traits from those with a poor aggregate. The traits weighted in the SI were: TRY (t ha<sup>-1</sup>); Alternaria blight severity scores (AUDPC); SPVD severity scores; harvest index (HI); and percentage dry mass composition (DM %). Standardised values were used to compute SI values for each genotype/progeny according to a modified formula of Ceballos et al. (2004).

The specific formula for the SI was:

$$\text{SI} = (\text{TRY} \times \text{W5}) + (\text{HI} \times \text{W4}) + (\text{DM} \times \text{W3}) - (\text{AUDPC} \times \text{W2}) - (\text{SPVD} \times \text{W1})$$

W1-5 = weights assigned to a particular trait where W is a weighting from 1 to 5. The selection index was used to select the best individual progeny from the different families.

Since the traits (variables) were measured in different units with large differences in their magnitude and variance, they were standardised to make them comparable. Standardisation was done separately for each site dataset after which the mean phenotypic values (P<sub>i</sub>) for each progeny was obtained.

The standardisation for each site was done as follows:

$$P_i = (x_{ij} - m_i) / s_i \text{ (Steel and Torrie, 1960)}$$

Where:

P<sub>i</sub> = Standardized phenotypic mean value;

x<sub>ij</sub> = Observed value of the trait i measured on genotype j;

$m_i$  = Overall mean of trait  $i$ ; and

$s_i$  = Standard deviation of trait  $i$  in a population.

The standardised phenotypic mean values were used to compute the SI for each genotype.

Heterosis for the individual genotype relative to the best parent of all parents (BPH%) was calculated according to Barth et al. (2003):

$$\text{BPH\%} = \frac{(G_i - \text{BP})}{(\text{BP})} \times 100$$

Where:  $G_i$  = Mean performance of the  $i^{\text{th}}$  selected progeny; BP = mean performance of the best parent.

Best parent heterosis was determined for only the top 20 best performing progeny selected using the selection index from the different 32 families.

#### 4.2.7 Data analysis

##### 4.2.7.1 Genetic data analysis

Data for each site were first analysed separately and the error variances of the individual sites were tested for homogeneity using Hartley's  $F_{\text{max}}$  test (Hartley, 1950). As the differences between the error variances were not significant ( $P > 0.05$ ) a combined analysis of the two sites was performed using the Residual Maximum Likelihood (REML) procedure in GENSTAT 14<sup>th</sup> Edition (Payne et al., 2011) to obtain family means. Genetic information was determined on a family mean basis. To obtain combining abilities an analysis of variance (ANOVA) of the North Carolina II mating design was performed on the individual and combined sets, using model 1 in SAS version 9.3 (SAS Institute, 2010) with parents considered as fixed effects and the sites as random effects. The ANOVA comparing sets was performed to provide information about set effects on combining ability and the contribution of the components of the treatment SS to the gene action underlying trait expression. The ANOVA of the individual sets (Set 1 and Set 2) was performed to provide set specific information on the combining ability effects and the contribution of the components of the treatment SS to the gene action underlying trait expression (Hallauer and Miranda, 1988).

The following linear model was used for the between set analysis:

$$Y_{ijkpq} = \mu + S_p + g_i(S_p) + g_j(S_p) + h_{ij}(S_p) + E_q + r_k(\text{SE})_{pq} + (\text{SE})_{pq} + (\text{Eg})_{iq}(S_p) + (\text{Eg})_{jq}(S_p) + (\text{Eh})_{ijq}(S_p) + e_{ijkpq}$$

Where:  $i = 1, 2, 3, 4$ ;  $j = 1, 2, 3, 4, 5$ ;  $r = 1, 2$ ;  $k = 1, 2$ ;  $p = 1, 2$ ;  $S = 1, 2$ .  $Y_{ijkpq}$  denotes the value of a family from the mating between the  $i^{\text{th}}$  female parent and the  $j^{\text{th}}$  male parent, in the  $k^{\text{th}}$  block, within set  $p$  and in the  $q^{\text{th}}$  site. The terms are defined as follows:  $\mu$  = Grand mean;  $S_p$  = the average effect of the  $p^{\text{th}}$  set;  $g_i(S_p)$  = the general combining ability (GCA) effect common to all  $F_1$  families of the  $i^{\text{th}}$  female parent nested within  $p^{\text{th}}$  set;  $g_j(S_p)$  = the GCA effect common to all  $F_1$  families of the  $j^{\text{th}}$  male parent nested within  $p^{\text{th}}$  set;  $h_{ij}(S_p)$  = the specific combining ability (SCA) effect specific to  $F_1$  families of the  $i^{\text{th}}$  female and  $j^{\text{th}}$  male parent nested within  $p^{\text{th}}$  set;  $E_q$  = average effect of  $q^{\text{th}}$  site;  $r_k(SE)_{pq}$  = the effect of the  $k^{\text{th}}$  replication nested within the  $p^{\text{th}}$  set and  $q^{\text{th}}$  site;  $(SE)_{pq}$  = the interaction between site and set effects;  $(Eg)_{jq}(S_p)$  and  $(Eg)_{iq}(S_p)$  = the interaction between site and GCA of the  $i^{\text{th}}$  female and  $j^{\text{th}}$  male parent, respectively nested within sets;  $(Eg)_{ijk}(S_p)$  = the interaction between site and SCA, nested within sets; and  $e_{ijkpq}$  = the random experimental error.

For the individual set analysis, the following linear model was used:

$$Y_{ijkpq} = \mu + (E)_q + r_k(E)_q + g_i + g_j + h_{ij} + (Eg)_{iq} + (Eg)_{jq} + (Eh)_{ijq} + e_{ijkpq}$$

Where:  $E_q$  = effects of the  $q^{\text{th}}$  site;  $rk(E)_q$  =  $k^{\text{th}}$  replication nested within the  $q^{\text{th}}$  site;  $g_i$  = GCA effect common to all  $F_1$  families of the  $i^{\text{th}}$  female parent ( $GCA_f$ );  $g_j$  = GCA effect common to all  $F_1$  families of the  $j^{\text{th}}$  male parent ( $GCA_m$ );  $h_{ij}$  = SCA effect specific to  $F_1$  families of the  $i^{\text{th}}$  female parent and  $j^{\text{th}}$  male parent;  $(Eg)_{iq}$  = interaction between  $GCA_f$  and  $q^{\text{th}}$  site;  $(Eg)_{jq}$  = interaction between  $GCA_m$  and  $q^{\text{th}}$  site;  $(Eh)_{ijq}$  = interaction between SCA and  $q^{\text{th}}$  site;  $E_{ijkpq}$  = random experimental error.

The main effects due to female and male parents are independent estimates of GCA effects while female x male interaction effects represent SCA effects. The GCA effects due to female parents are denoted as  $GCA_f$  and that due to male parents are denoted as  $GCA_m$  throughout this chapter.

Standard errors for the  $GCA_f$  and  $GCA_m$  effects and standard errors for the SCA effects of the crosses were calculated separately as the number of females and males was not equal using the method described by Cox and Frey (1984) as:

$$SE_{GCA} = \sqrt{MS_{fs} \left[ \frac{(f-1)}{mfrs} \right]} \quad \text{or} \quad SE_{GCA} = \sqrt{MS_{ms} \left[ \frac{(m-1)}{mfrs} \right]}$$

Where  $MS_{fs}$  and  $MS_{ms}$  are mean squares (MS) for female x site and male x site and  $mfrs$  = female x male x replication (site) x site.

Standard errors for SCA effects were calculated as:

$$SE_{SCA} = \sqrt{MS_{fms} \left[ \frac{(f-1)(m-1)}{mfrs} \right]}$$

The relative importance of additive (GCA) and non-additive (SCA) genetic effects in determining the performance of the progeny for each of the traits was determined by individually expressing the  $GCA_f$  SS,  $GCA_m$  SS, and the SCA SS as a percentage of the treatment (crosses) SS.

### 4.3 Results

#### 4.3.1 North Carolina II ANOVA for combined and individual sets of parents for eight traits evaluated at two sites

In the combined set ANOVA, the Site MS were significant ( $P < 0.05$ ) for all the traits (Table 4.4) indicating that there were significant differences between the site means. The sets MS were significant for all the traits except for MRN and TRY and HI. The Site x Set MS was significant ( $P \leq 0.05$ ) for AUDPC, UMRN, and TRY.

In the ANOVA for Set 1, the Site MS were significant ( $P < 0.05$ ) for all the traits (Table 4.5). The  $GCA_f$  MS were significant ( $P < 0.05$ ) for all traits except MRN, TRY and DM%. The  $GCA_m$  MS were only significant ( $P < 0.05$ ) for AUDPC and MRN and non-significant ( $P > 0.05$ ) for the other traits. The SCA MS were only significant ( $P \leq 0.05$ ) for AUDPC, SPVD score and HI. The Site x  $GCA_f$  MS was significant ( $P < 0.05$ ) for only AUDPC, UMRN and HI. The Site x  $GCA_m$  MS interaction was highly significant ( $P < 0.001$ ) for AUDPC, and non-significant ( $P > 0.05$ ) for the other traits. The Site x SCA MS was highly significant ( $P < 0.01$ ) for HI and non-significant ( $P > 0.05$ ) for the other traits.

In Set 2, the Site MS were significant ( $P < 0.05$ ) for all traits evaluated (Table 4.6). The  $GCA_f$  MS were significant ( $P < 0.05$ ) for all traits except for AUDPC and DM% (Table 4.6). The  $GCA_m$  MS were highly significant ( $P < 0.01$ ) for AUDPC, SPVD score and significant ( $P < 0.05$ ) for HI and non-significant ( $P > 0.05$ ) for the other traits. The SCA MS was highly significant ( $P < 0.001$ ) for AUDPC only. The Site x  $GCA_f$  MS were highly significant ( $P < 0.01$ ) only for SPVD score and MRN while the Site x  $GCA_m$  MS was highly significant for AUDPC ( $P < 0.01$ ) and non-significant ( $P > 0.05$ ) for the other traits. The Site x SCA MS were not significant for any of the traits.

From the combined sets analysis, the  $GCA_f$ /Set and  $GCA_m$ /Set SS accounted for over 60% of the treatment SS for all of the traits evaluated except DM% (Table 4.4). The  $GCA$ /Set SS of HI, UMRN, TRY and TRN had the highest contribution to the treatment SS of 85.0, 72.8, 72.4 and 68.0%, respectively. The SCA/Set contributed between 15.0 to 53.0% of the treatment SS, the highest contribution of 53.0% being recorded for DM%.

The  $GCA_f$  and  $GCA_m$  SS for Set 1 contributed over 50% of the treatment SS for the traits except DM% and HI (Table 4.5). The SCA SS contributed between 25.3 and 56.3% of the treatment SS, the highest contribution being 56.3% recorded for HI. In contrast to Set 1, the  $GCA_f$  and  $GCA_m$  SS for Set 2 contributed less than the SCA for AUDPC (46%) and DM% (49.7%) (Table 4.6). At 77.8% of the treatment SS, the  $GCA_f$  and  $GCA_m$  SS for HI predominated over the SCA SS in contrast to Set 1. For the rest of the traits,  $GCA_f$  and  $GCA_m$  SS in Set 2 accounted for higher proportions of the treatment SS than the SCA SS that is 60.9, 81.5, 83.8, 50.6 and 82.1% for SPVD, MRN, UMRN, TRN and TRY, respectively.



**Table 4.4 North Carolina II ANOVA mean squares and sum of squares for both sets of parents for eight traits evaluated at Namulonge and Kachwekano (2011A)**

Source of variation	DF	AUDPC	SPVD	MRN	UMRN	TRN	TRY	DM%	HI
Site	1	135399.6**	65.36**	5.87*	8.2 **	80.9**	6908.4**	117.3**	0.34**
Set	1	14316.7**	3.14**	0.17 <sup>NS</sup>	1.34**	5.8**	133.72 <sup>NS</sup>	47.7*	0.91 <sup>NS</sup>
Rep/Site*Set	4	8031.4**	1.97**	0.10 <sup>NS</sup>	0.89**	1.9*	123.6 <sup>NS</sup>	35.3**	0.01 <sup>NS</sup>
GCA <sub>f</sub> /Set	5	13671.2**	4.91**	0.14*	0.98**	8.0*	211.8*	3.1 <sup>NS</sup>	0.04**
GCA <sub>m</sub> /Set	7	11679.9**	0.34 <sup>NS</sup>	0.11*	0.27 <sup>NS</sup>	6.8 <sup>NS</sup>	104.2 <sup>NS</sup>	10.1 <sup>NS</sup>	0.02*
SCA/Set	18	4039.1**	0.82**	0.05 <sup>NS</sup>	0.14 <sup>NS</sup>	7.0 <sup>NS</sup>	37.8 <sup>NS</sup>	5.4 <sup>NS</sup>	0.01 <sup>NS</sup>
Site*Set	1	6922.5**	0.64 <sup>NS</sup>	0.09 <sup>NS</sup>	0.62*	3.5*	276.1*	5.7 <sup>NS</sup>	0.001 <sup>NS</sup>
Site*GCA <sub>f</sub> /Set	5	4313.1**	1.26**	0.11 <sup>NS</sup>	0.37*	1.0 <sup>NS</sup>	44.3 <sup>NS</sup>	1.3 <sup>NS</sup>	0.01 <sup>NS</sup>
Site*GCA <sub>m</sub> /Set	7	3552.9**	1.60 <sup>NS</sup>	0.03 <sup>NS</sup>	0.20 <sup>NS</sup>	0.5 <sup>NS</sup>	40.0 <sup>NS</sup>	11.5*	0.05 <sup>NS</sup>
Site*SCA/Set	18	1122.8**	0.33 <sup>NS</sup>	0.02 <sup>NS</sup>	0.17 <sup>NS</sup>	0.3 <sup>NS</sup>	39.9 <sup>NS</sup>	5.2 <sup>NS</sup>	0.01 <sup>NS</sup>
Error	60	24.2	24.20	0.22	0.37	0.7	8.2	2.3	0.08
Treatment SS		222820.1	41.6	2.30	9.40	21.9	2469.1	183.1	0.47
%SS due to GCA		67.4	64.6	64.3	72.8	68.0	72.4	47.0	85.0
%SS due to SCA		32.6	35.4	35.7	27.2	32.0	27.6	53.0	15.0

NS = not significant; \* = Significant at P≤0.05; \*\* = significant at P≤0.01; AUDPC = area under disease progress curve for Alternaria blight; SPVD = sweetpotato virus disease (score 1-9: 1 = no SPVD, and 9 = SPVD causing stunted growth); MRN = number of marketable storage roots per plant; UMRN = number of unmarketable storage roots per plant; TRN = total number of storage roots per plant; TRY = total storage root fresh mass (t ha<sup>-1</sup>); DM% = percentage dry mass composition; HI = harvest index; Site = Namulonge and Kachwekano; GCA<sub>f</sub> = female parent general combining ability; GCA<sub>m</sub> = male parent general combining ability; SCA = specific combining ability; %SS due to GCA and SCA expressed relative to the treatment SS

**Table 4.5 North Carolina II ANOVA means squares and sum of squares for Set 1 parents for eight traits evaluated at Namulonge and Kachwekano (2011A)**

Source	DF	AUDPC	SPVD	MRN	UMRN	TRN	TRY	DM%	HI
Site	1	54033.21***	34.95***	4.81***	8.62***	76.44**	6442.08*	113.07***	0.26***
Rep(Site)	2	9333.53***	1.54**	0.18 <sup>NS</sup>	1.34***	3.02**	191.34 <sup>NS</sup>	13.56 <sup>NS</sup>	0.01 <sup>NS</sup>
GCA <sub>f</sub>	3	22084.00***	5.23***	0.03 <sup>NS</sup>	1.11***	1.90*	65.19 <sup>NS</sup>	2.28 <sup>NS</sup>	0.02*
GCA <sub>m</sub>	4	16814.72***	0.40 <sup>NS</sup>	0.18*	0.36 <sup>NS</sup>	1.52 <sup>NS</sup>	149.43 <sup>NS</sup>	8.45 <sup>NS</sup>	0.01 <sup>NS</sup>
SCA	12	4434.22***	0.71**	0.06 <sup>NS</sup>	0.18 <sup>NS</sup>	0.33 <sup>NS</sup>	38.65 <sup>NS</sup>	4.26 <sup>NS</sup>	0.01*
Site*GCA <sub>f</sub>	3	6717.50***	0.57 <sup>NS</sup>	0.07 <sup>NS</sup>	0.52*	1.64 <sup>NS</sup>	20.90 <sup>NS</sup>	1.58 <sup>NS</sup>	0.01*
Site*GCA <sub>m</sub>	4	3880.14***	0.60 <sup>NS</sup>	0.02 <sup>NS</sup>	0.29 <sup>NS</sup>	0.73 <sup>NS</sup>	60.99 <sup>NS</sup>	13.19 <sup>NS</sup>	0.01 <sup>NS</sup>
Site*SCA	12	1135.04 <sup>NS</sup>	0.29 <sup>NS</sup>	0.02 <sup>NS</sup>	0.17 <sup>NS</sup>	0.32 <sup>NS</sup>	21.91 <sup>NS</sup>	3.84 <sup>NS</sup>	0.01**
Error	38	620.70	0.26	0.06	0.16	0.63	73.25	5.45	0.01
Treatment SS		186721.50	25.83	1.50	6.93	1.81	1257.05	9.75	0.19
%SS due to GCA		71.5	66.9	55.2	68.9	74.7	63.1	44.3	43.7
%SS due to SCA		28.5	33.1	44.8	31.1	25.3	36.9	55.7	56.3

NS = not significant; \* = Significant at  $P \leq 0.05$ ; \*\* = significant at  $P \leq 0.01$ ; AUDPC = area under disease progress curve for Alternaria blight; SPVD = sweetpotato virus disease (score 1-9: 1 = no SPVD, and 9 = SPVD causing stunted growth); MRN = number of market storage roots per plant; UMRN = number of unmarketable storage roots per plant; TRN = total number of storage roots per plant; TRY = total storage root fresh mass ( $t\ ha^{-1}$ ); DM% = percentage dry mass composition; HI = harvest index; Site = Namulonge and Kachwekano; GCA<sub>f</sub> = female parent general combining ability; GCA<sub>m</sub> = male parent general combining ability; SCA = specific combining ability; %SS due to GCA and SCA expressed relative to the treatment SS

**Table 4.6 North Carolina II ANOVA means squares and sum of squares for Set 2 parents for eight traits evaluated at Namulonge and Kachwekano (2011A)**

Source	DF	AUDPC	SPVD	MRN	UMRN	TRN	TRY	DM%	HI
Site	1	81394.74***	31.28***	1.75***	1.63***	19.38***	1693.49***	27.21*	0.11***
Rep(Site)	2	6729.30***	2.41**	0.02 <sup>NS</sup>	0.45*	0.72 <sup>NS</sup>	55.86 <sup>NS</sup>	57.09***	0.01 <sup>NS</sup>
GCA <sub>f</sub>	2	1051.97 <sup>NS</sup>	4.43**	0.30**	0.80**	1.17*	431.75**	4.25 <sup>NS</sup>	0.06**
GCA <sub>m</sub>	3	4833.42***	0.25***	0.01 <sup>NS</sup>	0.15 <sup>NS</sup>	0.25 <sup>NS</sup>	43.80 <sup>NS</sup>	12.30 <sup>NS</sup>	0.03*
SCA	6	3249.06***	1.03 <sup>NS</sup>	0.02 <sup>NS</sup>	0.07 <sup>NS</sup>	0.50 <sup>NS</sup>	36.19 <sup>NS</sup>	7.65 <sup>NS</sup>	0.01 <sup>NS</sup>
Site*GCA <sub>f</sub>	2	706.52 <sup>NS</sup>	2.29**	0.17**	0.15 <sup>NS</sup>	0.15 <sup>NS</sup>	79.42 <sup>NS</sup>	0.83 <sup>NS</sup>	0.00 <sup>NS</sup>
Site*GCA <sub>m</sub>	3	3116.49**	0.28 <sup>NS</sup>	0.00 <sup>NS</sup>	0.09 <sup>NS</sup>	0.19 <sup>NS</sup>	11.96 <sup>NS</sup>	9.20 <sup>NS</sup>	0.00 <sup>NS</sup>
Site*SCA	6	1098.43 <sup>NS</sup>	0.40 <sup>NS</sup>	0.03 <sup>NS</sup>	0.15 <sup>NS</sup>	0.31 <sup>NS</sup>	75.88 <sup>NS</sup>	7.96 <sup>NS</sup>	0.01 <sup>NS</sup>
Error	22	529.68	0.33	0.03	0.09	0.30	56.65	4.87	0.01
Treatment SS		36098.55	15.78	0.80	2.43	6.07	1212.01	91.31	0.28
%SS due to GCA		46.0	60.9	81.5	83.8	50.6	82.1	49.7	77.8
%SS due to SCA		54.0	39.1	18.5	16.2	49.4	17.9	50.3	22.2

NS = not significant; \* = Significant at  $P \leq 0.05$ ; \*\* = significant at  $P \leq 0.01$ ; AUDPC = area under disease progress curve for Alternaria blight; SPVD = sweetpotato virus disease (score 1-9: 1 = no SPVD and 9 = SPVD causing stunted growth); MRN = number of marketable storage roots per plant; UMRN = number of unmarketable storage roots per plant; TRN = total number of storage roots per plant; TRY = total storage root fresh mass ( $t\ ha^{-1}$ ); DM% = percentage dry mass composition; HI = harvest index; Site = Namulonge and Kachwekano; GCA<sub>f</sub> = female parent general combining ability; GCA<sub>m</sub> = male parent combining ability; SCA = specific combining ability. %SS due to GCA and SCA expressed relative to the treatment SS

### 4.3.2 General combining ability effects meaned over two sites

For brevity, only the GCA effects meaned over the two sites for the individual set analyses are considered. Since a low *Alternaria* blight score indicates resistance, a negative GCA effect for a parent indicates a contribution to increased disease resistance in its progeny (relative to the trial mean) which is desirable. Conversely, a positive GCA effect indicates an undesirable contribution to increased susceptibility in the progeny. In Set 1 (Table 4.7), the GCA effects for the female parents Semanda, Silk Omupya, and Kidodo and male parents Dimbuka and NASPOT 2 were significant for AUDPC, with only Silk Omupya and NASPOT 2 having highly significant ( $P < 0.01$ ), negative GCA effects. Bwanjule had high but non-significant, negative GCA effects. In Set 2 (Table 4.8), the GCA effects for AUDPC were not significant ( $P < 0.05$ ) for all the female and male parents. However, Budde and Silk Luwero had the largest, negative GCA effects of -20.1 and -13.8, respectively.

**Table 4.7 Performance and general combining ability effects of Set 1 parents for four traits meaned over two sites**

Parent	AUDPC		SPVD		MRN		UMRN	
	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
<b>Females</b>								
Semanda	192.5	<b>28.11*</b>	2.35	-0.31	0.37	-0.043	1.25	0.104
Silk Omupya	129.9	<b>-34.51**</b>	2.66	-0.22	0.38	-0.025	1.17	0.157
Kidodo	193.3	<b>28.80*</b>	2.22	-0.46	0.44	0.027	1.17	0.028
Bwanjule	142.0	-22.40	2.35	0.67	0.45	0.041	0.73	<b>-0.288*</b>
<b>SE</b>	<b>11.3</b>	<b>12.72</b>	<b>2.40</b>	<b>0.12</b>	<b>1.76</b>	<b>0.06</b>	<b>0.29</b>	<b>0.120</b>
<b>Males</b>								
Dimbuka	195.7	<b>31.24**</b>	2.46	-0.22	0.31	<b>-0.099**</b>	1.03	-0.117
NASPOT 2	112.5	<b>-51.97**</b>	2.84	0.16	0.47	<b>0.062**</b>	1.27	<b>0.280**</b>
NASPOT1	181.6	17.19	2.69	0.01	0.31	<b>-0.095**</b>	0.98	0.001
NASPOT 4	155.6	-8.84	2.57	-0.15	0.56	<b>0.151**</b>	1.21	0.063
Araka Red	176.8	12.37	2.70	0.02	0.39	-0.02	0.92	<b>-0.226*</b>
<b>SE</b>	<b>12.7</b>	<b>11.92</b>	<b>2.65</b>	<b>0.13</b>	<b>1.96</b>	<b>0.03</b>	<b>0.36</b>	<b>0.090</b>

\* = Significant at  $P \leq 0.05$ ; \*\* = significant at  $P \leq 0.01$ ; AUDPC = area under disease progress curve for *Alternaria* blight severity; SPVD = sweetpotato virus disease (scores 1-9, 1 = no SPVD and 9 = SPVD causing stunted growth); MRN = number of marketable storage roots per plant; UMRN = number of unmarketable storage roots per plant; GCA effects meaned over two sites were considered

The GCA effects for SPVD were not significant ( $P > 0.05$ ) for all the female and male parents in Set 1 (Table 4.7) and Set 2 (Table 4.8).

In Set 1, the  $GCA_r$  effects for MRN were not significant ( $P>0.05$ ) with those of Semanda and Silk Omupya, negative and those of Kidodo and Bwanjule, positive. All male parents, except parent Araka Red, had highly significant ( $P<0.01$ ) GCA effects for MRN. Dimbuka and NASPOT 1 had negative GCA effects whereas NASPOT 2 and NASPOT 4 had positive GCA effects. In Set 2, female parent Shock had significant positive GCA effects (0.16) for MRN (Table 4.8). Male parents, New Kawogo and Magabali had negative GCA effects while Silk Luwero and Budde had positive but non-significant GCA effects for MRN (Table 4.8). For this trait, parents with positive, significant GCA effects are desirable because they contribute to an increase in the number of roots in their progeny while parents with negative effects contribute to a reduction.

In Set 1, the GCA effects for UMRN were significant ( $P<0.05$ ) for Bwanjule among the females, and NASPOT 2 and Araka Red among the males (Table 4.7). Importantly, Bwanjule and Araka Red had negative GCA effects, which is desirable as these parents will contribute towards a reduction in UMRN in their progeny. Only Tanzania had highly significant ( $P<0.01$ ) GCA effects for UMRN in Set 2; however, they were positive which is not desirable for this trait (Table 4.8).

#### 4.8 Performance and general combining ability effects of Set 2 parents for four traits meaned over two sites

Parents	AUDPC		SPVD		MRN		UMRN	
	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
<b>Females</b>								
Tanzania	194.6	7.59	2.90	-0.06	0.24	-0.10	1.21	<b>0.32**</b>
Mbale	178.4	-8.65	3.52	0.56	0.28	-0.06	0.69	-0.20
Shock	185.9	1.06	2.47	-0.49	0.49	<b>0.16*</b>	0.78	-0.12
<b>SE</b>	<b>12.7</b>	<b>13.41</b>	<b>0.13</b>	<b>0.45</b>	<b>1.96</b>	<b>0.07</b>	<b>0.32</b>	<b>0.12</b>
<b>Males</b>								
New Kawogo	210.8	26.74	2.78	-0.18	0.33	-0.01	0.73	-0.18
Silk Luwero	173.2	-13.84	3.03	0.07	0.37	0.04	0.87	-0.03
Magabali	194.2	7.19	3.12	0.16	0.29	-0.05	0.90	0.12
Budde	167.0	-20.10	2.91	-0.05	0.35	0.02	0.99	0.09
<b>SE</b>	<b>14.6</b>	<b>14.90</b>	<b>0.16</b>	<b>0.28</b>	<b>2.27</b>	<b>0.03</b>	<b>0.36</b>	<b>0.11</b>

\* = Significant at  $P\leq 0.05$ ; \*\* = significant at  $P\leq 0.01$ ; AUDPC = area under disease progress curve for Alternaria blight; SPVD = sweetpotato virus disease (scores 1-9: 1 = no SPVD and 9 = SPVD causing stunted growth); MRN = number of marketable storage roots per plant; UMRN = number of unmarketable storage roots per plant; GCA effects meaned over two sites were considered

No parent had significant GCA effects for DM% in either set (Tables 4.9 and 4.10).

The best parents to be used when breeding for large TRN are those with large positive GCA effects for the trait. In Set 1, female parents Semanda and Kidodo (Table 4.9) had highly significant ( $P<0.01$ ), positive GCA effects for TRN. Similarly, male parents NASPOT 2 and NASPOT 4 had significant ( $P<0.05$ ), positive GCA effects for the trait. Since Bwanjule had highly significant ( $P<0.01$ ), negative GCA effects, it is not a desirable general combiner for this trait. Among the parents of Set 2, only female parent Tanzania had significant ( $P<0.05$ ) GCA effects for TRN (Table 4.10); however, it is not a good general combiner for this trait due to its negative GCA effects.

No parent in Set 1 (Table 4.9) had significant GCA effects for TRY. However, Kidodo had the highest positive GCA effect (0.35) for the trait. In this set, NASPOT 4 and NASPOT 2 had positive but non-significant GCA effects. In Set 2 (Table 4.10), Tanzania and Shock had significant ( $P<0.05$ ) GCA effects for TRY, but Tanzania had negative effects which are not desirable for this trait.

**Table 4.9 Performance and general combining ability effects of Set 1 parents for four traits meaned over two sites**

Parents	DM%		TRN		TRY		HI	
	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
<b>Females</b>								
Semanda	31.12	0.32	2.47	<b>0.22**</b>	14.39	-0.26	0.35	0.03
Silk Omupya	30.75	-0.05	2.26	0.01	13.06	-0.01	0.35	0.02
Kidodo	30.34	-0.46	2.46	<b>0.21**</b>	16.86	0.35	0.36	-0.02
Bwanjule	30.95	0.15	1.81	<b>-0.44**</b>	16.54	-0.08	0.30	-0.03
<b>SE</b>	<b>0.51</b>	<b>0.34</b>	<b>0.27</b>	<b>0.04</b>	<b>3.35</b>	<b>1.29</b>	<b>0.02</b>	<b>0.02</b>
<b>Males</b>								
Dimbuka	31.38	0.58	2.10	-0.16	12.04	-1.95	0.32	-0.01
NASPOT 2	29.88	-0.92	2.61	<b>0.34*</b>	17.79	1.59	0.36	<b>0.03*</b>
NASPOT 1	30.89	0.09	2.00	-0.25	12.47	-2.41	0.31	-0.02
NASPOT 4	31.58	0.78	2.56	<b>0.32*</b>	18.83	1.86	0.36	<b>-0.03*</b>
Araka Red	30.23	-0.57	1.99	-0.26	14.94	0.92	0.34	0.01
<b>SE</b>	<b>0.57</b>	<b>0.71</b>	<b>0.31</b>	<b>0.14</b>	<b>3.74</b>	<b>1.41</b>	<b>0.02</b>	<b>0.01</b>

\* = Significant at  $P\leq 0.05$ ; \*\* = significant at  $P\leq 0.01$ ; DM% = percentage dry mass composition; TRN = total number of storage roots per plant; TRY = total storage root fresh mass ( $t\ ha^{-1}$ ); HI = harvest index; GCA effects meaned over two sites were considered

The HI expresses the economic yield as a proportion of the total biomass; therefore a genotype that produces a high proportion of storage root mass in relation to the total biomass is more desirable. Only NASPOT 2 and NASPOT 4 of Set 1 had significant ( $P<0.05$ ) GCA effects for HI (Table 4.9). As a parent, NASPOT 2 with a positive GCA effect would be preferred to NASPOT 4 which had a negative GCA effect. In Set 2, female parents Mbale and Shock had highly significant ( $P<0.01$ ) GCA effects for HI (Table 4.10). The GCA effect for Shock was positive while that of Mbale was negative, thus Mbale was not a very good general combiner for the trait. Again, New Kawogo and Budde had significant ( $P<0.01$ ) GCA effects but only Budde's was positive and would therefore be a preferred general combiner.

**Table 4.10 Performance and general combining ability effects of Set 2 parents for four traits meaned over two sites**

Parent	DM%		TRN		TRY		HI	
	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
<b>Females</b>								
Tanzania	31.60	-0.50	2.06	-1.45*	7.16	<b>-2.95*</b>	0.31	-0.01
Mbale	32.62	0.52	1.53	-0.28	8.22	-1.88	0.26	-0.06**
Shock	31.92	-0.18	1.84	0.02	14.94	<b>4.83**</b>	0.39	0.07**
<b>SE</b>	<b>0.57</b>	<b>0.80</b>	<b>0.31</b>	<b>0.21</b>	<b>3.74</b>	<b>1.36</b>	<b>0.02</b>	<b>0.02</b>
<b>Males</b>								
New Kawogo	32.52	0.42	1.76	-0.05	9.32	-0.78	0.27	-0.05**
Silk Luwero	31.04	-1.06	1.72	-0.10	12.25	2.15	0.31	-0.01
Magabali	33.22	1.12	1.74	-0.07	8.77	-1.34	0.30	-0.01
Budde	31.40	-0.70	2.03	0.21	10.09	0.03	0.39	0.07**
<b>SE</b>	<b>0.66</b>	<b>0.80</b>	<b>0.35</b>	<b>0.17</b>	<b>4.32</b>	<b>1.58</b>	<b>0.02</b>	<b>0.02</b>

\* = Significant at  $P\leq 0.05$ ; \*\* = significant at  $P\leq 0.01$ ; DM% = percentage dry mass composition; TRN = total number of roots per plant; TRY = total storage root fresh mass ( $t\ ha^{-1}$ ); HI = harvest index; GCA effects meaned over two sites were considered

It is important to note that some genotypes with high HI have weak or underdeveloped foliage which makes propagation and maintenance of such genotypes difficult. Furthermore, HI on its own is obviously not a direct indicator of absolute yield and should therefore be used to evaluate genotypes in combination with other yield-related traits, in particular overall marketable root yield.

#### 4.3.3 Specific combining ability effects for individual sets meaned over two sites

Again, since there were no common parents across the two sets, only the SCA effects meaned over the two sites for the individual set analyses are considered. Among the 20 full-sib families in Set 1, the AUDPC value for Alternaria blight ranged from 96.9 in family Bwanjule x NASPOT 2 to 269.7 in family Kidodo x Dimbuka (Table 4.11). However, both families had positive SCA effects

with only that of Kidodo x Dimbuka highly significant ( $P < 0.01$ ). Of the 20 families in this set, only seven had significant ( $P < 0.05$ ) SCA effects of which three had desirable negative effects and four had undesirable positive effects. Family Kidodo x NASPOT 1 had the largest negative SCA effects (-67.12) and is therefore a more desirable family. Bwanjule x Dimbuka and Silk Omupya x Araka Red may be regarded as good families for this trait with SCA effects of -30.31 and -27.16, respectively. The *per se* performance (AUDPC means) of these families was good with Kidodo x NASPOT 1, Bwanjule x Dimbuka, Silk Omupya x Araka Red having mean AUDPC values of 143.3, 142.9 and 115.2 which were low compared to the other crosses. Families Silk Omupya x NASPOT 2, Kidodo x NASPOT 4 and Bwanjule x NASPOT 1 had significant ( $P < 0.05$ ), positive SCA effects, and Kidodo x Dimbuka had a significant ( $P < 0.01$ ), positive SCA effect and may therefore not be desirable families when breeding for resistance to Alternaria blight.

**Table 4.11 Performance and specific combining ability effects of Set 1 families for four traits meaned over two sites**

Family	AUDPC		SPVD		MRN		UMRN	
	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
Semanda x Dimbuka	219.5	-4.27	2.20	0.05	0.18	-0.09	1.09	-0.04
Semanda x NASPOT 2	124.3	-16.28	2.59	0.06	0.43	0.01	1.13	<b>-0.40*</b>
Semanda x NASPOT 1	220.0	10.25	2.10	0.26	0.33	0.05	1.09	-0.16
Semanda x NASPOT 4	173.8	-9.97	2.03	-0.22	0.45	-0.07	1.66	<b>0.35*</b>
Semanda x Araka Red	225.2	20.27	2.92	0.53	0.44	0.10	1.28	0.26
Silk Omupya x Dimbuka	150.6	-10.63	2.91	0.47	0.19	-0.09	1.22	0.04
Silk Omupya x NASPOT 2	106.7	<b>28.69*</b>	2.56	-0.26	0.33	<b>-0.12*</b>	1.24	<b>-0.34*</b>
Silk Omupya x NASPOT 1	169.9	22.83	2.92	0.26	0.35	0.06	1.18	<b>0.55**</b>
Silk Omupya x NASPOT 4	107.4	-13.73	2.59	0.05	0.76	<b>0.23**</b>	1.40	0.04
Silk Omupya x Araka Red	115.2	<b>-27.16*</b>	2.31	-0.37	0.29	-0.08	0.80	-0.28
Kidodo x Dimbuka	269.7	<b>45.21**</b>	2.00	-0.01	0.36	0.02	1.10	0.04
Kidodo x NASPOT 2	112.1	-19.20	2.81	-0.12	0.54	0.04	1.62	0.17
Kidodo x NASPOT 1	143.3	<b>-67.12**</b>	1.69	0.37	0.32	-0.02	1.56	-0.02
Kidodo x NASPOT 4	210.6	<b>26.26*</b>	2.47	0.37	0.5	-0.09	1.06	-0.18
Kidodo x Araka Red	220.5	14.85	2.13	-0.11	0.46	0.04	0.93	-0.02
Bwanjule x Dimbuka	142.9	<b>-30.31*</b>	2.74	-0.40	0.51	<b>0.16**</b>	0.70	-0.02
Bwanjule x NASPOT 2	96.9	6.80	3.39	-0.12	0.58	0.07	1.07	<b>0.57**</b>
Bwanjule x NASPOT 1	193.3	<b>34.04*</b>	4.03	0.67	0.28	-0.10	0.49	<b>-0.37*</b>
Bwanjule x NASPOT 4	130.7	-2.56	3.17	-0.07	0.54	-0.07	0.71	-0.21
Bwanjule x Araka Red	146.5	-7.97	3.44	0.07	0.37	-0.06	0.67	0.04
<b>Mean</b>	<b>164.0</b>		<b>2.65</b>		<b>0.41</b>		<b>1.15</b>	
<b>SE</b>	<b>25.3</b>	<b>12.98</b>	<b>0.27</b>	<b>0.88</b>	<b>0.41</b>	<b>0.05</b>	<b>0.64</b>	<b>0.16</b>

\* = Significant at  $P \leq 0.05$ ; \*\* = significant at  $P \leq 0.01$ ; AUDPC = area under disease progress curve for Alternaria blight severity; SPVD = sweetpotato virus disease score (score 1-9: 1 = no SPVD, and 9 = SPVD causing stunted growth); MRN = number of marketable storage roots per plant; UMRN = number of unmarketable storage roots per plant



Semanda was inconsistent as a parent, in some cases producing resistant families such as Semanda x NASPOT 2 (AUDPC of 124.3) with a negative SCA effect of -16.28 and in other cases producing very susceptible families such as Semanda x Dimbuka (219.5), Semanda x NASPOT 1 (220) and Semanda x Araka Red (225.2) with SCA effects of -4.27, 10.25 and -20.27, respectively. Kidodo was also inconsistent in that it produced resistant families Kidodo x NASPOT 2 (112.1) and Kidodo x NASPOT 1 (143.3) with SCA effects of -19.2 and -67.12, respectively, and susceptible families Kidodo x Dimbuka (269.7), Kidodo x NASPOT 4 (210.6), and Kidodo x Araka Red (220.5) with SCA effects of 45.21, 26.26 and 14.85, respectively. Kidodo x NASPOT 1 which had the highest significant ( $P < 0.01$ ), negative SCA effect of -67.12 and AUDPC of 143.3 was therefore one of the most desirable families along with Kidodo x NASPOT 2 with a SCA effect of -19.2 and AUDPC of 112.1.

In Set 2, the SCA effects for AUDPC of families Mbale x Silk Luwero and Shock x Magabali were highly significant ( $P < 0.01$ ) but with the effects being positive these families were undesirable (Table 4.12). The SCA effect of Mbale x Magabali was also significant ( $P < 0.05$ ) and being negative this was a desirable family. Shock x Silk Luwero had the lowest AUDPC value (142.4) with high but non-significant ( $P < 0.05$ ), negative SCA effects. All crosses with New Kawogo produced families with high AUDPC values (above 200) but, interestingly, only Mbale x New Kawogo had positive SCA effects. Shock performed inconsistently in crosses producing families with the highest AUDPC (231.5) for Shock x Magabali and also the lowest AUDPC value for Shock x Silk Luwero (142.4) and SCA effects of 36.15 and -22.14, respectively.

No families in Set 1 had significant SCA effects for SPVD (Table 4.11). However, Semanda x NASPOT 4, Silk Omupya x NASPOT 2, Silk Omupya x Araka Red, Kidodo x Dimbuka, Kidodo x NASPOT 2, Kidodo x Araka Red, Bwanjule x Dimbuka, Bwanjule x NASPOT 2 and Bwanjule x NASPOT 4 had the desired negative SCA effects. Similarly, no families in Set 2 had significant SCA effects for SPVD (Table 4.12). Families Tanzania x Silk Luwero, Tanzania x Budde, Mbale x Budde and Shock x Magabali had the desired negative SCA effects.

Of the Set 1 families, Silk Omupya x NASPOT 4 and Bwanjule x Dimbuka produced the highest MRN of 0.76 and 0.51, respectively with highly significant ( $P < 0.01$ ), positive SCA effects and were therefore the best families (Table 4.11). Silk Omupya x NASPOT 2 had a significant ( $P < 0.05$ ), but undesirable negative SCA effect for this trait. All Set 2 families had significant ( $P < 0.05$ ) SCA effects for MRN except Tanzania x New Kawogo, and Shock x Budde (Table 4.12). Of those families with significant ( $P > 0.05$ ) SCA effects, only Tanzania x Magabali, Mbale x New Kawogo, Mbale x Silk Luwero, Mbale x Budde and Shock x Silk Luwero had desirable positive SCA effects.

**Table 4.12 Performance and specific combining ability effects of Set 2 families for four traits meaned over two sites**

Family	AUDPC		SPVD		MRN		UMRN	
	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
Tanzania x New Kawogo	216.7	-4.77	3.1	0.43	0.23	0.01	0.81	-0.24
Tanzania x Silk Luwero	180.2	-0.62	2.7	-0.30	0.19	<b>-0.09*</b>	1.21	0.02
Tanzania x Magabali	193.0	-8.59	3.1	0.02	0.30	<b>0.11*</b>	1.16	0.22
Tanzania x Budde	188.5	13.97	2.7	-0.15	0.23	<b>-0.03*</b>	1.32	0.01
Mbale x New Kawogo	214.6	9.48	2.8	-0.49	0.29	<b>0.02*</b>	0.66	0.14
Mbale x Silk Luwero	197.0	<b>32.46**</b>	3.8	0.20	0.37	<b>0.10*</b>	0.71	0.06
Mbale x Magabali	158.1	<b>-27.55*</b>	4.3	0.58	0.12	<b>-0.11*</b>	0.73	-0.08
Mbale x Budde	143.9	-14.38	3.2	-0.29	0.32	<b>0.03*</b>	0.68	-0.11
Shock x New Kawogo	201.2	-4.71	2.4	0.06	0.47	<b>-0.02*</b>	0.71	0.10
Shock x Silk Luwero	142.4	-22.14	2.6	0.09	0.56	<b>0.03*</b>	0.67	-0.08
Shock x Magabali	231.5	<b>36.15**</b>	2.0	-0.60	0.45	<b>-0.04*</b>	0.77	-0.13
Shock x Budde	168.4	0.41	2.9	0.44	0.50	-0.01	0.99	0.11
<b>Mean</b>	<b>186.3</b>		<b>3.0</b>		<b>0.34</b>		<b>0.87</b>	
<b>SE</b>	<b>25.3</b>	<b>11.85</b>	<b>0.3</b>	<b>0.81</b>		<b>0.05</b>	<b>0.64</b>	<b>0.14</b>

\* = Significant at  $P \leq 0.05$ ; \*\* = significant at  $P \leq 0.01$ ; AUDPC = area under disease progress curve for Alternaria blight severity; SPVD = sweetpotato virus disease score (scores 1-9 used; 1 = no SPVD and 9 = SPVD causing stunted growth); MRN = number of marketable storage roots per plant; UMRN = number of unmarketable storage roots per plant

Of the Set 1 families, Semanda x NASPOT 2, Silk Omupya x NASPOT 2 and Bwanjule x NASPOT 1 had significant ( $P < 0.05$ ), negative SCA effects for UMRN whereas families Silk Omupya x NASPOT 1 and Bwanjule x NASPOT 2 had highly significant ( $P < 0.01$ ), positive SCA effects (Table 4.11). Semanda x NASPOT 4 had a significant ( $P < 0.05$ ), positive SCA effect. A family with a low mean UMRN and negative SCA effects is desired. Therefore, the best Set 1 family was Bwanjule x Dimbuka with the lowest mean UMRN of 0.7 and SCA effect of -0.02. There were no families in Set 2 (Table 4.12) with significant SCA effects for UMRN. However, families Tanzania x New Kawogo, Mbale x Magabali, Mbale x Budde, Shock x Silk Luwero and Shock x Magabali had desirable negative SCA effects.

There were no families in Set 1 with significant ( $P < 0.05$ ) SCA effects for DM% (Table 4.13). Thirteen of the 20 families had undesirable negative SCA effects for this trait. Similarly, there were no families in Set 2 with significant ( $P < 0.05$ ) SCA effects for DM% (Table 4.14). Of the 12 families, seven had undesirable negative SCA effects.

There were no families with significant ( $P < 0.05$ ) SCA effects for TRN in Set 1 (Table 4.13). Of the 20 families, 10 families had desirable positive SCA effects whereas the other 10 had undesirable negative SCA effects. In Set 2, five families had highly significant ( $P < 0.01$ ) SCA effects and two families had significant ( $P < 0.05$ ) SCA effects (Table 4.14). Of these seven families, only Shock x Silk Luwero had undesirable negative SCA effects.

There were no families in Set 1 with significant SCA effects for TRY (Table 4.13). However, Semanda x NASPOT 1, Semanda x Araka Red, Silk Omupya x NASPOT 1, Silk Omupya x NASPOT 4, and Bwanjule x Dimbuka had large positive SCA effects. In Set 2, no family had significant SCA effects for TRY (Table 4.14). However, seven families had positive SCA effects.

All families in Set 1 had highly significant ( $P < 0.01$ ), negative SCA effects for HI and were therefore undesirable for this trait (Table 4.13). In Set 2, of the 12 families, five (Tanzania x New Kawogo, Tanzania x Magabali, Mbale x Budde, Shock x Magabali, Shock x Budde) had highly significant ( $P < 0.01$ ) SCA effects and two (Mbale x New Kawogo and Mbale x Magabali) had significant ( $P < 0.05$ ) SCA effects (Table 4.14). Tanzania x Magabali, Mbale x New Kawogo and Shock x Budde had desirable positive SCA effects. Tanzania x New Kawogo, Mbale x Magabali, Mbale x Budde and Shock x Magabali had undesirable negative SCA effects.

**Table 4.13 Performance and specific combining ability effects of Set 1 families for four traits meaned over two sites**

Family	DM%		TRN		TRY		HI	
	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
Semanda x Dimbuka	31.44	-0.26	2.1	-0.19	8.08	-3.14	0.34	<b>-0.33**</b>
Semanda x NASPOT 2	30.29	0.09	2.4	-0.41	16.04	-0.92	0.37	<b>-0.33**</b>
Semanda x NASPOT 1	32.56	1.35	2.5	0.30	12.77	3.46	0.34	<b>-0.29**</b>
Semanda x NASPOT 4	30.96	-0.93	2.9	0.09	17.97	-0.04	0.31	<b>-0.33**</b>
Semanda x Araka Red	30.35	-0.20	2.4	0.21	17.11	2.99	0.39	<b>-0.30**</b>
Silk Omupya x Dimbuka	31.44	0.11	2.1	-0.01	8.00	-1.89	0.28	<b>-0.38**</b>
Silk Omupya x NASPOT 2	29.11	-0.72	2.4	-0.23	12.65	-2.99	0.34	<b>-0.36**</b>
Silk Omupya x NASPOT 1	29.77	-1.07	2.2	0.21	13.78	3.46	0.36	<b>-0.29**</b>
Silk Omupya x NASPOT 4	33.77	2.25	2.7	0.18	19.74	3.06	0.45	<b>-0.20**</b>
Silk Omupya x Araka Red	29.66	-0.52	1.8	-0.15	11.15	-1.64	0.31	<b>-0.38**</b>
Kidodo x Dimbuka	31.40	0.48	2.3	0.03	13.52	-0.17	0.34	<b>-0.28**</b>
Kidodo x NASPOT 2	29.36	-0.06	3.1	0.26	21.83	-0.45	0.40	<b>-0.22**</b>
Kidodo x NASPOT 1	30.42	-0.01	2.1	-0.11	13.48	-1.86	0.31	<b>-0.46**</b>
Kidodo x NASPOT 4	29.94	-1.17	2.8	-0.01	18.61	-1.86	0.41	<b>-0.46**</b>
Kidodo x Araka Red	30.58	0.81	2.0	-0.16	16.85	0.24	0.32	<b>-0.32**</b>
Bwanjule x Dimbuka	31.23	-0.30	1.8	0.16	18.57	5.20	0.31	<b>-0.30**</b>
Bwanjule x NASPOT 2	30.77	0.74	2.6	0.38	20.64	1.52	0.32	<b>-0.34**</b>
Bwanjule x NASPOT 1	30.80	-0.24	1.2	-0.39	9.86	-3.94	0.23	<b>-0.38**</b>
Bwanjule x NASPOT 4	31.63	-0.10	1.9	-0.26	19.00	-1.16	0.28	<b>-0.31**</b>
Bwanjule x Araka Red	30.33	-0.05	1.7	0.10	14.66	-1.61	0.34	<b>-0.30**</b>
<b>Mean</b>	<b>30.79</b>		<b>2.3</b>		<b>15.20</b>		<b>0.32</b>	
<b>SE</b>	<b>1.14</b>		<b>0.6</b>	<b>0.22</b>	<b>7.49</b>	<b>2.45</b>	<b>0.05</b>	<b>0.05</b>

\*\* = significant at  $P \leq 0.01$ ; DM% = percentage dry mass composition; TRN = total number of storage roots per plant; TRY = total storage root fresh mass ( $t \text{ ha}^{-1}$ ); HI = harvest index

**Table 4.14 Performance and specific combining ability effects of Set 2 families for four traits meaned over two sites**

Family	DM%		TRN		TRY		HI	
	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
Tanzania x New Kawogo	31.80	-0.23	2.1	<b>1.75**</b>	8.42	0.29	0.23	<b>-0.24**</b>
Tanzania x Silk Luwero	30.62	0.08	2.2	<b>1.91**</b>	7.98	-3.51	0.29	0.02
Tanzania x Magabali	33.11	0.38	2.1	<b>1.79**</b>	12.13	4.36	0.36	<b>0.22**</b>
Tanzania x Budde	30.88	-0.02	1.9	<b>1.36**</b>	9.82	-1.15	0.35	0.01
Mbale x New Kawogo	35.21	2.17	1.5	<b>1.91**</b>	10.25	1.05	0.22	<b>0.14*</b>
Mbale x Silk Luwero	31.21	-0.35	1.7	0.29	14.17	1.62	0.24	0.06
Mbale x Magabali	32.46	-1.28	1.3	-0.17	5.58	-3.25	0.26	<b>-0.08*</b>
Mbale x Budde	31.60	-0.32	1.6	-0.11	12.61	0.58	0.32	<b>-0.11**</b>
Shock x New Kawogo	30.56	-1.78	1.8	-0.02	16.27	-1.34	0.36	0.10
Shock x Silk Luwero	31.29	-0.27	1.2	<b>-0.50*</b>	22.14	1.88	0.41	-0.08
Shock x Magabali	34.10	1.06	1.8	-0.07	16.14	-1.11	0.29	<b>-0.13**</b>
Shock x Budde	31.72	0.50	2.5	<b>0.45*</b>	21.02	0.57	0.49	<b>0.11**</b>
<b>Mean</b>	32.05		<b>1.8</b>		13.10		<b>0.32</b>	
<b>SE</b>	<b>1.14</b>		<b>0.6</b>	<b>0.20</b>	<b>7.49</b>	<b>2.23</b>	<b>0.05</b>	<b>0.04</b>

\* = Significant at  $P \leq 0.05$ ; \*\* = significant at  $P \leq 0.01$ ; DM% = percentage dry mass composition; TRN = total number of storage roots per plant; TRY = total storage root fresh mass ( $t\ ha^{-1}$ ); HI = harvest index

#### 4.3.4 Performance of the families at individual sites

In order to identify families with superior performance at individual sites, family means for the different traits at each site were generated and discussed below.

For Set 1 at Namulonge (Table 4.15), the AUDPC values varied greatly ranging from 101.4 in the most resistant family (Bwanjule x NASPOT 2) to 202.2 in the most susceptible family (Kidodo x Dimbuka). The families of Silk Omupya had lower AUDPC values ranging from 103.7 to 138.2. Bwanjule families also had lower AUDPC values ranging from 101.4 in Bwanjule x NASPOT 2 to 167.5 in Bwanjule x NASPOT 1. In contrast, Kidodo families were inconsistent with Kidodo x NASPOT 2 (108.7) being resistant and Kidodo x Dimbuka (202.2) susceptible. All families of NASPOT 2 had low AUDPC values ranging from 101.4 to 114.7 and were the most resistant of all the families at this site.

#### 4.15 Mean performance for eight traits of Set 1 families evaluated at Namulonge (2011A)

Family	AUDPC	SPVD	MRN	UMRN	DM%	TRN	TRY	HI
Semanda x Dimbuka	157.0	2.17	0.32	1.65	30.74	3.20	13.17	0.43
Semanda x NASPOT 2	113.1	3.16	0.71	1.76	30.10	3.85	25.63	0.44
Semanda x NASPOT 1	159.1	2.70	0.54	1.57	30.30	1.92	20.64	0.42
Semanda x NASPOT 4	147.1	2.90	0.78	2.34	29.65	4.40	30.29	0.41
Semanda x Araka Red	164.8	3.29	0.70	1.62	29.50	3.38	25.72	0.49
Silk Omupya x Dimbuka	124.0	3.70	0.33	1.64	28.68	2.66	12.98	0.48
Silk Omupya x NASPOT 2	114.7	3.17	0.60	1.54	28.84	3.45	22.24	0.39
Silk Omupya x NASPOT 1	138.2	3.63	0.55	1.50	27.74	2.89	21.16	0.45
Silk Omupya x NASPOT 4	103.7	3.47	0.86	1.89	35.70	4.03	32.51	0.33
Silk Omupya x Araka red	127.3	3.38	0.40	0.72	28.47	2.09	14.65	0.43
Kidodo x Dimbuka	202.2	2.79	0.59	0.45	29.11	3.50	21.81	0.43
Kidodo x NASPOT 2	108.7	3.42	0.82	1.75	29.28	3.66	28.68	0.36
Kidodo x NASPOT 1	121.0	2.40	0.57	2.10	27.10	3.67	24.21	0.45
Kidodo x NASPOT 4	186.0	3.50	0.79	1.42	29.62	3.95	29.01	0.45
Kidodo x Araka red	151.0	2.90	0.82	1.24	29.10	3.04	29.20	0.39
Bwanjule x Dimbuka	130.0	3.70	0.82	0.91	29.98	2.59	29.46	0.29
Bwanjule x NASPOT 2	101.4	3.40	0.90	0.92	29.84	2.80	29.94	0.26
Bwanjule x NASPOT 1	167.5	4.30	0.46	0.75	29.71	1.98	17.37	0.34
Bwanjule x NASPOT 4	113.3	3.80	0.94	0.90	30.86	2.71	32.79	0.37
Bwanjule x Araka Red	138.5	4.60	0.61	0.77	28.10	2.20	22.39	0.36
<b>Mean</b>	<b>138.4</b>	<b>3.32</b>	<b>0.66</b>	<b>1.37</b>	<b>29.62</b>	<b>3.10</b>	<b>24.19</b>	<b>0.40</b>
<b>SE</b>	<b>25.3</b>	<b>0.48</b>	<b>3.92</b>	<b>0.64</b>	<b>2.06</b>	<b>0.61</b>	<b>7.49</b>	<b>0.05</b>

AUDPC = area under disease progress curve for Alternaria blight severity; SPVD = sweetpotato virus disease score (scores 1-9 used; 1 = no SPVD and 9 = SPVD causing stunted growth); MRN = number of marketable storage roots per plant; UMRN = number of unmarketable storage roots per plant; DM% = percentage dry mass composition; TRN = total number of storage roots per plant; TRY = total storage root fresh mass (t ha<sup>-1</sup>); HI = harvest index

Generally, Set 2 families exhibited lower levels of resistance to Alternaria blight with mean AUDPC of 145.1 compared to 138.4 for Set 1 (Table 4.16). Mbale x Magabali had the lowest AUDPC value (101.6) and Shock x Magabali the highest value (175.3). Shock x Budde had the highest TRY of 31.1 t ha<sup>-1</sup>, whereas Mbale x Magabali had the lowest TRY of 7.5 t ha<sup>-1</sup>.

#### 4.16 Mean performance for eight traits of Set 2 families evaluated at Namulonge (2011A)

Family	AUDPC	SPVD	MRN	UMRN	DM%	TRN	TRY	HI
Tanzania x New Kawogo	173.9	4.10	0.28	0.78	32.0	2.05	12.41	0.28
Tanzania x Silk Luwero	147.9	3.40	0.37	1.71	29.61	3.20	12.49	0.37
Tanzania x Magabali	160.8	3.81	0.39	5.20	33.8	2.70	17.03	0.39
Tanzania x Budde	161.0	3.50	0.39	1.67	27.9	2.83	10.97	0.39
Mbale x New Kawogo	163.0	4.04	0.29	0.87	31.9	2.25	17.04	0.29
Mbale x Silk Luwero	128.5	4.71	0.31	0.91	29.4	2.55	23.26	0.31
Mbale x Magabali	101.6	6.12	0.27	0.72	31.5	3.21	7.54	0.27
Mbale x Budde	145.9	3.97	0.38	0.96	30.9	2.22	19.16	0.38
Shock x New Kawogo	135.8	2.75	0.43	0.91	29.4	2.53	26.28	0.43
Shock x Silk Luwero	106.3	3.32	0.39	0.78	31.3	2.54	22.97	0.39
Shock x Magabali	175.3	2.39	0.39	0.51	33.6	2.63	28.16	0.39
Shock x Budde	141.4	3.17	0.51	0.84	30.7	2.83	31.13	0.51
<b>Mean</b>	<b>145.1</b>	<b>3.77</b>	<b>0.37</b>	<b>1.32</b>	<b>30.0</b>	<b>2.63</b>	<b>19.04</b>	<b>0.37</b>
<b>SE</b>	<b>25.3</b>	<b>0.48</b>	<b>3.92</b>	<b>0.63</b>	<b>2.1</b>	<b>0.61</b>	<b>7.49</b>	<b>0.05</b>

AUDPC = for Alternaria blight severity; SPVD = sweetpotato virus disease (scores used; 1 = no SPVD and 9 = SPVD causing stunted growth); MRN = number of marketable storage roots per plant; UMRN = number of unmarketable storage roots per plant; DM% = dry mass percentage; TRN = total number of storage roots per plant; TRY = total storage root fresh mass (t ha<sup>-1</sup>); HI = harvest index

The mean AUDPC values for Set 1 families were higher at Kachwekano than at Namulonge (Tables 4.15 and 4.17). The lowest AUDPC at Namulonge was 101.4 for family Bwanjule x NASPOT 2 and the same family had the lowest AUDPC value at Kachwekano but with an unexpectedly lower value of 96.6. However, most of the AUDPC values for other families were higher with Kidodo x Dimbuka the most susceptible family both at Kachwekano (337.9) and at Namulonge (202.2). Similarly, for Set 1 the mean TRY of 6.22 t ha<sup>-1</sup> at Kachwekano was very low compared to 24.19 t ha<sup>-1</sup> at Namulonge.

#### 4.17 Mean performance for eight traits of Set 1 families evaluated at Kachwekano (2011A)

Family	AUDPC	SPVD	MRN	UMRN	DM%	TRN	TRY	HI
Semanda x Dimbuka	281.2	1.9	0.05	0.85	31.9	1.08	2.96	0.24
Semanda x NASPOT 2	151.6	2.3	0.16	0.52	30.8	1.01	6.28	0.31
Semanda x NASPOT 1	281.2	1.5	0.28	0.61	34.7	0.98	4.86	0.26
Semanda x NASPOT 4	200.1	1.2	0.11	0.96	32.3	1.37	5.46	0.22
Semanda x Araka Red	286.7	2.5	0.19	0.93	31.2	1.47	8.49	0.28
Silk Omupya x Dimbuka	176.9	2.1	0.06	0.86	34.4	1.05	2.98	0.22
Silk Omupya x NASPOT 2	100.0	1.9	0.06	0.95	29.2	1.33	3.10	0.20
Silk Omupya x NASPOT 1	201.3	2.2	0.16	0.87	31.7	1.56	6.38	0.34
Silk Omupya x NASPOT 4	108.5	1.7	0.15	0.91	33.0	1.47	6.92	0.44
Silk Omupya x Araka Red	104.0	1.3	0.18	0.90	33.6	1.62	7.64	0.28
Kidodo x Dimbuka	337.9	1.2	0.13	0.57	32.2	1.09	5.23	0.25
Kidodo x NASPOT 2	137.0	2.2	0.27	1.50	29.4	2.51	14.91	0.45
Kidodo x NASPOT 1	164.1	1.0	0.07	0.19	33.6	0.53	2.79	0.17
Kidodo x NASPOT 4	236.9	1.4	0.21	0.71	30.1	1.69	8.20	0.37
Kidodo x Araka Red	290.8	1.4	0.10	0.67	32.0	1.05	4.43	0.26
Bwanjule x Dimbuka	155.7	1.9	0.20	0.50	32.7	1.05	7.71	0.34
Bwanjule x NASPOT 2	96.6	3.5	0.27	1.21	31.9	2.32	11.43	0.38
Bwanjule x NASPOT 1	219.4	3.8	0.06	0.25	31.9	0.40	2.31	0.13
Bwanjule x NASPOT 4	147.9	2.5	0.14	0.53	32.7	1.04	5.29	0.19
Bwanjule x Araka Red	155.5	2.3	0.31	0.58	29.9	1.11	6.94	0.31
<b>Mean</b>	<b>191.7</b>	<b>2.0</b>	<b>0.16</b>	<b>0.75</b>	<b>32.0</b>	<b>1.29</b>	<b>6.22</b>	<b>0.28</b>
<b>SE</b>	<b>19.9</b>	<b>0.4</b>	<b>0.08</b>	<b>0.29</b>	<b>0.6</b>	<b>0.44</b>	<b>3.82</b>	<b>0.06</b>

AUDPC = for Alternaria blight severity; SPVD = sweetpotato virus disease score (scores 1-9 used; 1 = no SPVD and 9 = SPVD causing stunted growth); MRN = number of marketable storage roots per plant; UMRN = number of unmarketable storage roots per plant; DM% = percentage dry mass composition; TRN = total number of storage roots per plant; TRY = total storage root fresh mass ( $t\ ha^{-1}$ ); HI = harvest index

As was the case in Set 1, higher Alternaria blight severity levels were recorded at Kachwekano in Set 2 families than at Namulonge (Tables 4.16 and 4.18). Shock x Magabali was the most susceptible family with an AUDPC of 289.4.

#### 4.18 Mean performance for eight traits of Set 2 families evaluated at Kachwekano (2011A)

Family	AUDPC	SPVD	MRN	UMRN	DM%	TRN	TRY	HI
Tanzania x New Kawogo	261.8	2.2	0.11	0.84	31.8	1.26	4.47	0.22
Tanzania x Silk Luwero	212.6	1.9	0.08	0.70	31.8	1.14	3.46	0.20
Tanzania x Magabali	226.7	2.3	0.17	0.89	30.4	1.48	7.24	0.21
Tanzania x Budde	216.6	2.0	0.20	0.93	34.1	1.46	8.70	0.32
Mbale x New Kawogo	270.0	2.0	0.08	0.48	34.6	0.71	3.42	0.12
Mbale x Silk Luwero	252.1	2.9	0.12	0.52	34.0	0.92	5.10	0.15
Mbale x Magabali	214.3	2.4	0.06	0.77	33.7	1.03	3.60	0.25
Mbale x Budde	142.2	2.4	0.16	0.39	32.4	1.05	6.06	0.27
Shock x New Kawogo	266.8	2.0	0.16	0.51	34.5	1.01	6.33	0.28
Shock x Silk Luwero	179.6	2.0	0.37	0.46	30.2	2.06	12.67	0.44
Shock x Magabali	289.4	1.7	0.09	0.64	34.5	1.06	4.03	0.19
Shock x Budde	196.3	1.7	0.26	1.15	33.2	2.05	11.02	0.46
<b>Mean</b>	<b>227.4</b>	<b>2.1</b>	<b>0.16</b>	<b>0.69</b>	<b>32.9</b>	<b>1.27</b>	<b>6.34</b>	<b>0.26</b>
<b>SE</b>	<b>19.9</b>	<b>0.4</b>	<b>0.08</b>	<b>0.29</b>	<b>1.2</b>	<b>1.22</b>	<b>3.82</b>	<b>0.06</b>

AUDPC = for Alternaria blight severity; SPVD = sweetpotato virus disease (scores 1-9 used: 1 = no SPVD and 9 = SPVD causing stunted growth); MRN = number of marketable storage roots per plant; UMRN = number of unmarketable storage roots per plant; DM% = percentage dry mass composition; TRN = total number of roots per plant; TRY = total storage root fresh mass (t ha<sup>-1</sup>); HI = harvest index

#### 4.3.5 Best parent heterosis of individual progeny

Unlike the preceding sections in which determinations were based on family means, determinations in this section are based on the values of the individual progeny genotypes in each of the 32 different families. A SI (Section 4.1.6) was used to rank the individual progeny across the 32 families of both sets for five of the eight traits, and BPH% was calculated for the top 20 progeny (Table 4.19). Of the top 20 progeny, three had Bwanjule as the female parent (Set 1), six had Shock as the female parent (Set 2) and four had Mbale as the female parent (Set 2). The SI ranked progeny 27 from family Bwanjule x NASPOT 4 as the best. A negative BPH% for AUDPC indicated a progeny that was more resistant than the best parent. Similarly, a negative BPH% for SPVD score indicated a progeny that was more resistant than the best parent. Eleven of the top 20 progeny recorded BPH% in the desired negative direction for Alternaria blight. The BPH% for Alternaria blight ranged from -76.0 (progeny 19 of Bwanjule x NASPOT 2) to 99.8% (progeny 29 of Shock x New Kawogo). The BPH% for TRY ranged from -85.9 (progeny 4 of Kidodo x NASPOT 1) to 96.9% (progeny 14 of Kidodo x NASPOT 4). The BPH% for DM% ranged from -12.1 (progeny 22 of Sock x Budde) to 31.8% (Progeny 30 of Mbale x Budde). Progeny 30 of Mbale x Budde had the lowest BPH% for HI of -40.4%, whereas progeny 21 of Semanda x NASPOT 1 had the highest BPH for HI% of 56.1%. The BPH% for the SPVD ranged from -55.0 in progeny 2 of Semanda x Araka Red, to 41.3% in progeny 23 of Shock x Silk Luwero and progeny 26 of Mbale x Budde.



**Table 4.19 Best parent heterosis for the top 20 F<sub>1</sub> progeny selected using a selection index**

Genotype	Progeny number	SI	BPH%				
			AUDPC	SPVD	TRY	DM%	HI
Bwanjule x NASPOT 4	27	19.9	-11.7	-38.0	48.2	27.5	15.7
Shock x Silk Luwero	23	17.7	-47.7	35.2	-52.4	22.2	-13.4
Bwanjule x NASPOT 2	19	17.4	-76.0	-54.5	-29.8	12.3	-9.0
Shock x Silk Luwero	1	16.7	62.8	35.2	73.4	19.0	38.2
Kidodo x NASPOT 1	4	16.6	-49.1	-17.1	-85.9	3.7	9.0
Semanda X Araka Red	2	15.6	-41.0	-55.0	5.3	12.1	-27.0
Semanda x NASPOT 4	8	15.6	-31.4	0.0	78.5	3.2	20.2
Shock x Budde	28	15.5	-50.1	-27.5	58.6	-0.8	27.0
Silk Omupya x NASPOT 4	22	15.4	-36.7	-53.4	62.8	-1.9	9.0
Mbale x New Kawogo	24	15.4	-7.2	-27.5	57.6	8.0	2.2
Mbale x Budde	30	15.1	6.5	41.3	-48.4	31.8	-40.4
Tanzania X Silk Luwero	14	14.0	10.8	-13.8	68.1	-6.8	44.9
Shock x New Kawogo	29	14.0	99.8	-27.5	65.5	9.5	17.9
Semanda x NASPOT 1	21	14.0	42.6	-54.5	89.1	-12.1	56.1
Bwanjule X Dimbuka	16	13.8	10.1	-38.0	-6.3	-8.9	31.5
Kidodo x NASPOT 4	14	13.6	16.1	13.8	96.9	11.9	4.5
Mbale x New Kawogo	20	13.6	14.1	13.8	47.2	11.9	4.5
Shock x Budde	22	13.6	-4.2	-41.3	91.6	-9.2	33.7
Mbale x Budde	26	13.4	9.9	0.0	-57.6	-0.7	22.4
Shock x Silk Luwero	29	13.4	-45.0	41.3	5.3	4.2	-6.7

SI = Selection index value for specific progeny from a particular family; AUDPC = for *Alternaria* blight severity; BPH% = best parent heterosis as a percentage; SPVD = sweetpotato virus disease; TRY = total storage root fresh mass (t ha<sup>-1</sup>); DM% = percentage dry mass composition; HI = harvest index

#### 4.4 Discussion

This study was carried out to understand the gene action controlling the inheritance of resistance to *Alternaria* blight, and sweetpotato yield components. This information would inform future breeding programmes. Just as importantly, the F<sub>1</sub> progeny may be used as sources of new genetic variation in breeding for resistance to *Alternaria* blight and SPVD and improved agronomic performance. In addition, the promising F<sub>1</sub> genotypes can be further evaluated for varietal potential.

##### 4.4.1 North Carolina II ANOVA for eight traits evaluated at two sites

The significance of the genotype GCA MS and SCA MS interactions with sites for all the traits indicated that the families (and therefore the genotypes within families) responded differently to change in sites (Table 4.4). Significant genotype x environment interaction presents challenges to selection as it reduces the correlation between the phenotype and genotype thereby potentially

leading to selection of inferior progeny. This demands that breeders test their selections for stability of performance across a range of environments.

The significant differences in performance between the parents within the sets for AUDPC, SPVD, UMRN, TRN and HI indicated that the parents within the two sets were of divergent variability which may allow for high levels of heterosis to be expressed in the progeny of crosses between these parents (Table 4.4). According to Prasad and Singh (1986) and Martin et al. (1995) the degree of heterosis is related to the magnitude of genetic divergence between the parents thus the greater the genetic variability the higher the heterosis.

That the  $GCA_f$ /Set MS for all traits except DM% were larger than the  $GCA_m$ /Set MS was indicative of greater variation in the mean performance as parents (relative to the overall mean of all parents) of the female parents (Table 4.4). The Site x  $GCA_f$ /Set MS was significant for only AUDPC, SPVD and UMRN. This indicated that the  $GCA_f$  was not consistent for these three traits but was consistent for other traits across the sites. The Site x  $GCA_m$ /Set MS was significant for only AUDPC and DM% indicating that the  $GCA_m$  was only consistent across the sites for the other traits. Non-additive gene action is apparently important in the expression of AUDPC and SPVD given the significance of the SCA MS for these two traits. The significance of Site x SCA/Set MS for AUDPC indicates that contribution of non-additive genetic effects of the parents in specific crosses is not consistent across the sites for Alternaria blight resistance. The  $GCA_f$ /Set and  $GCA_m$ /Set SS accounted for the greater proportion of phenotypic (treatment) variation in all the traits except DM% where the SCA/Set accounted for 53.0%. Therefore both additive and non-additive gene action play a role in the phenotypic expression of these traits but the additive variance component is relatively more important than the non-additive variance component except for DM%.

The significance ( $P < 0.05$ ) of the  $GCA_f$  MS in Set 1 for AUDPC, SPVD, UMRN, TRN and HI indicated that additive genetic variance contributed by the female parents is very important in controlling the expression of these traits (Table 4.5). Similarly, significance ( $P < 0.05$ ) of the  $GCA_m$  MS for AUDPC indicated that the male parents in Set 1 contributed significant additive genetic effects to the expression of this trait. Significance ( $P < 0.05$ ) of the SCA MS for AUDPC, SPVD and HI indicated that the non-additive gene action is important in the expression of these three traits for the parents in Set 1 (Table 4.5). Significance ( $P < 0.05$ ) of the Site x  $GCA_f$  MS for AUDPC, UMRN and HI indicated that the additive genetic effects for the female parents in Set 1 was not consistent across the sites for these three traits but was consistent for the other traits evaluated. The Site x  $GCA_m$  MS was highly significant ( $P < 0.01$ ) for AUDPC indicating that the additive genetic effects of male parents in Set 1 were not consistent across the sites only for AUDPC but consistent for the

other traits. The Site x SCA MS was only significant for HI indicating that the effect of non-additive gene action for this trait varied with change in site.

Significance ( $P < 0.05$ ) of the  $GCA_f$  MS in Set 2 for SPVD, MRN, UMRN, TRN, TRY and HI indicated that additive genetic variance contributed by the female parents is very important in controlling the expression of these traits (Table 4.6). Similarly, significance ( $P < 0.05$ ) of the  $GCA_m$  for AUDPC, SPVD and HI indicated that additive genetic variance due to male parents in Set 2 was very important in the expression of these three traits. The SCA MS was only significant ( $P < 0.001$ ) for AUDPC indicating that the non-additive gene action was important in the expression of this trait for the parents in Set 2. Furthermore, significance ( $P < 0.05$ ) of the Site x  $GCA_f$  MS for SPVD and MRN indicated that the effect of the additive action for female parents in Set 2 for these two traits varied with change in site. Similarly, significance of Site x  $GCA_m$  for AUDPC indicated that the additive gene action due to male parents in Set 1 for AUDPC was not consistent over sites.

#### **4.4.2 Mean performance, and general and specific combining ability effects for the eight traits**

##### **4.4.2.1 Area under disease progress curve**

The parental AUDPC values for Alternaria blight ranged from 112.5 to 195.7 in Set 1 (Table 4.7) and 167.0 to 210.8 in Set 2 (Table 4.8). This wide range in AUDPC values is very encouraging in that it indicates that selection of genotypes for high resistance to Alternaria blight from within the available germplasm is possible. The significant ( $P < 0.05$ ), positive GCA effects for AUDPC in three of the Set 1 parents Semanda, Kidodo and Dimbuka of 28.11, 28.8 and 31.24, respectively implies that they are not good general combiners when breeding for Alternaria blight resistance since they contribute towards higher susceptibility. Conversely, Silk Omupya, NASPOT 2 with highly significant ( $P < 0.01$ ) and large negative GCA effects of -34.51 and -51.97, and Bwanjule with non-significant but large GCA effects of -22.4 are good general combiners when breeding for resistance to the disease.

Set 1 families exhibited considerable variation in terms of reaction to Alternaria blight. The AUDPC values ranged from 96.9 for the most resistant family (Bwanjule x NASPOT 2) to 269.7 for the most susceptible family (Kidodo x Dimbuka) (Table 4.11). Family Bwanjule x NASPOT 2 had a non-significant ( $P < 0.05$ ), positive SCA effect of 6.8 for AUDPC but parent Bwanjule had a large negative GCA effect of -22.40 and parent NASPOT 2 also had the highest significant ( $P < 0.01$ ), negative GCA effect of -51.97. Similarly, parents Silk Omupya and NASPOT 2 with significant ( $P < 0.05$ ), negative GCA effects produced progeny with a low AUDPC (106.7) but with significant

( $P < 0.05$ ), positive SCA effects. The positive SCA effects of these crosses were unexpected since both parents had negative GCA effects. A similar scenario was reported by Mwanga et al. (2002) for SPVD where two very good combiners for SPVD produced susceptible progeny with undesirable SCA effects. The difference here, however, is that despite the positive SCA effects, the progeny of these crosses had high levels of resistance to the disease.

The susceptible family Kidodo x NASPOT 4 with an AUDPC of 210.6 and a significant ( $P < 0.05$ ), positive SCA effect of 26.26 (Table 4.11) resulted from a cross between a female parent with a significant ( $P < 0.05$ ), positive GCA effect of 28.80 and a male parent with a non-significant ( $P > 0.05$ ), negative GCA effect of -8.84 (Table 4.7). Conversely, family Bwanjule x Dimbuka with a significant ( $P < 0.05$ ), negative SCA effect of -30.31 (Table 4.11) was the result of a cross between a female parent with a non-significant ( $P > 0.05$ ), negative GCA effect of -22.40 and a male parent with a highly significant ( $P < 0.01$ ), positive GCA effect of 31.24 (Table 4.7). The implication being that sometimes parents with positive GCA effects may be of value in the development of resistant *Alternaria* blight genotypes and conversely, some parents with negative GCA effects may not be very useful in the development of *Alternaria* blight resistant genotypes. Therefore parents should not be eliminated from the crossing program solely on the basis of GCA alone but after a thorough evaluation of the *per se* performance of their progeny.

Female parents Silk Omupya and Bwanjule (Table 4.7) across all males produced families with the lowest AUDPC values (Table 4.11) and were therefore the best combiners for resistance to *Alternaria* blight. Similarly, male parent NASPOT 2 (Table 4.7) produced the most resistant families across all females (Table 4.11). All these parents had significant ( $P < 0.05$ ), negative GCA effects for the disease and thus were the best at transmitting resistance to *Alternaria* blight to their progeny. These parents should be used as sources of resistance to the disease.

The GCA and SCA MS were both significant for AUDPC implying that both additive and non-additive gene actions were important for this trait. The GCA SS contributed 71.5% in Set 1 and 46% in Set 2 of the treatment SS for this trait indicating that additive gene action and non-additive gene action were both important and the predominance of either depends on the parents used. However, results reported by Simon and Strandberg (1998) for *A. dauci* in carrots (*Daucus carota* L.) indicated that additive gene action was more predominant. Maiero et al. (1990) also reported resistance to early blight (*A. solani*) in tomato (*Solanum lycopersicum* L.) to be predominantly controlled by additive gene action. Furthermore, Christ and Haynes (2001) reported both additive and non-additive gene action to be important in conditioning the resistance to early blight (*A. solani*) of diploid potato with the additive component predominant.

Greater severity of *Alternaria* blight was recorded at Kachwekano than Namulonge. Similar findings have been reported by Mwanga et al. (2007b) and Osiru et al. (2007a) for these two sites. The highest AUDPC value at Kachwekano was 337.9 for family Kidodo x Dimbuka (Table 4.17). The same family was also the most susceptible at Namulonge with an AUDPC value of 202.2 (Table 4.15). This means that this is a poor family in terms of resistance to *Alternaria* blight but, interestingly, it was not the lowest yielder at both sites. It may be exhibiting some level of disease tolerance that enables it to produce a fair yield equivalent to 90.2% of the average yield despite being severely infected.

#### **4.4.2.2 Sweetpotato virus disease**

The phenotypic expression of SPVD at the two sites was significantly ( $P < 0.05$ ) different for both sets (Table 4.5 & 4.6). Significance ( $P < 0.01$ ) of the  $GCA_f$  MS compared to non-significance of the male  $GCA_m$  MS in Set 1 indicated that additive gene action was contributed mainly by the female parents in this set. However, significance ( $P < 0.01$ ) of both  $GCA_f$  and  $GCA_m$  MS for Set 2 parents indicated that both female and male parents in this set contributed significant additive gene action. Significance ( $P < 0.01$ ) of the SCA MS for Set 1 indicated that non-additive gene action was also important. Non-significance of the SCA MS for Set 2 implied that for the parents in Set 2, the non-additive gene action was not important. Furthermore, the significance ( $P < 0.01$ ) of the Site x  $GCA_f$  MS for Set 2 indicated that the extent of the additive gene action in the expression of resistance through to susceptibility to SPVD in the progeny of this set was dependent on the female parent of a cross and the site at which the progeny were grown. The GCA SS comprised 66.9% of the treatment SS for Set 1 and 60.9% for Set 2 compared to the SCA SS of 33.1 and 39.1%, respectively. This means both the additive and the non-additive gene action were important in the expression of this trait with the additive component predominant over the non-additive component. This is similar to the findings of Mihovilovich et al. (2000) and Mwanga et al. (2002).

#### **4.4.2.3 Number of marketable roots per plant**

The mean MRN was significantly different ( $P < 0.01$ ) between the two sites for both sets (Tables 4.5 & 4.6). The significant ( $P < 0.05$ )  $GCA_f$  and  $GCA_m$  MS in Set 1 indicates the importance of additive gene action while the non-significant SCA MS indicates the relative non-importance of non-additive gene action in the expression of this trait (Table 4.5). The GCA SS comprised 55.2% of the treatment SS compared to 44.8% for SCA for Set 1, and 81.5% compared to 18.5% for Set 2. This indicates that the additive gene action was relatively more important than the non-additive gene action for this trait particularly for Set 2 families. The GCA effects were highly significant ( $P < 0.01$ ) for four of the five male parents in Set 1 (Table 4.7) and one female parent in Set 2 (Table 4.8).

For this trait positive GCA effects in the parents are desirable to contribute to increased MRN in their  $F_1$  progeny.

#### **4.4.2.4 Number of unmarketable roots per plant**

The mean UMRN was significantly ( $P < 0.01$ ) different between the two sites for both sets (Tables 4.5 & 4.6). The significance ( $P < 0.01$ ) of the  $GCA_f$  MS and non-significance of the  $GCA_m$  MS in both sets implied that the female parents contributed the additive genetic effects for this trait. The significant ( $P < 0.05$ ) Site x  $GCA_f$  MS for Set 1 implies differential contribution to the progeny of additive gene action by the female parents in this set across the two sites. Non-significance of both the  $GCA_m$  and Site x  $GCA_m$  MS in both sets indicated additive gene action contributed by the male parents was non-significant either on average across sites or in interaction with sites. The SCA MS for both sets were non-significant ( $P > 0.05$ ) indicating the relative non-importance of non-additive gene action in the expression of the trait. Non-additive gene action in the production of unmarketable roots was also not conditional on the site in which the sets of families were grown as evidenced by the non-significant Site x SCA MS. The GCA SS comprised 68.9% of the treatment SS compared to 31.1% for SCA SS in Set 1, and 83.8% compared to 16.2% in Set 2. Therefore, UMRN is controlled by both additive and non-additive gene action with additive gene action predominating.

#### **4.4.2.5 Total root number per plant**

The mean TRN was highly significantly ( $P < 0.01$ ) different between the two sites for both sets (Tables 4.5 & 4.6). Significance ( $P < 0.05$ ) of the  $GCA_f$  MS in Set 1 (Table 4.5) and Set 2 (Table 4.6) and non-significance of the  $GCA_m$  MS as well as SCA MS in both sets indicates that TRN was influenced by additive gene action contributed by the female parents in both sets. In addition, the non-significance of Site x  $GCA_f$  MS in both sets indicates that the contribution of additive gene action by the female parents was not site dependent. The highly significant ( $P < 0.01$ ), positive  $GCA_f$  effects for parents Semanda and Kidodo (Set 1), and the significant ( $P < 0.05$ ) positive  $GCA_m$  effects for parents NASPOT 2 and NASPOT 4 (Set 1) (Table 4.9) means that these parents are good general combiners in that they make a positive contribution towards higher TRN in their progeny. On the other hand, crossing parents with negative GCA effects for TRN (Table 4.8) resulted in progeny with highly significant ( $P < 0.01$ ), desirable positive SCA effects, namely: Tanzania x New Kawogo (1.75), Tanzania x Silk Luwero (1.91), Tanzania x Magabali (1.79), Tanzania x Budde (1.36), and Mbale x New Kawogo (1.91) (Table 4.14). Apparently the interaction between the two parents of each cross with undesirable additive effects produced desirable non-additive effects in their progeny. This once again highlights the unpredictability of desirable non-additive gene action being expressed in the progeny of parents with desirable and/or undesirable

additive gene action. The family Shock x Budde (0.45) from parents with positive GCA effects recorded the highest mean of 2.5 for TRN and a positive SCA effect of 0.45. This cross demonstrates the importance of both additive and non-additive gene action in maximising TRN. The GCA SS comprised 74.7% of the treatment SS versus 25.3% for SCA for Set 1, and similarly 50.6% versus to 49.4% for Set 2. This further indicates that both additive and non-additive gene action influence this trait but that additive gene action is more prominent, particularly in Set 1.

#### **4.4.2.6 Total storage root yield**

The significance ( $P < 0.01$ ) of the Site MS for TRY for both sets indicates that the families on average will yield differently when there is a change in site (Tables 4.5 & 4.6). Significance ( $P < 0.01$ ) of the  $GCA_f$  MS in Set 2 and non-significance ( $P > 0.05$ ) of  $GCA_m$  implies that the additive gene action is important but is mainly due to the female parent. The Site x  $GCA_f$  MS was non-significant for both sets implying that the additive effects of the female parents were consistently expressed regardless of the site in which their progeny were evaluated. The GCA SS comprised 63.1% of the treatment SS and 36.9% for SCA for Set 1 and correspondingly 83.1% and 17.9% for Set 2 implying that both additive and non-additive gene action were important for this trait but with the additive component predominating. Vimala and Lakshmi (1991) similarly reported on the predominance of additive gene action in the expression of this trait. Conversely, an earlier study by Chen et al. (1989) showed that non-additive genetic variance was more important than additive variance indicating low narrow-sense heritability for this trait. On the other hand, Pillai and Amma (1989) found that additive genetic variance and non-additive genetic variance were equally important for TRY.

#### **4.4.2.7 Percentage dry mass composition**

The DM% was significantly ( $P < 0.01$ ) different between the two sites for both sets (Tables 4.5 and 4.6). The  $GCA_f$  and  $GCA_m$ , SCA MS and their interactions with site were non-significant ( $P > 0.05$ ) for both sets (Table 4.5 and 4.6). The DM% ranged from 29.1 for cross Silk Omupya x NASPOT 2 (Table 4.13) to 35.2% for cross Mbale x New Kawogo (Table 4.14). This high DM% is typical of most of the Ugandan sweetpotato genotypes (Mwanga et al., 2007a) and has also been reported by Tumwegamire et al. (2011) in East African sweetpotato germplasm. Since the SCA SS at 55.7% accounted for a greater proportion of the treatment SS than the GCA SS at 44.3% for Set 1, and 50.3% versus 49.7% for Set 2, non-additive gene action was relatively more important than additive gene action in determining the variation in DM%. Similar results have been reported by Mariscal and Carpena (1988) in sweetpotato and by Kamau et al. (2010) in cassava where SCA SS accounted for 55 and 61.0% of the treatment SS, respectively. However, this is contrary to Chiona (2009) who reported that additive gene action was more important than non-additive

gene action for DM% in sweetpotato with GCA SS comprising 92.0% of the treatment SS and SCA comprising the remaining 8%. Similarly, Feng et al. (1988) and Dai et al. (1988) reported additive gene effects for dry mass to be more important than non-additive gene effects.

#### **4.4.2.8 Harvest index**

Significance ( $P < 0.05$ ) of the  $GCA_f$  MS and non-significance ( $P > 0.05$ ) of the  $GCA_m$  MS in Set 1 indicates that the additive gene action determining the expression of HI in the families of this set was mainly contributed by the female parents (Table 4.5). Significance ( $P < 0.05$ ) of the SCA MS in Set 1 indicates that the non-additive gene action is also important for this set of parents. In Set 2, the  $GCA_f$  and  $GCA_m$  MS were both significant ( $P < 0.05$ ) whereas that of SCA was not significant ( $P < 0.05$ ) (Table 4.6). This indicates that additive gene action was important in determining the HI of the families of this set. In Set 1 (Table 4.13), all of the families had negative SCA effects implying a positive contribution of non-additive gene action to HI. However, in Set 2 Tanzania x Magabali, Mbale x New Kawogo and Shock x Budde had positive SCA effects indicating a positive contribution of non-additive gene action to HI (Table 4.14). The GCA SS comprised 43.7% of treatment SS versus 56.3% for SCA in Set 1, and correspondingly 77.8% versus 22.2% for Set 2. Therefore both additive and non-additive gene action are important in the expression of this trait but the relative predominance of additive gene action or non-additive gene action depends on the parents under consideration. It should be noted, however, that since Alternaria blight and SPVD diseases reduce leaf photosynthetic activity and therefore root bulking and dry mass accumulation, it is likely that HI will be negatively affected by the presence of either or both these diseases.

#### **4.4.2.9 Heterosis of the crosses**

The SI was used to identify the best progeny within the families based on the traits under consideration. Bwanjule, Shock and Mbale were the female parents of nine of the top 20 progeny (Table 4.19). This indicates that these two parents have a higher breeding value than the rest. According to Falconer and Mackey (1996) heterosis is a function of increasing genetic diversity among parents. Most of the top performing progeny from families of Set 1 were from crosses between landraces and the improved cultivars (NASPOTs). On the other hand, most of the top performing progeny of Set 2 families were from crosses between Shock as a female and Budde and Silk Luwero as the males (Table 4.19). For resistance to Alternaria blight and SPVD, a negative heterosis is desired which indicates that the disease severity is lower in the progeny than in the best parent. Encouragingly most of the genotypes recorded BPH% in the desired direction for the five traits considered (Table 4.19) indicating genetic improvement over not only the particular parents of each progeny but also over the parent with the best overall performance. However, five of the 20 genotypes selected using the SI had lower TRY than the best parent. This



was because these genotypes had scored highly for the other traits. This was a weakness inherent in generating a cumulative score of the weighted traits in the SI; nevertheless, the SI assisted in selecting genotypes with the best overall weighted score for the evaluated traits. The overall scores or values for genotypes generated from selection indices should always be considered in conjunction with the performances for critically important traits (which are usually component traits of the SI) such as marketable yield. In future breeding work, other methods such as independent culling could also be considered.

#### **4.5 Conclusion**

It was apparent that both additive and non-additive gene actions were important for the phenotypic expression of the traits under consideration although additive gene action generally predominated. With respect to *Alternaria* blight, the implication of both additive and non-additive gene action contributing to the expression of resistance to the disease is that improved cultivars with good resistance levels to the disease can be obtained by careful selection of progeny expressing both gene actions. Both additive and non-additive gene action will be conserved in the best performing progeny through vegetative propagation. Predominance of additive gene action for any trait generally means that the performance of the parents of the crosses can be used to predict performance of the progeny. Conversely, predominance of non-additive gene action means progeny performance may not be accurately predicted based on parental performance. There were also instances in this study that proved exceptions to the rule where resistant progeny with desirable SCA effects were obtained from parents whose GCA effects were not desirable. Therefore, before discarding any parents it is important to evaluate the *per se* performance of their progeny and to not depend entirely on the magnitude and significance of GCA effects alone.

Female parents Silk Omupya and Bwanjule produced the most *Alternaria* resistant families across all male parents while male parent NASPOT 2 produced the most *Alternaria* resistant families across all female parents (Table 4.11). Bwanjule x NASPOT 4 was the best family across traits. Based on BPH%, the best performing parents across all traits were Shock, Bwanjule, Mbale, Silk Luwero and NASPOT 2. The best genotype across traits were progeny 27 from Bwanjule x NASPOT 4, progeny 23 from Shock x Silk Luwero, progeny 19 from Bwanjule x NASPOT 2, progeny 1 from Shock x Silk Luwero and progeny 4 from Kidodo x Silk Luwero.

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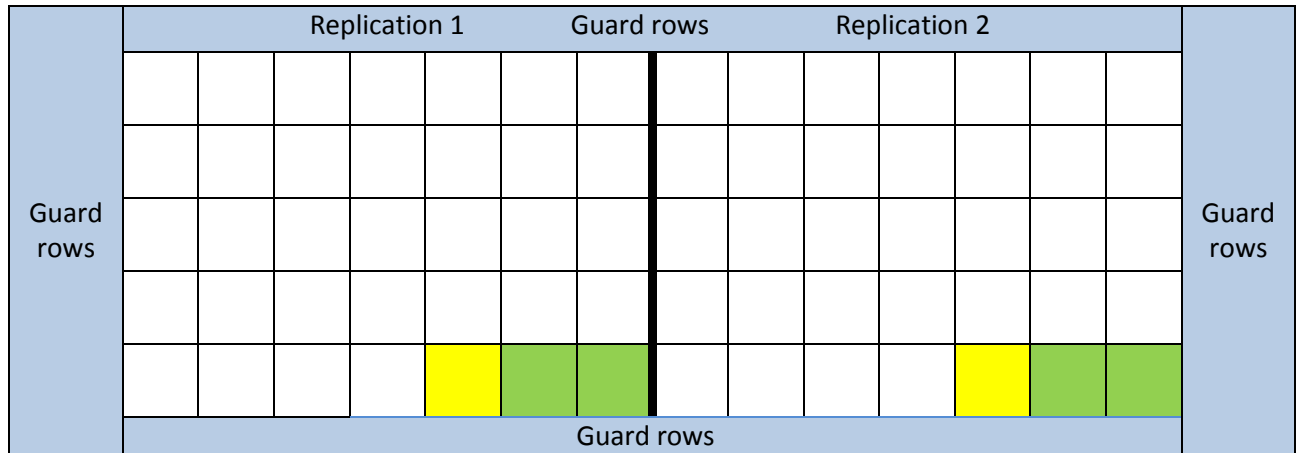
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## Appendices

### Appendix 4.1. Row x column (5x7) design for the F<sub>1</sub> progeny evaluation trial at Namulonge and Kachwekano (2011A)



Yellow shaded plots were planted to the parents and data collected from them. The green shaded plots were also planted to the parents but no data was collected from them. Each family was represented by 30 genetically unique genotypes (siblings) and each genotype by five plants in the trial, thus a total of 150 plants per family

## Chapter 5

### Evaluation and participatory selection of selected sweetpotato F<sub>1</sub> genotypes at three sites in Uganda

#### Abstract

Most of the important traits in sweetpotato (*Ipomoea batatas* (L.) Lam) are sensitive to environmental change. This necessitates evaluating new sweetpotato genotypes in different environments to identify those with stable performance for important traits before they can be recommended to farmers. Depending on their stability, genotypes can either be recommended for wide or specific release. In addition to stability and general performance, these new genotypes must have farmer and consumer preferred traits to enhance their adoption. Therefore, farmers should participate at an appropriate stage in the evaluation and selection of new genotypes. This study was conducted to: evaluate promising sweetpotato F<sub>1</sub> genotypes for total storage root yield (TRY), *Alternaria* leaf petiole and stem blight (*Alternaria* spp.) resistance and other traits; and identify those genotypes with wide and specific adaptation in association with performance for farmer preferred traits. A total of 21 promising F<sub>1</sub> genotypes from previously evaluated crosses, Tanzania (resistant check) and NASPOT 1 (susceptible check) were evaluated during the second rains of 2011 at three sites, Namulonge, Kachwekano and Serere using a randomised complete block design with three replications. Scientists and farmers evaluated the agronomic performance and also quality traits of the genotypes before and at harvest. Throughout the trials and at harvest, the severity of *Alternaria* leaf petiole and stem blight was greater at Kachwekano (the high disease pressure site) than Namulonge and Serere. Across sites, Tanzania had the lowest area under the disease progress curve (AUDPC). At Namulonge several genotypes had lower AUDPC values than Tanzania and were thus more resistant. Generally higher TRY ranging from 12.3 to 25.5 t ha<sup>-1</sup> were recorded at Namulonge than at Kachwekano and Serere. Genotypes G14, G16, G24, G29, G49, G59 and G69 were the most stable across the sites for low *Alternaria* leaf petiole and stem blight severity and can, therefore, be recommended for cultivation in both low and high disease pressure areas. Genotypes G67, G13, G14, G24, G29 and G53 were the most stable across the sites for TRY and therefore the most widely adapted of the F<sub>1</sub> genotypes for this trait, while G68, G60 and G58 were specifically adapted to Kachwekano and Serere. In the participatory selection, before harvest and at harvest, Spearman's rank correlation of the scientists and farmers' mean ranking of the genotypes at each site was positive and significant. This indicated that the scientists are capable of selecting for farmer preferred attributes. The study identified five F<sub>1</sub> genotypes G13, G14, G24, G49 and G69 with better performance than the existing cultivars.

## 5.1 Introduction

Plant breeders desire stable genotypes with good performance under all conditions within the target production regions. Stable genotypes with high yield potential can only be identified by testing them in a series of environments (Martin et al., 1988) and it is always important to test genotypes in environments which reveal their maximum genetic potential in terms of the traits under consideration (Frey, 1964). The major objective of any crop improvement programme is the development of cultivars with high yield potential and other desirable traits, and the ability to withstand seasonal fluctuations over a wide range of environments (Kamalam et al., 1978). Landraces are less responsive to improved conditions but produce yields that are just acceptable at poor sites whereas improved cultivars are more responsive to improved conditions but may perform poorly under poor conditions (Kanua and Floyd, 1988). This has obvious implications for the intended release of new cultivars to farmers in target production environments. Most of the important sweetpotato traits, including yield, are strongly affected by environmental conditions associated with sites and years (Ngeve, 1993). In most cases, high yielding genotypes are not yield stable and those that are yield stable are low yielding (Ngeve, 1993; Manrique and Hermann, 2000). However, breeding sweetpotato for high yield and wide adaptation is possible (Grüneberg et al., 2005). In sweetpotato, attention needs to be paid to testing in low-yielding, marginal environments if farmers working in such environments are the main beneficiaries of the new cultivars. Hence, yield testing in early stages of a sweetpotato breeding program should use at least one favourable environment and one less favourable environment (Grüneberg et al., 2005).

In Uganda, the National Sweetpotato Program released 20 sweetpotato cultivars between 1995 and 2011 and all these releases were made after conducting on-station, on-farm and standard multi-locational yield trials focusing mainly on high yield, high dry mass, resistance to pests and diseases (Mwanga et al., 2011). Of all these released cultivars, only one, NASPOT 11, had been bred through a participatory plant breeding process (Mwanga et al., 2011), but efforts were made to incorporate farmer preferred attributes in the other cultivars. Despite releasing all these cultivars, farmers still demand new ones to meet their ever changing preferences and some of the cultivars have not been well received for example, NASPOT 2, NASPOT 5 and Sowola 6 (Abidin et al., 2002). For this reason, many farmers have continued to cultivate their landraces which underscores the need to involve farmers in genotype selection so that their preferences are considered. This approach allows incorporation of farmers' knowledge, identification of farmers' selection criteria and priorities.



Participation of farmers can allow for exploitation of specific adaptation effects within sites and facilitate seed supply to farmers (Ceccarelli et al., 2000).

Evaluation by farmers helps scientists to design, test and recommend new technologies in light of information about farmers' requirements and needs. It facilitates close interaction among farmers, researchers and other role players in crop genetic improvement, allowing researchers to respond more closely to the needs and preferences of resource-poor farmers and their market clients (Sperling et al., 2001). Farmers can be involved in evaluating materials grown on the research station and also collaborate by growing and selecting breeding materials in their own field (Ceccarelli et al., 2000). The cultivars obtained from this process are developed more rapidly, are more diverse and have higher adoption rates (Witcombe et al., 2003). Consideration of farmers' concerns and conditions leads to technologies that become widely adapted and more productive and leads to sustainable agricultural systems (Odendo et al., 2002).

The F<sub>1</sub> genotypes previously selected (Chapter 4) were used in this study. The study was carried out to identify superior genotypes as possible candidates for advanced yield and on-farm trials. The main objective of this study was to evaluate and identify genotypes with wide and specific stable performance over three sites for *Alternaria* leaf petiole and stem blight (commonly referred to as *Alternaria* blight) resistance, TRY and other farmer preferred traits.

## **5.2 Materials and Methods**

### **5.2.1 Genotypes and sites**

Twenty one F<sub>1</sub> genotypes, one resistant check (Tanzania) and one susceptible check (NASPOT 1) were planted at three sites during the second rain season of 2011 (2011B) (second rain season starts in September to January). The first site was the National Crops Resources Research Institute (NaCRRI), at Namulonge (0°32' N, 32°35' E; 1150 metres above sea level (masl)). The second site was Kachwekano Zonal Agricultural Research and Development Institute (KAZARDI) (01°16'S, 29°57'E; 2200 masl) and the third site was at the National Semi-Arid Resources Research Institute at Serere (NaSARRI) (1°32'N, 33°27'E; 1140 masl). A randomized complete block design with three replications was used for the trial and the same randomization was applied at all three sites (Appendix 5.11). Seventeen vine-tip cuttings per genotype, each 0.30 m in length, were planted 0.30 m apart in each of four, 5 m long ridged rows spaced 1 m apart per plot providing for 68 hills per genotype. No fertilizer or supplementary irrigation was applied and the plots were hand weeded. No artificial inoculation with *Alternaria bataticola* (one of the species within *Alternaria* that causes *Alternaria* blight) was done thus all disease infection was by natural spread.

## 5.2.2 Data Collection

### 5.2.2.1 Disease rating

Rating for Alternaria blight was conducted at three weekly intervals from two months after planting (MAP) until four data sets were obtained. Alternaria blight and sweetpotato virus disease (SPVD) rating was done as previously described (Chapter 3, section 3.2.5).

### 5.2.2.2 Harvest data

At Namulonge and Serere, the trials were harvested at 5 MAP and at Kachwekano at 7 MAP. At harvest, the number of storage roots, total storage root mass (TRY (t ha<sup>-1</sup>)), number of marketable storage roots, mass of marketable storage roots (MRY (t ha<sup>-1</sup>)), number and mass of unmarketable storage roots (t ha<sup>-1</sup>), shoot mass (t ha<sup>-1</sup>) and total biomass (t ha<sup>-1</sup>) were recorded. The genotypes were also evaluated for weevil damage, cracking and storage root defects. Two medium size roots were randomly selected per genotype for dry mass composition (DM%) determination. Dry mass composition was determined as described by Islam et al. (2002):

$$\text{Dry mass(\%)} = \frac{\text{Dry mass}}{\text{Fresh mass}} \times 100$$

The harvest index (HI) was calculated as:

$$\text{Harvest index(\%)} = \frac{\text{Total storage root fresh mass}}{\text{Total biomass (roots + vines)}} \times 100$$

### 5.2.2.3 Participatory selection data

In addition to collecting disease and agronomic data, participatory selection of the F<sub>1</sub> genotypes was also performed at two of the three sites namely, Namulonge and Kachwekano. The genotypes were separately evaluated before harvest and at harvest by a group of five scientists and a group of 10 farmers (five males and five females) at each site. The groups of scientists and farmers at both sites were different. The five scientists at NaCRRI, Namulonge and five scientists at KAZARDI, Kachwekano had a minimum qualification of a bachelor's degree in agricultural sciences and were employed by the National Agricultural Research Organisation (NARO). The selected farmers were knowledgeable about sweetpotato production and consumer preferences. At each site, the evaluation before harvest was carried out two days before harvesting the trial. Before the evaluation process was carried out, both groups at each site were familiarised with the selection procedure and criteria. Both groups used the same evaluation criteria. The traits considered were: Alternaria blight severity, SPVD severity; growth habit (spreading, erect);

leaf morphological traits (broad, small leaves, leaf colour); and general acceptability as a new cultivar (i.e. whether each participant considered the genotype suitable to become a cultivar). A rating scale of 1-5 was used for all the traits. For diseases, a severely infected genotype was scored 1 and a symptomless genotype, 5. For leaf morphology traits (broad or small leaves, leaf colour), and growth habit, 1 = poor and 5 = excellent.

For selection at harvest, the two groups at each site separately listed the traits that they wanted to use in the evaluation process and ranked them in order of importance. On this basis, each group developed a list of top five traits for scoring the genotypes (Table 5.7). For each trait, the participants individually scored each harvested plot in all three replications on a scale of 1-5 where 1 = trait absent and 5 = the genotype expressed the trait at a satisfactory level. Then the mean score for each trait was separately determined for each of the two groups per site. Roots were sampled from each plot of each genotype, boiled, taste tested and then scored for the following attributes: appearance of the flesh after cooking, sweetness, dry mass (hardness), fibre content and acceptability as a new cultivar. The same rating scale of 1-5 was used as above.

### 5.2.3 Data analysis

#### 5.2.3.1 AMMI analysis for the three sites data

The genotype x environment interaction (GEI) and associated stability of the genotypes across three sites for area under the disease progress curve (AUDPC) for *Alternaria* blight severity scores, SPVD severity scores, TRY, MRY, HI and DM% were analysed using the additive main effects and multiplicative interaction (AMMI) procedure in GENSTAT version 14 (Payne et al., 2011) based on the standard AMMI model (Gauch and Zobel, 1996):

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^N \lambda_n \gamma_{gn} \eta_{en} + \theta_{ge} + \xi_{ij}$$

Where:  $Y_{ge}$  is the yield (or other traits) of genotype  $g$  in environment,  $e$ ;  $\mu$  is the grand mean;  $\alpha_g$  is the genotype mean deviation;  $\beta_e$  is the environment mean deviation;  $N$  is the number of interaction principal component analysis (IPCA) axes retained in the model;  $\lambda_n$  is the eigenvalue of the interaction principal component analysis axis (IPCA)  $n$ ;  $\gamma_{gn}$  and  $\eta_{en}$  are genotype and environment IPCA scores for the  $n^{\text{th}}$  IPCA axis;  $\theta_{ge}$  is the residual of the GEI unaccounted for by the IPCA axes; and  $\xi_{ij}$  is the experimental error.

The AMMI analysis partitions the GEI sum of squares (SS) into IPCA axes. Only IPCA1 and IPCA2 were significant and the non-significant IPCA3 was considered as “statistical noise” and accounted for by the residual term. The interaction patterns of the genotypes and the

environments were graphically represented in a biplot of the respective IPCA1 scores (y-axis) versus the genotype and environmental means (x-axis) for the two main traits considered in this study, namely *Alternaria* blight AUDPC and TRY. In the biplot, displacement in the horizontal plane reflects differences in the mean performance, while displacement in the vertical plane reflects differences in interaction effects (Zobel et al., 1988).

### 5.2.3.2 Analysis of participatory selection data

The scores for each trait for each genotype at each of the two sites for each group were analysed by ANOVA in GENSTAT version 14 to obtain the mean scores for each trait per genotype, evaluation group and site. Weights were assigned to each scored trait such that the trait ranked first by a group was assigned a weight of 5 and that ranked fifth was assigned a weight of 1. For each genotype, the mean score for each trait was multiplied by the assigned weight then all five weighted scores were summed up to obtain an aggregate score for each genotype.

Aggregate weighting index used for the both the scientist and farmer groups:

$$\sum ATW = (AT_1 * W_5) + (AT_2 * W_4) + (AT_3 * W_3) + (AT_4 * W_2) + (AT_5 * W_1)$$

Where:  $AT_{1...5}$  = Attributes ranked 1...5; and  $W_5...W_1$  = assigned weight ranging from 5 to 1.

The aggregate scores of the genotypes at each site for each group were ranked to determine two separate rank orders (one per group) of the genotypes at each site. The ranks for each genotype per group were summed across the two sites (Kang, 1993) and the genotype with the lowest rank sum was the best over the two sites.

## 5.3 Results

### 5.3.1 Genotype x environment interaction and stability of the genotypes

#### 5.3.1.1 *Alternaria* blight

The genotypes, environments and genotype x environment interaction (GEI) mean squares (MS) were highly significant ( $P < 0.001$ ) for AUDPC (Table 5.1). The genotypes, environments and GEI accounted for 16.4, 24.5 and 21.8% of the total SS for AUDPC. Only IPCA1 was significant and accounted for 72.0% of the GEI SS. The genotype G14 had the smallest IPCA1 score of 0.00525 and was therefore the most stable (in terms of the interaction pattern captured by IPCA1) for *Alternaria* blight (Table 5.2). Genotype G28 with an IPCA1 value of -3.41636 was the least stable. NASPOT 1 (susceptible check) with the highest mean AUDPC value of 86.7 across the three sites was more susceptible than all the  $F_1$

genotypes evaluated. Tanzania (resistant check) was more resistant than any of the F<sub>1</sub> genotypes with the lowest mean AUDPC value of 46.1 across the three sites. Across the sites, G49, G13, G67, G14 and G65 had the lowest AUDPC values of 46.6, 48.7, 48.7, 49.1 and 51.1, respectively. Genotype G58 had the highest mean AUDPC value of 79.8 among the genotypes. At individual sites, G49, G13 and G14 were ranked the most resistant at Namulonge, Kachwekano and Serere, respectively. Genotype G58 was the most susceptible among the genotypes at Namulonge and Kachwekano with AUDPC values of 83.4 and 109.2, respectively. Genotype G68 had the highest AUDPC value of 80.3 at Serere. Of the three sites, genotypes at Kachwekano recorded the highest *Alternaria* blight severity with an average AUDPC value of 76.6.

**Table 5.1 AMMI analysis for Alternaria blight severity, sweetpotato virus disease severity score and total storage root yield for 23 sweetpotato genotypes evaluated at Namulonge, Kachwekano and Serere (2011B)**

Source of variation	df	AUDPC				SPVD				Total storage root yield (t ha <sup>-1</sup> )			
		SS	MS	% Total SS	% G x E SS	SS	MS	% Total SS	% G x E SS	SS	MS	% Total SS	% G x E SS
Total	206	126650	615			262.1	1.27			13574	65.9		
Treatments	68	79424	1168***	62.7		107.4	1.58*	41.0		10535	154.9***	77.6	
Genotypes	22	20809	946***	16.4		27.6	1.26	10.5		1312	59.7***	9.7	
Environments	2	31049	15525***	24.5		20.9	10.45***	8.0		6489	3244.7***	47.8	
Interaction	44	27566	626**	21.8		58.9	1.34	22.5		2734	62.1***	20.1	
IPCA1	23	19857	863***		72.0	39.9	1.73		67.8	1716	74.6***		62.8
IPCA2	21	7709	367		28.0	19.0	0.90		32.2	1018	48.5***		37.2
Error	132	46789	354			148.2	1.12			2701	20.5		

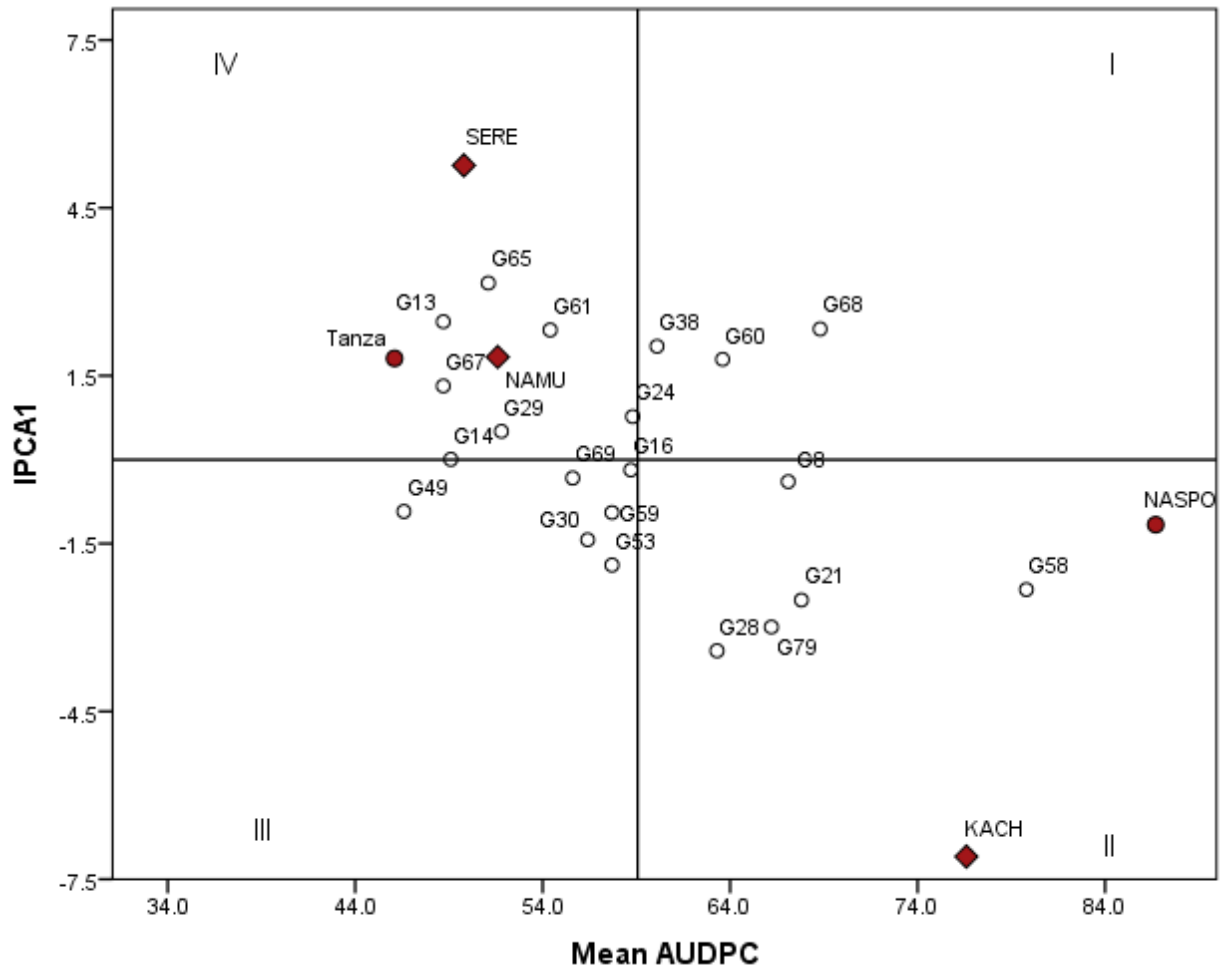
\* = significant at 0.05; \*\* = significant at P<0.01; \*\*\* = significant at P<0.001; AUDPC = area under disease progress curve for Alternaria blight severity; SPVD = sweetpotato virus disease severity scores (scores 1-9 used; 1 = no SPVD and 9 = SPVD causing stunted growth); df = degrees of freedom; SS = sum of squares; MS = mean square; % Total SS = percentage of total sum of squares; % G x E SS = percentage of genotype x site sum of squares

## 5.2 Mean AMMI performance estimates and ranking of the genotypes for Alternaria blight severity at Namulonge, Kachwekano and Serere (2011B)

Genotype	Overall mean AUDPC	IPCA1	IPCA2	Namulonge		Kachwekano		Serere	
				Mean	Rank	Mean	Rank	Mean	Rank
G8	67.1	-0.39336	1.83402	48.3	8	90.1	18	63.0	20
G13	48.7	2.46564	-1.92151	56.3	18	45.5	1	44.3	9
G14	49.1	0.00525	-1.71079	51.0	10	63.7	7	32.7	1
G16	58.7	-0.18533	-1.51633	59.1	20	74.9	13	42.0	8
G21	67.8	-2.50861	-0.17353	56.4	19	102.6	19	44.3	10
G24	58.8	0.77041	1.21857	45.6	5	72.6	10	58.3	18
G28	63.3	-3.41636	-0.77916	53.7	16	103.6	20	32.7	1
G29	51.8	0.50558	-1.29120	52.2	13	63.5	6	39.7	5
G30	56.4	-1.43335	0.07224	45.6	6	84.0	16	39.7	5
G38	60.1	2.02679	0.42608	53.7	17	63.7	8	63.0	20
G49	46.6	-0.92678	1.82993	26.8	1	73.3	12	39.7	5
G53	57.7	-1.88434	-0.80294	51.0	11	87.1	17	35.0	3
G58	79.8	-2.32293	-2.78913	83.4	23	109.2	22	46.7	12
G59	57.7	-0.94515	1.41543	40.3	4	83.9	15	49.0	13
G60	63.6	1.79363	-1.85431	69.6	22	65.3	9	56.0	16
G61	54.4	2.31667	-0.01823	51.0	12	55.2	4	57.0	17
G65	51.1	3.15645	0.61656	45.6	7	46.9	2	60.7	19
G67	48.7	1.31573	1.03116	37.6	2	58.3	5	50.3	14
G68	68.8	2.33462	2.15257	53.2	14	72.9	11	80.3	23
G69	55.6	-0.32871	1.71497	37.6	3	77.9	14	51.3	15
G79	66.2	-2.99241	0.82728	48.3	9	106.0	21	44.3	11
NASPOT 1	86.7	-1.16207	1.79274	66.7	21	115.0	23	78.3	22
Tanzania	46.1	1.80864	-2.07441	53.3	15	47.3	3	37.7	4
<b>Mean</b>	<b>59.3</b>			<b>51.6</b>		<b>76.6</b>		<b>49.8</b>	

AUDPC = area under disease progress curve for Alternaria blight severity; IPCA = Interaction principal component analysis

In the AMMI biplot of IPCA1 versus AUDPC mean values for genotypes and environments (Figure 5.1), genotypes on the right hand side of the vertical line are the most susceptible to Alternaria blight and those on the left are the most resistant. Genotypes closest to the horizontal line are more stable for the expression of Alternaria blight across the three sites. Genotypes G8 and NASPOT 1 are stable for the disease but they had above average AUDPC values. Genotypes G14, G16, G24, G29, G49, G59 and G69 are stable for the disease with below average AUDPC values.



**Figure 5.1 Biplot of IPCA1 scores versus genotype and environment AUDPC means**

**Key**

Check genotypes: NASPO = NASPOT 1; Tanza = Tanzania ●

F<sub>1</sub> test genotypes: G8, G13, G14, G16, G21, G24, G28, G29, G30, G38, G49, G53, G58, G59, G60, G61, G65, G67, G68, G69 and G79 ○

Site: NAMU = Namulonge; KACH = Kachwekano; SERE = Serere ◆

None of the sites was very stable for Alternaria blight severity but Namulonge was more stable than Serere and had several genotypes specifically adapted to it (Figure 5.1). Kachwekano was a high disease pressure site and the least stable with high interaction with the genotypes.

**5.3.1.2 Sweetpotato virus disease**

The MS for the environments were highly significant ( $P < 0.001$ ) for SPVD and not significant ( $P > 0.05$ ) for the genotypes and GEI (Table 5.1). Very low severity levels of SPVD were recorded for these genotypes with a mean score of 1.9 across sites (Appendix 1). Serere recorded the highest SPVD severity with a mean score of 2.3 while Namulonge had the lowest



mean severity score of 1.6. Plants were not inoculated with SPVD and the precaution was taken to select vines that were visually free of symptoms of SPVD and its component diseases. Generally, this resulted in low infection levels for SPVD and because of these low SPVD levels, confounding was not reported. Nevertheless, such low SPVD levels were unexpected but were probably largely due to the prevailing weather conditions during that season in combination with the low inoculum levels.

### **5.3.1.3 Total storage root yield**

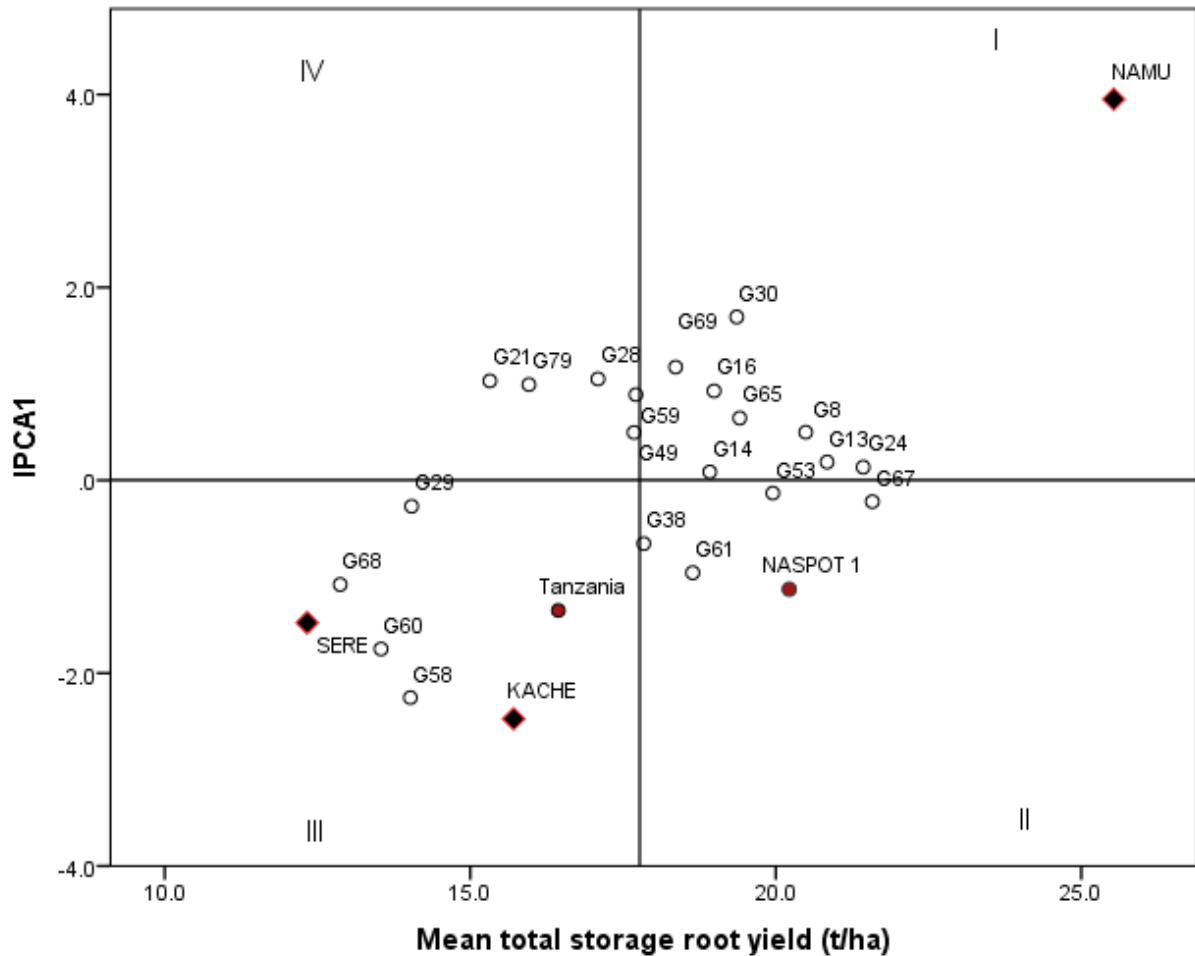
The genotypes, environments and GEI MS were highly significant ( $P < 0.001$ ) for TRY (Table 5.1). The genotypes, environments and GEI SS accounted for 9.7, 47.8 and 20.1% of the total SS for TRY, respectively. Both IPCA1 and IPCA2 were significant and accounted for 62.8 and 37.2% of the GEI SS. Genotypes G14 and G13 were the most stable for TRY across the sites with IPCA1 scores of 0.08633 and 0.18901, respectively (Table 5.3). Genotypes G58 and G60 were the least stable with IPCA1 values of 2.2542 and -1.74938, respectively. Across sites, G67, G24, G13, G53 and G65 had the highest TRY of 21.6, 21.4, 20.8, 19.9 and 19.4 t ha<sup>-1</sup>, respectively. Genotypes G68, G60, G58, G29 and G21 had the lowest TRY of 12.9, 13.5, 14.0, 14.0 and 15.3 t ha<sup>-1</sup>, respectively across sites. The mean TRY across genotypes of 25.5 t ha<sup>-1</sup> recorded at Namulonge was the highest of the three sites while the 12.3 t ha<sup>-1</sup> recorded at Serere was the lowest. The most outstanding genotypes at Namulonge were G30, G69 and G16 with yields of 34.0, 31.3 and 30.6 t ha<sup>-1</sup>, respectively. There was no consistency in the ranking of the genotypes in that highly ranked genotypes at one site ranked poorly at the other sites.

Most of the genotypes were clustered around the intersection of the vertical and horizontal lines of the biplot in quadrant 1 (Figure 5.2). The further genotypes in quadrants I and II were from the vertical line the higher their yields and the further away from the horizontal line the more unstable. The further genotypes in quadrants III and IV were from the vertical line the lower their yields and the further away from the horizontal line the more unstable. Genotypes G53, G67, G14, G13, G29 and G24 were closest to the horizontal line and were the most stable for TRY, while G58 and G30 were the furthest from the horizontal line and the least stable for TRY. Genotypes G59, G49 and G38 are average yielders. Genotype 67 was the highest yielding of the F<sub>1</sub> genotypes and was stable. NASPOT 1 was high yielding but unstable while Tanzania was low yielding and unstable. Namulonge was a very high yielding environment but unstable with very low interaction with the genotypes. Kachwekano and Serere were low yielding and unstable environments but with genotypes G68, G60 and G58 specifically adapted to them.

**5.3 Mean AMMI performance estimates and ranking of the genotypes for total storage root yield (t ha<sup>-1</sup>) at Namulonge, Kachwekano and Serere (2011B)**

Genotype	Overall Mean	IPCA1	IPCA2	Namulonge		Kachwekano		Serere	
				Mean	Rank	Mean	Rank	Mean	Rank
G8	20.5	0.49816	0.02743	30.2	4	17.2	8	14.1	7
G13	20.8	0.18901	-0.29646	29.1	7	17.4	7	16.0	4
G14	18.9	0.08633	1.44211	27.7	11	20.5	3	8.6	20
G16	19.0	0.92707	0.52908	30.6	3	16.0	13	10.4	15
G21	15.3	1.03024	-1.23778	26.4	14	7.2	23	12.3	11
G24	21.4	0.13619	-0.90956	29.2	6	16.4	11	18.7	2
G28	17.1	1.05036	-1.81533	28.0	10	7.4	22	15.9	5
G29	14.0	-0.26961	0.32112	20.8	19	13.4	18	7.9	22
G30	19.4	1.69363	0.54536	34.0	1	14.5	14	9.6	18
G38	17.8	-0.65650	0.38515	23.1	18	18.4	5	12.0	12
G49	17.7	0.49669	-0.40570	27.1	13	13.2	19	12.7	10
G53	20.0	-0.13348	-1.50316	26.3	15	14.0	17	19.5	1
G58	14.0	-2.25420	-1.11901	12.2	23	14.4	15	15.5	6
G59	17.7	0.88763	-0.14469	28.8	9	13.0	20	11.3	13
G60	13.5	-1.74938	0.12783	14.4	22	16.1	12	10.2	16
G61	18.6	-0.95907	1.59782	23.3	16	23.3	1	9.3	19
G65	19.4	0.64465	0.87561	30.1	5	18.1	6	10.1	17
G67	21.6	-0.22108	1.00442	28.9	8	22.7	2	13.1	9
G68	12.9	-1.08135	0.27452	16.4	21	14.2	16	8.0	21
G69	18.4	1.17342	1.16814	31.3	2	16.5	10	7.3	23
G79	16.0	0.99172	-0.44067	27.3	12	10.2	21	10.4	14
NASPOT 1	20.2	-1.13006	-0.19483	23.3	17	20.3	4	17.0	3
Tanzania	16.4	-1.35035	-0.23140	18.7	20	17.0	9	13.7	8
<b>Mean</b>	<b>17.9</b>			<b>25.5</b>		<b>15.7</b>		<b>12.3</b>	

IPCA = Interaction principal component analysis



**Figure 5.2 Biplot of IPCA1 scores versus genotype and environment mean total storage root yield ( $t\ ha^{-1}$ )**

**Key**

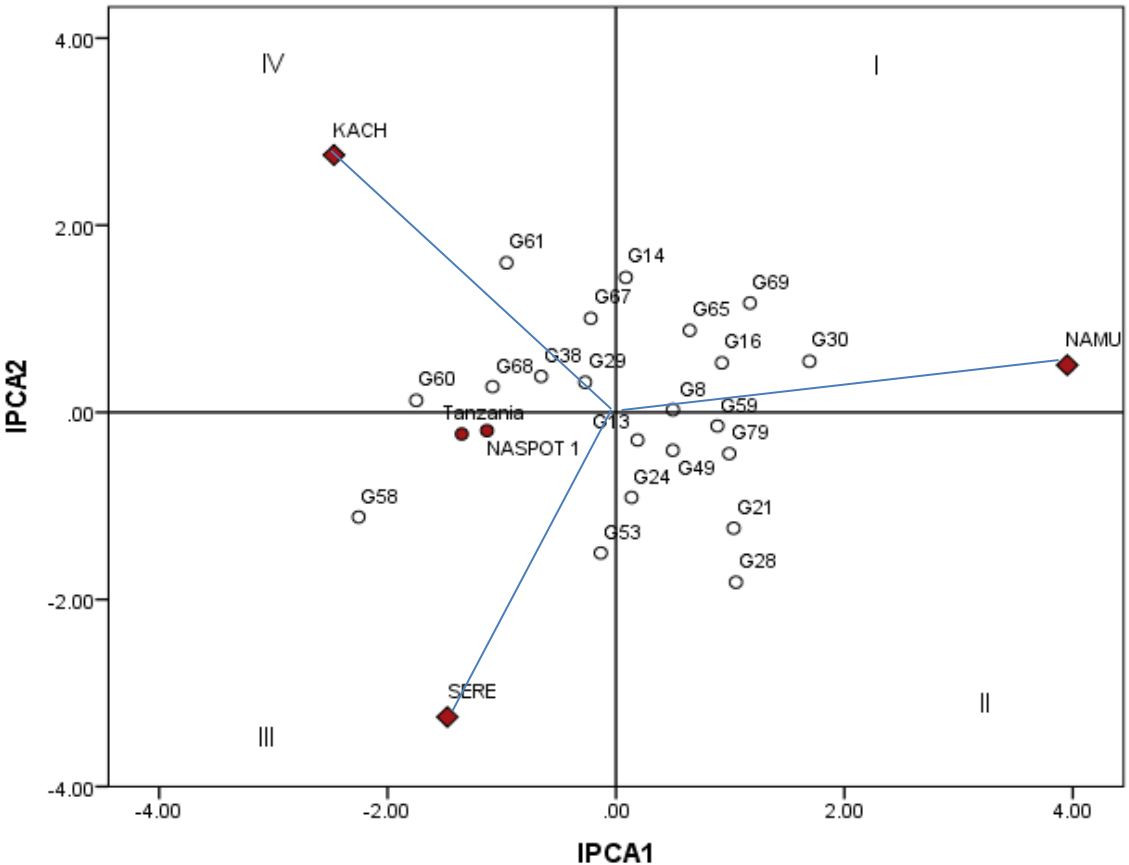
Check genotypes: NASPOT 1; Tanzania ●

F<sub>1</sub> test genotypes: G8, G13, G14, G16, G21, G24, G28, G29, G30, G38, G49, G53, G58, G59, G60, G61, G65, G67, G68, G69 and G79 O

Site: NAMU = Namulonge; KACH = Kachwekano; SERE = Serere ◆

In the AMMI biplot of the two significant axes IPCA1 vs IPCA2 for TRY, the genotypes and the three environments generally dispersed around the origin (centre) of the biplot (the sites more so than the genotypes) indicating strong interactions between the genotypes and environments in response to the abiotic or biotic factors underlying or driving the IPCA1 & 2 scores (Figure 5.3). Genotypes or environments with coordinates that are close to each other in an IPCA1 vs IPCA2 biplot have similar interaction response patterns while those distant from each have different patterns. Genotypes near the origin are non-sensitive to environmental interactive forces and those distant from the origin are sensitive and have large interactions. Genotypes G13, G8, G49 and G29 were positioned close to the origin indicating minimal interaction of these genotypes

with the environments. The remaining 17 genotypes and checks (Tanzania and NASPOT 1) were positioned further away from the origin and therefore had strong interactions with some of the environments. The longer the vector from the origin to the coordinates of an environment the stronger the interaction that environment exerts on the genotypes. Genotypes that fall in the same quadrant as an environment have positive interaction with that environment whereas those in the diagonally opposite quadrant to an environment have negative interaction with that environment.



**Figure 5.3 Biplot of IPCA1 scores versus IPCA2 scores for genotype and environment mean total storage root yield ( $t\ ha^{-1}$ )**

**Key**

- Check genotypes: NASPOT 1; Tanzania ●
- F<sub>1</sub> test genotypes: G8, G13, G14, G16, G21, G24, G28, G29, G30, G38, G49, G53, G58, G59, G60, G61, G65, G67, G68, G69 and G79 ○
- Site: NAMU = Namulonge; KACH = Kachwekano; SERE = Serere ◆

#### **5.3.1.4 Marketable root yield**

The effects of genotypes, environments and GEI were significant for MRY (Table 5.4). Environments effects were more important than the genotypes and GEI effects with each respectively contributing 43.0, 12.5 and 19.3% to the total SS. Both IPCA1 and IPCA2 were highly significant ( $P < 0.001$ ) and accounted for 66.4 and 33.7% of the GEI SS. Across the three environments G67, NASPOT 1, G24, G53 and G65 had the highest mean MRY of 9.2, 8.9, 8.8, 8.7 and 8.7 t ha<sup>-1</sup>, respectively (Appendix 5.2). At Namulonge, G30, G16, G24 and G65 had the highest MRY of 15.0, 13.1, 12.9 and 12.7 t ha<sup>-1</sup>, respectively. At Kachwekano, G65, G60, G13 and NASPOT 1 had the highest MRY of 9.9, 9.2, 8.9, 8.0 t ha<sup>-1</sup>, respectively. At Serere, genotypes G49, NASPOT 1, G53 and G8 had the highest MRY of 8.5, 7.7, 6.9 and 6.8 t ha<sup>-1</sup>, respectively.

#### **5.3.1.5 Harvest index**

Effects of the environments were highly significant ( $P < 0.001$ ) and that of the genotypes and GEI were not significant ( $P < 0.001$ ) (Table 5.4). The environments accounted for 12.6% of the total SS. Genotype G79 had the highest mean HI of 0.64 (Appendix 5.3). Genotype G21 had the lowest mean HI of 0.41. Genotypes G38, G24, G13 and NASPOT1 had the lowest IPCA1 scores of 0.0097, 0.00592, 0.00788 and 0.0090, respectively. Genotypes G16, G59 and G79 had the highest HI at Namulonge, Kachwekano and Serere of 0.67, 0.74 and 0.75, respectively.

#### **5.3.1.6 Dry mass composition**

The environments effects were significant ( $P < 0.05$ ) for DM% whereas the genotypes and GEI effects were not significant (Table 5.4). Only IPCA1 was significant accounting for 65.3% of the total GEI SS. The check cultivars, Tanzania and NASPOT 1, had lower IPCA1 values than all the F<sub>1</sub> genotypes and were thus more stable for DM% than the F<sub>1</sub> genotypes. Genotype G58 with a mean DM% across sites of 33.7% was the most stable among the F<sub>1</sub> genotypes with an IPCA1 score of -0.05866 (Appendix 5.4). Genotype G68 recorded the highest mean DM% of 33.9% across sites while G60 had the lowest at 29.9%. Genotypes at Serere had the highest mean DM% of 33.2% with G14 and G69 having the highest values of 37.3 and 36.5%, respectively.

**Table 5.4 AMMI analysis for marketable storage root yield, harvest index and dry mass composition for 23 sweetpotato genotypes evaluated at Namulonge, Kachwekano and Serere (2011B)**

Source of variation	df	Marketable storage root yield (t ha <sup>-1</sup> )				Harvest index				Dry mass composition			
		SS	MS	% Total SS	% G x E SS	SS	MS	% Total SS	% G x E SS	SS	MS	% Total SS	% G x E SS
Total	206	2585.1	12.55			6.254	0.034			3159.9	15.34		
Treatments	68	1934.8	28.45***	74.8		2.607	0.038*	41.7		1256.2	18.47	39.8	
Genotypes	22	323.1	14.69***	12.5		0.454	0.021	7.3		244.0	11.09	7.8	
Environments	2	1112.5	556.25***	43.0		0.785	0.392***	12.6		95.8	47.90*	3.0	
Interaction	44	499.2	11.35***	19.3		1.368	0.031	21.9		916.4	20.83	29.0	
IPCA1	23	331.2	14.40***		66.4	0.804	0.035		58.8	598.0	26.00*		65.3
IPCA2	21	168.0	8.00***		33.7	0.564	0.027		41.2	318.4	15.16		34.7
Error	132	581.8	4.44*			3.523	0.028			1809.0	13.70		

\* = significant at P<0.05; \*\* = significant at P<0.01; \*\*\* = significant at P<0.001; df = degrees of freedom; SS = sum of squares; MS = mean square; % Total SS = percentage of total sum of squares; % G x E SS = percentage of genotype x site sum of squares

## **5.3.2 Participatory selection**

### **5.3.2.1 Genotype evaluation before harvest**

For the evaluation done before harvest, the scientists and farmers at both sites selected different genotypes (Table 5.5). Based on the selection index, the scientists at Namulonge ranked NASPOT 1, G58, G79, G69 and G2 and at Kachwekano ranked G60, G67, NASPOT 1, G49 and G16 as their most preferred genotypes. Similarly, the farmers at Namulonge ranked G58, G59, NASPOT 1, G21 and G29 and at Kachwekano G14, G29, NASPOT 1, G60 and G16 as their most preferred genotypes. NASPOT 1, G21, G53, G58 and 65 were ranked as the best across the groups and sites.

**Table 5.5 Scientists and farmers' selection and ranking of genotypes before harvest at Namulonge and Kachwekano (2011B)**

Genotype	Namulonge scientists		Namulonge farmers		Kachwekano scientists		Kachwekano farmers		Rank sum	Overall rank
	Aggregate	Rank	Aggregate	Rank	Aggregate	Rank	Aggregate	Rank		
G8	36	10	27	8	23	22	16	9	49	14
G13	37	5	28	4	23	22	15	11	42	9
G14	20	23	24	12	29	10	30	1	46	11
G16	24	21	20	18	34	5	21	5	49	15
G21	38	5	28	4	29	10	21	5	24	2
G24	32	13	17	21	29	10	13	17	61	20
G28	23	22	25	11	30	9	12	21	63	21
G29	27	19	28	4	29	10	29	2	35	6
G30	37	5	21	17	29	10	13	17	49	16
G38	32	13	27	8	25	20	14	13	54	18
G49	31	16	22	15	35	4	18	8	43	10
G53	37	5	28	4	29	10	16	9	28	3
G58	47	2	32	1	28	17	14	13	33	4
G59	31	16	32	1	26	18	12	21	56	19
G60	33	12	16	22	42	1	24	3	38	8
G61	34	11	18	19	24	21	13	17	68	22
G65	38	4	27	8	34	5	13	17	34	5
G67	27	19	22	15	39	2	14	13	49	17
G68	31	16	16	22	29	10	12	21	69	23
G69	45	3	24	12	31	7	14	13	35	7
G79	45	3	23	14	26	18	15	11	46	12
NASPOT 1	50	1	30	3	39	2	24	3	9	1
Tanzania	32	15	18	19	31	7	21	5	46	13

Aggregate = sum of the weighted attributes for each genotype per group; Rank sum = sum of the genotype rank across the four groups



The Spearman's correlation between scientists and farmers' rankings at Namulonge was significant ( $P < 0.05$ ) and positive ( $r = 0.324$ ). The Spearman's correlation between scientists and farmers' rankings at Kachwekano was significant ( $P < 0.05$ ) and positive ( $r = 0.282$ ) (Table 5.6).

**Table 5.6 Spearman's rank correlations between the scientists and farmers' genotype rankings before harvest at Namulonge and Kachwekano (2011B)**

NS	-			
NF	<b>0.342*</b>	-		
KS	-0.153	<b>-0.305*</b>	-	
KF	-0.04	0.103	<b>0.283*</b>	-
	NS	NF	KS	KF

NS = Namulonge scientists; NF = Namulonge farmers; KS = Kachwekano scientists; KF = Kachwekano farmers;  
\* = Significant at  $P < 0.05$

### 5.3.2.2 Genotype evaluation at harvest

For the evaluation at harvest, each group listed their own set of traits that they considered important in desirable sweetpotato genotypes and ranked these attributes (Table 5.7). Storage root yield was the most important trait ranked first by all four groups followed by root size, weevil resistance, root shape and skin colour.

**Table 5.7 Attributes used by scientists and farmers at harvest for the participatory selection process at Namulonge and Kachwekano (2011B)**

Namulonge scientists		Namulonge farmers		Kachwekano scientists		Kachwekano farmers	
Attribute	Rank	Attribute	Rank	Attribute	Rank	Attribute	Rank
Root yield	1	High root yield	1	High yield	1	High yield	1
Large roots	2	No weevil damage	2	No weevil damage	2	Large roots	2
Root shape	3	Big roots	3	Large roots	3	Root shape	3
Root number	4	Skin colour (red/cream)	4	Shape of roots	4	Straight roots	4
Skin colour (red)	5	Long straight roots	5	Root skin colour	5	No cracking	5
No surface defects	6	Flesh colour (white)	6	No cracking	6		
Root flesh colour	7	Quantity of sap	7	Flesh colour	7		
Sap content	8	No cracking	8				

At harvest, on the basis of the selection index, the ranked order of the scientists' selected genotypes at Namulonge was: G30, G28, G49, G67 and G24; and at Kachwekano was: G29, G49, G30, NASPOT 1 and G14 (Table 5.8). The ranked order of the farmers' selections at Namulonge was: G8, G30, G53, G29 and G49; and at Kachwekano was: G21, G24, G30, G29 and G14.

**Table 5.8 Scientists and farmers' selection and ranking of genotypes at harvest at Namulonge and Kachwekano (2011B)**

Genotype	Namulonge scientists		Namulonge farmers		Kachwekano scientists		Kachwekano farmers		Across four groups	
	Aggregate	Rank	Aggregate	Rank	Aggregate	Rank	Aggregate	Rank	Rank Sum	Final rank
G8	52.0	16	71.3	1	36.7	18	23.6	22	57	16
G13	41.6	23	60.3	22	38.3	14	34.0	13	72	23
G14	52.7	14	64.7	16	49.6	5	42.7	5	40	7
G16	47.0	22	64.3	18	44.3	9	37.7	10	59	18
G21	48.7	19	64.7	15	34.3	23	50.0	1	58	17
G24	61.3	5	65.3	12	47.7	6	49.0	2	25	4
G28	67.4	2	66.3	8	40.3	11	40.0	7	28	5
G29	56.4	12	67.7	4	56.0	1	44.7	4	21	2
G30	70.0	1	68.7	2	52.7	3	47.0	3	9	1
G38	47.7	20	64.3	19	39.0	12	30.0	19	70	22
G49	66.7	3	67.3	5	55.4	2	36.7	11	21	3
G53	57.4	10	67.7	3	35.0	20	21.0	23	56	13
G58	58.6	6	56.3	23	35.0	20	31.0	16	65	20
G59	57.7	8	65.3	10	35.7	19	40.6	6	43	8
G60	47.3	21	65.3	11	45.4	7	40.0	7	46	9
G61	57.0	11	67.0	6	34.6	22	32.3	15	54	11
G65	52.3	15	62.6	20	37.3	15	35.0	12	62	19
G67	62.7	4	67.0	7	37.0	16	30.0	19	46	10
G68	50.0	18	65.7	9	38.7	13	31.0	16	56	14
G69	58.6	7	64.7	17	41.7	10	27.0	21	55	12
G79	51.0	17	65.0	14	37.0	16	30.7	18	65	21
NASPOT1	57.7	8	65.2	13	52.1	4	39.6	9	34	6
Tanzania	53.4	13	60.4	21	44.5	8	32.9	14	56	15

Aggregate score based on weighted selection index (Individual trait scores provided in Appendices 5.6 and 5.7)

At harvest, the Spearman's correlation between scientists and farmers' rankings at Namulonge was highly significant ( $P < 0.01$ ) and positive ( $r = 0.412$ ) and that between scientists and farmers at Kachwekano was also highly significant ( $P < 0.01$ ) and positive ( $r = 0.440$ ) (Table 5.9). The other rank correlations were non-significant.

### 5.9 Spearman's rank correlation between the scientists and farmers' genotype rankings at Namulonge and Kachwekano at harvest (2011B)

NS	-			
NF	<b>0.412**</b>	-		
KS	0.206	0.093	-	
KF	0.115	0.028	<b>0.440**</b>	-
	NS	NF	KS	KF

NS = Namulonge scientists; NF = Namulonge farmers; KS = Kachwekano scientists; KF = Kachwekano farmers;

\*\* = significant at  $P < 0.01$

The quality traits (mostly organoleptic) of the genotypes that were evaluated at harvest included sweetness (taste), root firmness (hardness), root fibre content, appearance and general acceptability based on taste and appearance (Appendices 5.8 and 5.9). At Namulonge, scientists ranked G24, NASPOT 1, Tanzania, G38 and G28 as the best and at Kachwekano G68, NASPOT1, G14, G60 and G29 were ranked as the best genotypes. Farmers at Namulonge ranked NASPOT 1, G28 and G38, G68 and Tanzania as the best genotypes, and at Kachwekano G14, G29, G68, G60 and NASPOT 1 were ranked as the best. Genotypes NASPOT 1, G68, G24, G60 and G53 were the best ranked across the groups.

**Table 5.10 Scientists and farmers' selection and ranking of quality traits of genotypes at harvest at Namulonge and Kachwekano (2011B)**

Genotype	Namulonge scientists		Namulonge farmers		Kachwekano scientists		Kachwekano farmers		Rank sum	Overall rank
	Aggregate	Rank	Aggregate	Rank	Aggregate	Rank	Aggregate	Rank		
G8	47.0	13	39.5	18	41.0	18	39.5	18	67	19
G13	42.0	20	35.0	21	40.5	19	45.5	11	71	21
G14	39.5	21	43.0	12	55.5	3	56.5	1	37	6
G16	37.5	23	42.5	13	45.0	16	43.0	15	67	20
G21	45.0	16	32.0	23	35.5	23	33.0	21	83	23
G24	61.5	1	50.0	6	48.5	10	44.5	12	29	3
G28	54.5	5	55.5	2	38.0	21	42.0	16	44	9
G29	43.5	17	42.5	14	55.0	5	55.0	2	38	7
G30	51.0	7	48.5	8	50.5	8	31.5	22	45	12
G38	55.0	4	53.5	3	46.0	14	30.5	23	44	10
G49	43.5	18	39.0	19	47.0	12	41.5	17	66	18
G53	47.5	11	49.5	7	50.5	9	49.5	7	34	5
G58	46.5	15	47.5	10	38.5	20	51.5	6	51	14
G59	43.5	19	48.5	9	45.5	15	47.5	9	52	15
G60	48.5	9	40.0	16	55.5	4	53.5	4	33	4
G61	48.5	10	46.0	11	51.0	7	44.0	14	42	8
G65	49.0	8	41.5	15	48.5	11	37.0	19	53	17
G67	53.5	6	40.0	17	46.5	13	48.5	8	44	11
G68	47.5	12	52.5	4	62.0	1	54.0	3	20	2
G69	38.0	22	36.5	20	36.0	22	44.0	13	77	22
G79	47.0	14	34.0	22	51.5	6	46.0	10	52	16
NASPOT 1	58.5	2	57.0	1	56.0	2	53.0	5	10	1
Tanzania	58.0	3	51.0	5	43.5	17	36.5	20	45	13

Aggregate score based on weighted selection index (individual trait scores provided in Appendix 5.8 and 5.9)

The positive Spearman's correlation ( $r=0.605$ ) between scientists and farmers' rankings at Namulonge was highly significant ( $P<0.01$ ) (Table 5.11). The positive Spearman's rank correlation ( $r=0.552$ ) between scientists and farmers' ranking at Kachwekano was also significant ( $P<0.01$ ).

**Table 5.11 Spearman's rank correlation between scientist and farmers' genotype rankings for quality traits at harvest at Namulonge and Kachwekano (2011B)**

NS	-			
NF	0.605**	-		
KS	0.217	0.275*	-	
KF	-0.229	0.058	0.552**	-
	NS	NF	KS	KF

KF= Kachwekano farmers; KS= Kachwekano scientists; NF = Namulonge farmers; NS = Namulonge scientists;

\*\* =significant at  $P<0.01$ ; \* = significant at  $P <0.05$

## 5.4 Discussion

The objectives of this study were to evaluate and identify  $F_1$  genotypes with wide and specific stable performance over three sites for *Alternaria* blight resistance, TRY and other farmer preferred traits. Additionally, the ranking of the genotypes by two different groups of scientists and farmers at two of the sites for selected traits were compared using Spearman's rank correlations.

### 5.4.1 Performance and stability of the genotypes

The severity of the disease was higher at Kachwekano than at the other two sites (Table 5.2). The AMMI analysis revealed that the *Alternaria* blight was influenced more by environmental effects, than by the GEI effects and least by genotypes effects. During the 2011B season, Kachwekano did not receive as much rainfall as Namulonge but the disease was more severe at this site. During the PRA conducted in 2010, some farmers in Luwero reported the disease to be more severe during the dry season than during the wet season. It is possible that the disease infected the crop during the first month after planting when there was sufficient moisture and the symptoms became visible later on when the crop was stressed due to insufficient moisture. Mwanga et al. (2007b) described Serere as a low pressure area for *Alternaria* blight. However, this study has provided an indication that the effect of *Alternaria* blight under natural infestation in Serere is increasing since the severity was not significantly less than that of Namulonge. However, this can only be confirmed after

obtaining data for two or more seasons. Should the trend be confirmed, farmers at Serere will require *Alternaria* blight resistant genotypes and this would necessitate evaluation of all the popular sweetpotato genotypes in the area for resistance to the disease in order to identify those with good levels of resistance.

Resistance of the genotypes across sites to *Alternaria* blight was not consistent, with some genotypes having lower AUDPC values at one site and higher values at another site. However, some genotypes maintained lower AUDPC values across sites and if these genotypes can maintain this consistency in subsequent evaluations (particularly over more seasons) and also meet the required performance levels for other important traits then they will be recommended to the farmers for cultivation in all the tested and similar sites/environments. Those that have consistent, good performance at particular sites will be recommended for those sites. Genotypes G49, G67, G69, 59 and G24 were the best genotypes at Namulonge. Genotypes G13 and G65 performed better than the check, Tanzania at Kachwekano. Similarly, G14, G28 and G53 were also better than the Tanzania at Serere. Thus these genotypes are well adapted to those sites. Genotypes G49, G13, G67 and G14 recorded lower mean AUDPC values across sites and should be further evaluated for even wider adaptation.

The AMMI biplot provided an indication of the stability of the different genotypes for *Alternaria* blight. In this context, stability means a genotype that maintains the same level of disease severity, either high or low across sites. Genotypes that are stable for low *Alternaria* blight severity and good yields are desired for this programme. Stability of genotypes G14, G16, G24, G29, G49, G59 and G69 for low *Alternaria* blight severity implies that these genotypes can be grown in all of the test sites and maintain low disease severities. They can also be used as sources of resistance in breeding for *Alternaria* blight resistance. Genotypes NASPOT 1 and G8 expressed stable but above average AUDPC values. This implies that these genotypes can only be grown in areas of low *Alternaria* blight pressure or may need fungicide protection when grown in high disease pressure areas. Kachwekano is a high *Alternaria* blight pressure site; therefore it is ideal for evaluating the resistance of germplasm to the disease while Namulonge and Serere are ideal for germplasm multiplication.

The high significance ( $P < 0.001$ ) of the effects of genotypes, environments and GEI for TRY implied that all these factors are important in determining the expression of this trait. However, environmental effects were more important than genotypes and GEI effects. Namulonge was the highest yielding site with a mean TRY of  $25.5 \text{ t ha}^{-1}$  and Serere was the lowest yielding site with a

mean of 12.3 t ha<sup>-1</sup>. The cause of such high variation in yield was in all likelihood the amount of rainfall received during the season. At Kachwekano and Serere, the crops received reasonable amounts of rainfall only during the first month after planting but very little in the subsequent months unlike Namulonge which had good rainfall for the first three months after planting (Appendix 5.10). The yield recorded at Namulonge which ranged between 12.2 (G58) and 34.0 t ha<sup>-1</sup> (G30) is an indication of the high yield potential of this set of genotypes. However, the full genotype yield potential was not realised at the other two sites due to moisture stress and, since this evaluation was done over one season, it may not provide a definitive indication of the actual yield potential of these genotypes at those sites. However, the best genotypes for TRY across the three sites were G67 (21.6 t ha<sup>-1</sup>) and G24 (21.4 t ha<sup>-1</sup>).

The AMMI biplot provided an indication of the stability of the genotypes for TRY. Genotypes G53, G67, G14, G13, and G29 were very close to the horizontal line and therefore the most stable. These genotypes are widely adapted and can be grown at any of the three test sites and should give good yields. Provided the necessary agronomic requirements are available, they can be recommended to farmers at all three sites. Genotypes G68, G60 and G58 were low yielding and specifically adapted to the low yield potential sites of Kachwekano and Serere and may not perform well outside these sites. In Uganda, superiority of a genotype in terms of yield and stability amounts to nothing if it falls short with respect to DM%. Most Ugandans prefer genotypes with high DM% and the National Sweetpotato Program has also adopted 30% as the benchmark for DM% (Mwanga et al., 2007a). In this study, all the genotypes had acceptable levels of DM% and there were no significant differences ( $P < 0.05$ ) among them. Genotypes G68, G58 and G13 had the highest mean DM% of 33.9, 33.7 and 33.7%, respectively.

Only the environments effects were significant ( $P < 0.001$ ) for HI. Thus for this set of genotypes the environment may be the main determining factor in the expression of HI. The average HI of the genotypes ranged from 41% (G21) to 64% (G79). These are good HI indicating a fair to predominant distribution of assimilates to the roots over the foliage. According to Bhagsari and Ashley (1990), a high HI (>50%) in sweetpotato indicates that storage roots constitute the main sink for photosynthate. They further showed that HI is positively correlated with TRY and dry mass yield. Therefore, a high HI is generally a good indicator of a high yielding genotype. A low HI associated with high above ground biomass can also be useful where sweetpotato foliage is used as livestock feed. Genotypes G21 and G49 with a larger proportion of foliage than storage roots would be most suited for this purpose. The best five genotypes overall in terms of HI were G79, G38, G24, G8 and Tanzania.



### 5.4.2 Participatory clonal selection

This was a preliminary study and a follow up on the participatory rural appraisal carried out in January 2010. At the two selection stages, before harvest and at harvest, the scientists and farmers at the two sites ranked some of the genotypes similarly and in other instances differently. The significant ( $P < 0.05$ ), positive Spearman's rank correlation between scientists and farmers at each site ( $r = 0.342$  for Namulonge,  $r = 0.283$  for Kachwekano) indicated that the two groups ranked many genotypes in the same way before harvest. Therefore, at each site the scientists in this study are capable of selecting genotypes that have farmer preferred traits. The groups of scientists at the two sites selected different genotypes and so did the farmers. Since they based their selection on crop vigour, the cause of the difference in genotype selection was likely to be the differences in the performances of the genotypes across the sites due to the poor weather conditions at Kachwekano, which did not receive enough rainfall during the trial (Appendix 5.10). Ranking of genotypes before harvest may be influenced by the amount of aboveground foliage produced particularly the leaves which at that stage are the economic yield component of the crop. On the other hand, farmers may prefer genotypes with more upright growth habit than prostrate growth habit with spreading vines. However, the aboveground characteristics of any genotype may not always be a good indicator of belowground performance.

At harvest, most of the attributes identified by the scientists and farmers were similar but the ranking of the genotypes differed. Just as in any formal selection system where yield is considered as a major criterion (Joshi et al., 1997), yield was ranked the number one trait by the groups. Scientists and farmers at both sites preferred high-yielding genotypes with large storage roots which implies the converse that high yielding genotypes that produce small roots are not preferred. This is certainly the case where the farmers are market oriented. The buyers select and pay only for the large roots and leave the small ones or take them at no cost. Abidin et al. (2002) in north-eastern Uganda, also reported that farmers prefer genotypes that produce numerous, large storage roots, which tend to also have large overall yields. Similarly, Ndirigwe et al. (2005) in Rwanda reported that farmers rejected one cultivar which was high yielding because it had small size storage roots. In addition to storage root size, shape of the storage root was identified as an important trait by all groups except farmers at Namulonge. Grooved roots are not preferred because they are difficult to peel and will not be bought in the market unless they are the only ones available. Skin colour was important to all groups except the Kachwekano farmers. Red skin colour was mostly preferred by the groups and this is also the market preference. That skin colour was not identified as an important trait by the Kachwekano farmers, was probably because most of them

produce for home consumption. In previous studies by Abidin et al. (2002) in north-eastern Uganda, the preferred skin colour was white/tan and flesh colour was yellow. Therefore, the importance of skin colour depends on region where the evaluation is carried out. According to Ndirigwe et al. (2005), in Rwanda the reddish skin is also preferred by both the farm household and the market.

At harvest, the significant ( $P < 0.01$ ), positive Spearman's rank correlation coefficient between scientists and farmers at Namulonge ( $r = 0.412$ ) and between scientists and farmers at Kachwekano ( $r = 0.440$ ), indicated that it is possible for the evaluation to be carried out by scientists only and successfully identify farmer preferred traits. This would obviously enable considerable savings for research budgets and will facilitate quicker selection processes. However, it is important to emphasise that these conclusions are drawn from a limited study on a small sample of scientists and farmers.

For the cooking qualities of the genotypes, the farmers also represented the consumer since they also consume sweetpotato and they interact frequently with other consumers. The highly significant ( $P < 0.01$ ), positive Spearman's rank correlations between the rankings of scientists and farmers at Namulonge ( $r = 0.605$ ) and scientists and farmers at Kachwekano ( $r = 0.552$ ) for cooking quality traits indicates that the scientists at each site are capable of selecting for the same cooking qualities preferred by farmers. Therefore, it is not necessary to use site specific groups in the selection process. NASPOT 1, which is a popular cultivar, emerged as the best genotype across the groups for cooking quality traits with G68 and G24 ranked second and third. However, Gibson et al. (2008) do not recommend carrying out cooking quality taste tests when the number of genotypes in the programme is still as large as was the case in the current study. Furthermore, they argue that since genotypes are taste tested at the same time, without the sauces usually eaten with sweetpotato or conditions that do not wholly simulate home cooking and eating, such results may not necessarily provide a true indication of the preferred genotypes. They recommend that fewer genotypes be taste tested by farmers one at a time with their preferred sauce in order to allow farmers to more carefully decide on which ones to select. However, since NASPOT 1, already the most popular cultivar in Uganda, was ranked as the best by the groups this provides some validation of the outcome of the current study.

## **5.5 Conclusion**

Some of the  $F_1$  genotypes selected from the crosses conducted in this breeding programme are highly adaptable and have farmer preferred attributes. Genotypes that exhibited stability for resistance to *Alternaria* blight as well as stability for high yield were G14, G16, G24, G49 and G59.

These genotypes can be recommended to farmers on a trial basis at the three test sites and other associated sites. However, a full investigation of the stability of these genotypes across a representative range of environments will have to be performed. Stability for the scientist and farmer evaluated traits will be the basis upon which any genotype will be advanced.

Many breeders involve farmers at the advanced selection stage of a breeding programme as they can raise the breeders' awareness of traits that they may not have thought to be important. On the basis of this and other studies, it is recommended that farmers' involvement should be at advanced stages of evaluation when the number of genotypes has been reduced. At this stage, in addition to on-station evaluation, farmers can be given planting materials of promising genotypes to plant in their own fields or small plots. This is a quick way of disseminating new cultivars in a country such as Uganda which lacks organised seed distribution channels for new cultivars. The good correlations between scientist and farmer rankings of genotypes at each of the two sites in this study demonstrated that the identification of selection criteria and application thereof by scientists and farmers is not that different. The practical implication of this study is that selection within sites can be generally carried out by experienced scientists who have a good understanding of the production requirements of sweetpotato and consumer preferences. Importantly, the selection has to be conducted by site specific sets of scientists.

Overall, genotype G49 was ranked well both for stability by GEI analysis and for scientist and farmer preferred traits by the participatory selection process. In the participatory process it was ranked tenth before harvest and third at harvest. It is an above average yielder with good yield stability, and is stable *Alternaria* blight with below average AUDPC value. This genotype will be recommended for cultivation by selected farmers on a trial basis before, hopefully being released for cultivation on a wide scale.

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## Appendices

### Appendix 5.1 Mean AMMI performance estimates and ranking of the genotypes for sweetpotato virus disease score at Namulonge, Kachwekano and Serere (2011B)

Genotype	Mean SPVD	IPCA1	IPCA2	Namulonge		Kachwekano		Serere	
				Mean	Rank	Mean	Rank	Mean	Rank
G8	1.3	-0.01957	-0.12729	1.3	4	1.3	2	1.7	6
G13	2.0	-0.63277	-0.39805	2.3	20	2.3	20	1.3	1
G14	1.9	-0.14939	0.29899	2.0	18	1.3	2	2.3	10
G16	2.2	0.47151	0.05500	1.3	4	2.0	15	3.3	20
G21	1.7	-0.38595	-0.39269	1.7	11	2.0	15	1.3	1
G24	1.7	0.35452	-0.37663	0.7	1	2.0	15	2.3	10
G28	2.1	0.10256	-0.03882	1.7	11	2.0	15	2.7	17
G29	1.7	-0.13913	-0.38734	1.3	4	2.0	15	1.7	6
G30	2.4	0.58851	0.48664	1.7	11	1.7	11	4.0	21
G38	2.0	0.35452	-0.37663	1.0	2	2.3	20	2.7	17
G49	1.7	0.22726	-0.12194	1.0	2	1.7	11	2.3	10
G53	1.6	-0.64304	0.28829	2.3	20	1.0	1	1.3	1
G58	1.8	-0.02470	0.21588	1.7	11	1.3	2	2.3	10
G59	2.1	0.11026	-0.55357	1.3	4	2.7	22	2.3	10
G60	2.9	0.84560	-0.19435	1.3	4	3.0	23	4.3	23
G61	2.1	-0.64561	0.45987	3.0	23	1.3	2	2.0	8
G65	1.7	-0.14683	0.12741	1.7	11	1.3	2	2.0	8
G67	1.9	0.22469	0.04965	1.3	4	1.7	11	2.7	17
G68	1.4	-0.39108	-0.04953	1.7	11	1.3	2	1.3	1
G69	1.6	-0.51578	0.03359	2.0	18	1.3	2	1.3	1
G79	1.9	-0.02213	0.04430	1.7	11	1.7	11	2.3	10
NASPOT 1	1.7	0.10000	0.13276	1.3	4	1.3	2	2.3	10
Tanzania	2.6	0.33655	0.82445	2.3	20	1.3	2	4.0	21
<b>Mean</b>	<b>1.9</b>			<b>1.6</b>		<b>1.7</b>		<b>2.3</b>	

SPVD = sweetpotato virus disease; IPCA = interaction principal component analysis

**Appendix 5.2 Mean AMMI performance estimates and ranking of the genotypes for marketable root yield at Namulonge, Kachwekano and Serere (2011B)**

Genotype	Mean MRY	IPCA1	IPCA2	Namulonge		Kachwekano		Serere	
				Mean	Rank	Mean	Rank	Mean	Rank
G8	8.0	0.26655	-0.09111	11.9	9	6.2	13	6.8	4
G13	8.3	0.20239	-0.43669	12.0	7	8.4	3	3.5	20
G14	7.9	0.22915	1.00385	12.0	8	6.3	12	4.3	15
G16	7.9	0.73312	0.31811	13.1	2	2.6	23	5.1	12
G21	6.1	0.57387	-0.88863	10.7	14	6.9	9	6.5	5
G24	8.8	0.36285	-0.15218	12.9	3	3.2	22	6.1	7
G28	6.7	0.38110	-0.99570	10.7	15	5.4	17	2.6	23
G29	5.2	-0.31283	0.40357	7.7	20	5.6	16	4.1	18
G30	8.2	1.33223	0.24965	15.0	1	7.5	7	4.9	13
G38	7.3	-0.40511	0.36300	9.5	17	5.2	18	5.2	11
G49	6.4	-0.28693	-0.31376	8.8	19	5.8	15	8.5	1
G53	8.7	-0.00865	-0.98150	11.7	11	6.0	14	6.9	3
G58	5.4	-1.95133	-0.70710	3.3	23	5.2	19	4.9	14
G59	7.4	0.61506	-0.14368	12.2	5	7.0	8	4.2	17
G60	5.7	-1.14907	0.32887	6.0	22	9.2	2	4.0	19
G61	7.5	-0.60177	1.00363	9.3	18	7.7	5	5.8	8
G65	8.7	0.27051	0.22399	12.7	4	9.9	1	5.7	9
G67	9.2	-0.16850	0.77941	12.2	6	3.8	21	3.4	21
G68	4.8	-0.35859	-0.22077	7.0	21	6.9	10	3.3	22
G69	7.2	0.36673	0.69144	11.5	12	4.0	20	4.2	16
G79	6.6	0.71885	-0.26712	11.7	10	6.3	11	5.7	10
NASPOT 1	8.9	-0.36846	-0.23561	11.1	13	8.0	4	7.7	2
Tanzania	7.9	-0.44116	0.06830	10.0	16	7.7	6	6.1	6
<b>Mean</b>	<b>7.3</b>			<b>10.7</b>		<b>6.3</b>		<b>5.3</b>	

MRY = Marketable storage root yield ( $t\ ha^{-1}$ ); IPCA = Interaction principal component analysis

**Appendix 5.3 Mean AMMI performance estimates and ranking of the genotypes for harvest index at Namulonge, Kachwekano and Serere (2011B)**

Genotype	Mean HI	IPCA1	IPCA2	Namulonge		Kachwekano		Serere	
				Mean	Rank	Mean	Rank	Mean	Rank
G8	0.52	0.07328	-0.15515	0.51	19	0.52	5	0.52	4
G13	0.48	-0.00788	-0.11948	0.51	18	0.43	17	0.48	5
G14	0.44	0.07653	0.11216	0.55	16	0.47	13	0.32	22
G16	0.54	-0.14692	0.14088	0.74	1	0.44	15	0.45	9
G21	0.41	-0.29187	0.19643	0.68	2	0.22	23	0.32	20
G24	0.54	-0.00906	-0.27900	0.51	17	0.49	9	0.63	2
G28	0.45	-0.30192	0.06670	0.67	3	0.25	22	0.42	12
G29	0.47	0.07454	0.16882	0.60	7	0.50	8	0.32	21
G30	0.47	0.04141	0.07699	0.57	11	0.47	12	0.36	17
G38	0.55	0.00970	-0.14792	0.57	12	0.52	7	0.56	3
G49	0.43	-0.17749	-0.02983	0.57	13	0.30	21	0.43	11
G53	0.48	-0.04443	0.10012	0.63	5	0.43	16	0.39	15
G58	0.46	0.18570	-0.08914	0.44	23	0.53	4	0.40	13
G59	0.48	0.36133	0.08924	0.47	22	0.67	1	0.30	23
G60	0.50	0.06216	0.07044	0.60	9	0.52	6	0.40	14
G61	0.47	0.06144	0.05198	0.56	15	0.48	10	0.38	16
G65	0.48	0.02811	0.16788	0.63	4	0.48	11	0.33	18
G67	0.49	-0.04668	0.00624	0.59	10	0.43	18	0.44	10
G68	0.46	-0.12641	-0.08104	0.56	14	0.35	20	0.47	6
G69	0.48	0.26513	0.08739	0.51	20	0.61	2	0.32	19
G79	0.64	-0.07113	-0.30657	0.62	6	0.55	3	0.75	1
NASPOT 1	0.47	0.00592	-0.12205	0.50	21	0.43	19	0.47	7
Tanzania	0.51	-0.02144	-0.00508	0.60	8	0.47	14	0.46	8
<b>Mean</b>	<b>0.49</b>			<b>0.57</b>		<b>0.46</b>		<b>0.43</b>	

HI = harvest index; IPCA = Interaction principal component analysis



**Appendix 5.4 Mean AMMI performance estimates and ranking of the genotypes for dry mass composition at Namulonge, Kachwekano and Serere (2011B)**

Genotype	Mean DM%	IPCA1	IPCA2	Namulonge		Kachwekano		Serere	
				Mean	Rank	Mean	Rank	Mean	Rank
G8	31.78	0.16958	0.05815	31.0	15	31.2	16	33.2	16
G13	33.65	0.52972	0.26498	33.0	4	31.9	14	36.0	3
G14	32.83	1.24063	0.53150	32.1	11	29.2	21	37.3	1
G16	31.69	-1.15286	0.43654	33.3	2	32.9	10	28.9	21
G21	30.44	0.83484	-1.78987	24.4	23	32.3	13	34.7	7
G24	32.28	0.33643	-1.05599	28.6	22	33.6	6	34.7	7
G28	31.97	0.46043	0.03677	30.8	16	30.8	18	34.3	12
G29	32.39	-0.81098	0.19995	33.0	5	33.4	8	30.8	17
G30	32.56	-0.97129	-0.14032	32.5	9	34.6	2	30.6	19
G38	31.22	0.68430	1.18391	32.7	7	27.3	23	33.7	15
G49	32.31	0.14484	-0.23493	30.8	17	32.3	12	33.8	14
G53	32.86	-1.10122	-0.52396	32.0	12	35.9	1	30.7	18
G58	33.72	-0.05866	-0.11939	32.8	6	33.9	4	34.5	9
G59	32.42	0.81576	-0.29568	30.1	19	31.3	15	35.9	4
G60	29.92	-1.59838	-0.21881	30.3	18	33.3	9	26.1	23
G61	30.75	-0.55831	1.04322	33.2	3	29.6	20	29.5	20
G65	30.94	-1.09370	0.08929	31.6	14	32.8	11	28.5	22
G67	31.31	1.08659	0.17134	29.8	21	28.7	22	35.4	5
G68	33.94	0.28638	1.22688	35.9	1	30.8	19	35.2	6
G69	33.39	0.78134	0.34466	32.7	8	31.0	17	36.5	2
G79	32.83	0.07752	-0.81750	30.0	20	34.2	3	34.3	10
NASPOT 1	33.17	-0.05146	-0.19536	32.0	13	33.5	7	34.0	13
Tanzania	33.50	-0.05146	-0.19536	32.3	10	33.8	5	34.3	10
<b>Mean</b>	<b>32.30</b>			<b>31.5</b>		<b>32.1</b>		<b>33.2</b>	

DM% = percentage dry mass composition; IPCA = Interaction principal component analysis

**Appendix 5.5 The IPCA1 scores for Namulonge, Kachwekano and Serere for Alternaria blight severity, total storage root yield, dry mass composition, harvest index, marketable storage root yield and sweetpotato virus disease severity scores (2011B)**

Site	AUDPC		TRY		DM%		HI		MRY		SPVD	
	Means	IPCA1	Mean	IPCA1	Mean	IPCA1	Mean	IPCA1	Mean	IPCA1	Mean	IPCA1
Kachwekano	76.63	-7.09417	15.71	-2.47422	32.09	-1.96267	0.4585	0.58176	6.289	-1.51554	1.739	0.02808
Namulonge	51.57	1.83453	25.53	3.95115	31.51	-1.06082	0.5734	-0.36142	10.566	2.63692	1.623	-1.36410
Serere	49.83	5.25964	12.33	-1.47693	33.16	3.02348	0.4313	-0.22034	5.193	-1.12138	2.348	1.33602

AUDPC = area under disease progress curve for Alternaria blight severity; TRY = total storage root fresh mass (t ha<sup>-1</sup>); DM% = dry mass composition; HI = harvest index; MRY = marketable storage root yield (t ha<sup>-1</sup>); SPVD = sweetpotato virus disease; IPCA = Interaction principal component analysis

**Appendix 5.6 Mean trait scores for scientists and farmers at Namulonge at harvest (2011B)**

Genotype	Namulonge scientists						Namulonge farmers					
	Yield	Skin colour	No root defects	No. of roots	Root shape	Aggregate	Yield	Large roots	Skin colour	Long, straight roots	No weevil damage	Aggregate
G8	3.7	4.7	3.0	4.0	3.0	<b>52.0</b>	5.0	4.7	4.3	3.7	5.0	<b>71.3</b>
G13	3.3	3.0	2.3	3.3	2.0	<b>41.6</b>	4.3	4.7	2.7	2.0	4.3	<b>60.3</b>
G14	3.7	4.0	3.3	4.0	3.0	<b>52.7</b>	4.3	4.7	3.7	3.0	4.7	<b>64.7</b>
G16	2.7	4.0	3.0	4.3	3.0	<b>47.0</b>	4.3	4.0	3.7	3.3	5.0	<b>64.3</b>
G21	3.0	4.3	3.3	4.0	2.7	<b>48.7</b>	4.7	3.7	3.7	3.0	5.0	<b>64.7</b>
G24	4.0	4.7	3.7	5.0	4.0	<b>61.3</b>	4.3	4.3	4.3	4.7	4.3	<b>65.3</b>
G28	4.7	4.7	4.3	4.0	4.7	<b>67.4</b>	4.3	4.7	4.0	4.0	4.7	<b>66.3</b>
G29	2.7	4.0	4.7	3.7	4.3	<b>56.4</b>	4.7	4.3	4.7	4.7	4.3	<b>67.7</b>
G30	5.0	5.0	4.0	5.0	4.7	<b>70.0</b>	4.3	4.7	4.7	3.7	5.0	<b>68.7</b>
G38	2.7	4.3	2.7	3.7	4.0	<b>47.7</b>	4.3	4.3	4.3	3.7	4.3	<b>64.3</b>
G49	4.0	4.7	4.7	4.7	4.7	<b>66.7</b>	4.3	5.0	3.7	3.3	5.0	<b>67.3</b>
G53	3.7	3.0	4.0	4.0	4.0	<b>57.4</b>	4.6	5.0	4.0	4.0	4.5	<b>67.7</b>
G58	3.3	4.7	4.7	2.3	4.7	<b>58.6</b>	3.0	4.0	3.3	2.7	5.0	<b>56.3</b>
G59	3.7	3.7	4.0	4.3	3.7	<b>57.7</b>	4.7	5.0	3.7	2.3	4.3	<b>65.3</b>
G60	2.3	4.0	4.0	2.3	3.7	<b>47.3</b>	4.3	4.3	3.7	3.3	5.0	<b>65.3</b>
G61	3.3	5.0	4.3	3.0	4.0	<b>57.0</b>	4.7	4.3	4.0	2.7	5.0	<b>67.0</b>
G65	3.0	3.3	3.7	3.7	4.0	<b>52.3</b>	4.3	4.3	3.7	2.7	4.5	<b>62.6</b>
G67	3.7	5.0	4.0	4.7	4.7	<b>62.7</b>	4.3	4.3	4.0	4.3	5.0	<b>67.0</b>
G68	3.3	3.7	3.3	2.7	3.7	<b>50.0</b>	4.7	4.3	3.7	3.3	4.7	<b>65.7</b>
G69	3.3	4.3	4.0	4.3	4.3	<b>58.6</b>	4.7	3.7	3.0	4.3	5.0	<b>64.7</b>
G79	3.0	3.0	4.0	3.0	3.7	<b>51.0</b>	4.3	4.7	3.3	2.7	5.0	<b>65.0</b>
NASPOT 1	3.3	4.0	3.3	3.0	3.6	<b>57.7</b>	4.3	4.5	4.6	4.3	3.3	<b>65.2</b>
Tanzania	3.0	3.5	2.3	2.7	3.3	<b>53.4</b>	4.0	4.3	4.3	3.8	2.7	<b>60.4</b>
<b>Mean</b>	<b>3.4</b>	<b>4.1</b>	<b>3.8</b>	<b>3.8</b>	<b>3.8</b>		<b>4.4</b>	<b>4.4</b>	<b>4.4</b>	<b>3.4</b>	<b>4.7</b>	
<b>SE</b>	<b>0.5</b>	<b>0.4</b>	<b>0.3</b>	<b>0.5</b>	<b>0.4</b>		<b>0.5</b>	<b>0.5</b>	<b>0.5</b>	<b>0.7</b>	<b>0.3</b>	

**Appendix 5.7 Mean trait scores for scientists and farmers at Kachwekano at harvest (2011B)**

Genotype	Kachwekano scientists						Kachwekano farmers					
	Yield	Large roots	No weevil damage	Root colour	Root shape	Aggregate score	Yield	Large roots	Skin colour	Long, straight roots	No cracking	Aggregate score
G8	1.7	2.0	4.0	2.3	2.0	<b>36.7</b>	1.3	1.3	1.7	1.3	2.7	<b>23.6</b>
G13	2.0	2.0	3.3	3.0	3.0	<b>38.3</b>	2.0	2.0	2.0	2.3	3.0	<b>34.0</b>
G14	3.3	3.3	3.7	3.7	2.3	<b>49.6</b>	2.7	2.7	2.7	2.3	3.7	<b>42.7</b>
G16	2.3	2.3	4.0	3.7	3.0	<b>44.3</b>	2.0	2.7	2.3	2.3	3.0	<b>37.7</b>
G21	2.0	2.3	2.7	2.7	2.0	<b>34.3</b>	3.3	3.0	3.7	2.7	2.3	<b>50.0</b>
G24	3.7	3.3	3.0	3.3	2.0	<b>47.7</b>	3.7	3.0	2.7	3.0	1.7	<b>49.0</b>
G28	2.3	2.3	3.3	3.0	2.7	<b>40.3</b>	2.7	2.3	2.0	2.7	3.3	<b>40.0</b>
G29	3.0	4.0	4.7	3.0	3.7	<b>56.0</b>	2.7	2.7	2.7	3.0	3.7	<b>44.7</b>
G30	3.7	3.7	3.7	3.3	2.7	<b>52.7</b>	3.0	2.7	3.3	3.0	2.3	<b>47.0</b>
G38	2.7	2.3	3.3	2.7	1.3	<b>39.0</b>	2.3	1.7	1.7	1.7	1.7	<b>30.0</b>
G49	3.7	4.0	4.0	3.7	2.7	<b>55.4</b>	2.3	1.7	2.7	2.3	3.3	<b>36.7</b>
G53	1.0	1.0	4.7	2.3	3.0	<b>35.0</b>	1.3	1.3	1.0	1.3	2.0	<b>21.0</b>
G58	1.0	1.3	4.0	4.0	3.0	<b>35.0</b>	1.7	1.7	2.3	2.0	3.0	<b>31.0</b>
G59	1.7	1.7	4.0	2.3	2.0	<b>35.7</b>	3.0	2.3	2.3	2.0	3.3	<b>40.6</b>
G60	2.7	2.7	3.7	3.3	3.0	<b>45.4</b>	2.7	2.3	2.7	2.3	2.3	<b>40.0</b>
G61	1.3	1.3	4.7	2.7	1.3	<b>34.6</b>	2.3	1.3	1.7	2.3	3.3	<b>32.3</b>
G65	2.0	2.3	3.3	3.7	1.7	<b>37.3</b>	2.3	1.7	3.0	1.7	2.7	<b>35.0</b>
G67	1.3	1.3	4.0	3.0	3.7	<b>37.0</b>	2.0	2.0	1.0	2.0	3.0	<b>30.0</b>
G68	1.7	1.3	4.3	3.7	2.7	<b>38.7</b>	1.7	1.7	2.3	2.0	3.0	<b>31.0</b>
G69	2.0	2.0	4.0	3.7	3.0	<b>41.7</b>	1.7	1.3	1.7	2.0	2.3	<b>27.0</b>
G79	1.7	1.7	3.7	3.0	3.0	<b>37.0</b>	2.0	1.7	1.7	2.0	3.0	<b>30.7</b>
NASPOT 1	16.5	16.0	10.0	6.0	3.6	<b>52.1</b>	2.7	2.2	2.4	2.2	3.5	<b>39.6</b>
Tanzania	15.0	14.0	6.9	5.3	3.3	<b>44.5</b>	2.2	1.8	2.0	1.9	3.0	<b>25.7</b>
<b>Mean</b>	<b>2.2</b>	<b>2.3</b>	<b>3.8</b>	<b>3.1</b>	<b>2.6</b>		<b>2.2</b>	<b>2.3</b>	<b>3.8</b>	<b>3.1</b>	<b>2.6</b>	
<b>SE</b>	<b>0.5</b>	<b>0.5</b>	<b>0.5</b>	<b>0.4</b>	<b>0.5</b>		<b>0.5</b>	<b>0.5</b>	<b>0.5</b>	<b>0.4</b>	<b>0.5</b>	

**Appendix 5.8 Mean scores for sweetpotato organoleptic traits tested by scientists and farmers at Namulonge (2011B)**

Genotype	Namulonge scientists						Namulonge farmers					
	Appearance	Dry mass	Fibre content	Acceptability	Sweetness	Aggregate	Appearance	Dry mass	Fibre content	Acceptability	Sweetness	Aggregate
G8	4.0	3.5	3.5	3.5	4.5	<b>47.0</b>	3.0	3.0	3.0	2.5	2.0	<b>39.5</b>
G13	5.0	4.0	4.5	3.5	3.0	<b>42.0</b>	3.0	3.0	3.5	3.5	3.5	<b>35.0</b>
G14	2.5	3.0	3.5	4.5	3.0	<b>39.5</b>	3.5	3.0	3.0	2.5	2.5	<b>43.0</b>
G16	2.5	2.5	3.0	4.0	2.0	<b>37.5</b>	2.5	2.5	4.0	3.0	2.5	<b>42.5</b>
G21	4.0	2.5	3.5	4.0	3.0	<b>45.0</b>	2.5	2.0	3.0	2.5	1.5	<b>32.0</b>
G24	3.5	3.5	3.5	4.5	3.5	<b>61.5</b>	3.5	2.5	4.5	4.5	2.5	<b>50.0</b>
G28	3.0	3.5	3.5	3.5	3.0	<b>54.5</b>	4.5	2.5	4.0	4.5	4.0	<b>55.5</b>
G29	2.5	3.0	4.0	4.5	3.0	<b>43.5</b>	3.0	4.0	2.5	3.0	2.0	<b>42.5</b>
G30	4.0	3.0	4.0	4.0	2.5	<b>51.0</b>	3.0	2.5	4.0	3.0	3.5	<b>48.5</b>
G38	3.0	2.5	3.0	3.5	3.0	<b>55.0</b>	3.5	3.5	3.5	4.5	3.5	<b>53.5</b>
G49	4.0	2.5	3.5	3.0	3.0	<b>43.5</b>	3.5	2.5	3.0	3.0	2.0	<b>39.0</b>
G53	3.5	3.0	4.0	4.0	2.5	<b>47.5</b>	4.0	2.5	2.5	2.0	1.5	<b>49.5</b>
G58	3.0	2.0	3.5	4.0	3.0	<b>46.5</b>	3.0	3.5	4.5	4.0	2.5	<b>47.5</b>
G59	3.5	3.0	4.5	5.0	3.5	<b>43.5</b>	3.5	2.5	3.5	3.5	3.5	<b>48.5</b>
G60	3.5	2.5	4.5	3.0	3.5	<b>48.5</b>	2.5	3.0	2.5	3.0	2.5	<b>40.0</b>
G61	3.0	3.0	3.5	2.5	2.5	<b>48.5</b>	4.5	2.5	3.0	3.0	3.0	<b>46.0</b>
G65	4.0	3.5	4.5	4.0	3.0	<b>49.0</b>	2.0	2.0	3.5	4.0	3.0	<b>41.5</b>
G67	5.0	4.0	4.5	4.5	3.5	<b>53.5</b>	2.5	2.5	3.0	3.5	2.5	<b>40.0</b>
G68	3.0	2.5	3.5	3.5	3.0	<b>47.5</b>	3.5	3.0	4.0	4.0	3.5	<b>52.5</b>
G69	2.5	2.0	3.0	3.0	2.5	<b>38.0</b>	2.5	2.5	2.5	4.0	2.0	<b>36.5</b>
G79	3.0	2.5	2.5	3.5	2.5	<b>47.0</b>	2.0	2.5	3.0	3.5	1.5	<b>34.0</b>
NASPOT 1	3.0	2.0	4.0	3.5	2.5	<b>58.5</b>	3.0	3.5	4.0	4.0	3.0	<b>57.0</b>
Tanzania	3.0	3.0	4.0	4.5	2.5	<b>58.0</b>	4.5	2.5	4.5	4.5	4.0	<b>51.0</b>

**Appendix 5.9 Mean scores for sweetpotato organoleptic traits tested by scientists and farmers at Kachwekano (2011B)**

Genotype	Kachwekano scientists						Kachwekano farmers					
	Appearance	Dry mass	Fibre content	Acceptability	Sweetness	Aggregate	Appearance	Dry mass	Fibre content	Acceptability	Sweetness	Aggregate
G8	2.0	3.0	3.0	3.5	2.5	<b>41.0</b>	3.5	2.5	3.0	3.5	2.0	<b>39.5</b>
G13	1.5	3.5	3.5	3.0	2.0	<b>40.5</b>	2.5	3.5	3.0	2.0	2.5	<b>45.5</b>
G14	2.5	4.0	4.5	3.5	3.5	<b>55.5</b>	3.5	4.0	4.0	4.0	3.5	<b>56.5</b>
G16	1.5	4.0	3.0	4.5	2.5	<b>45.0</b>	2.5	3.5	3.5	3.5	2.0	<b>43.0</b>
G21	1.5	3.0	3.0	4.0	1.5	<b>35.5</b>	2.5	3.5	4.0	3.5	2.0	<b>33.0</b>
G24	2.5	4.0	4.0	3.0	2.5	<b>48.5</b>	2.5	3.0	2.0	2.5	1.5	<b>44.5</b>
G28	1.5	3.0	3.0	4.0	2.0	<b>38.0</b>	3.0	2.5	2.5	3.5	3.0	<b>42.0</b>
G29	2.5	4.0	4.0	4.5	3.5	<b>55.0</b>	3.5	3.5	3.5	2.5	2.0	<b>55.0</b>
G30	1.5	3.5	4.0	4.0	3.5	<b>50.5</b>	2.0	2.0	3.0	3.0	1.5	<b>31.5</b>
G38	1.5	3.0	4.0	4.0	3.0	<b>46.0</b>	1.5	2.5	3.0	3.5	1.0	<b>30.5</b>
G49	2.5	3.0	3.0	3.5	3.5	<b>47.0</b>	4.0	4.0	4.5	3.0	2.5	<b>41.5</b>
G53	1.5	3.5	4.0	4.0	3.5	<b>50.5</b>	3.5	3.5	4.0	4.0	2.5	<b>49.5</b>
G58	1.5	2.5	3.0	4.0	2.5	<b>38.5</b>	4.0	3.0	3.0	5.0	3.5	<b>51.5</b>
G59	1.5	3.5	3.0	4.5	3.0	<b>45.5</b>	3.5	3.0	3.5	3.0	3.0	<b>47.5</b>
G60	2.0	4.0	4.0	3.5	4.0	<b>55.5</b>	4.5	4.0	4.0	4.0	2.5	<b>53.5</b>
G61	2.5	4.0	4.5	4.0	2.5	<b>51.0</b>	2.5	4.0	3.0	4.0	2.0	<b>44.0</b>
G65	2.0	3.0	4.5	4.0	3.0	<b>48.5</b>	2.5	3.0	2.0	4.0	2.0	<b>37.0</b>
G67	2.5	3.5	4.0	3.0	2.5	<b>46.5</b>	2.5	3.5	3.5	4.0	3.0	<b>48.5</b>
G68	3.0	4.0	4.5	4.0	4.5	<b>62.0</b>	3.0	4.0	3.5	4.0	3.5	<b>54.0</b>
G69	1.5	3.5	3.0	2.5	1.5	<b>36.0</b>	4.0	4.0	3.5	3.0	3.5	<b>44.0</b>
G79	2.0	4.0	3.5	3.5	3.5	<b>51.5</b>	3.0	3.5	2.5	3.5	3.0	<b>46.0</b>
NASPOT 1	1.5	3.0	3.0	4.5	3.0	<b>43.5</b>	3.0	3.5	2.5	4.0	2.0	<b>53.0</b>
Tanzania	2.5	4.0	3.5	4.5	4.0	<b>56.0</b>	2.5	2.0	2.5	3.5	2.5	<b>36.5</b>

**Appendix 5.10 Rainfall (mm) received at each site from planting to harvesting**

	2011			2012				
	Oct	Nov	Dec	Jan	Feb	Mar	Apr	May
Namulonge	99.8	226.0	104.1	3.4	87.7	39.8		
Kachwekano		161.3	54.7	2.8	59.9	110.6	217.0	147.0
Serere		162.2	37.1	0.0	17.6	109.6	217.5	

# Chapter 6

## General overview

### 6.1 Introduction

Alternaria leaf petiole and stem blight (*Alternaria* spp.) (commonly referred to as Alternaria blight) is the most important fungal disease of sweetpotato in Uganda. Yield losses of up to 54% in susceptible genotypes have been associated with the disease under natural infection (Osiru et al., 2007). Of the available control options, especially for resource poor farmers, host plant resistance is the most recommended. Recent studies have shown differences in Alternaria blight severity among the landraces and improved cultivars grown in Uganda (Osiru et al., 2009). These differences can be exploited by identifying the most resistant genotypes so that they can be released to farmers in high disease pressure areas as well as using them as sources of resistance in breeding for Alternaria blight resistance. There is very limited information on the mode of inheritance of resistance to Alternaria blight. This necessitates that the mode of inheritance of resistance to Alternaria blight be investigated, an understanding of which will assist in implementing effective and efficient breeding strategies for the development of resistant genotypes. As previous research has shown (Gibson et al., 2008), farmers desire genotypes that have acceptable performance under the prevailing production constraints but also have farmer-preferred traits. These preferred traits must be identified by breeders so as to incorporate them into new genotypes.

The objective of this study was to contribute to the development of high yielding, Alternaria blight resistant sweetpotato genotypes with farmer and consumer desired traits that will enhance sweetpotato productivity and income generation particularly among the resource poor farming communities in Uganda. To accomplish this objective, there were four main components to the study:

- 1) establish farmers preferred sweetpotato traits, production constraints and Alternaria blight awareness through a participatory rural appraisal (PRA) in central and south-western Uganda;
- 2) evaluate sweetpotato germplasm for Alternaria blight resistance, storage root yield and other agronomic traits, and stability over two sites and three seasons;
- 3) generate F<sub>1</sub> genotypes to determine the combining ability of 16 parents and the modes of inheritance of: resistances to Alternaria blight and sweetpotato virus disease (SPVD); total storage root yield (TRY); number of marketable storage roots per plant (MRN); number of



unmarketable storage roots per plant (UMRN); total number of roots per plant (TRN); dry mass composition (DM%); and harvest index (HI); and

4) determine the adaptability and farmer acceptability of selected F<sub>1</sub> genotypes at three sites.

This overview summarises the outcomes of these four components of the study.

## **6.2 Summary of findings**

### **6.2.1 Farmer preferences**

Using individual household interviews and focus group discussions, a PRA was conducted in Luwero district (central Uganda) and Kabale district in south-western Uganda to: identify sweetpotato attributes preferred by the local farmers; their perceptions of sweetpotato production constraints; their awareness of *Alternaria* blight resistance; and their mechanisms/strategies for coping with the disease. The findings were:

- Farmers in Kabale plant mainly landraces whereas farmers in Luwero plant both landraces and improved cultivars.
- The most important traits in sweetpotato for farmers in Luwero were high yield, early maturity and sweetness (taste) and in Kabale, sweetness (taste), high yield and early maturity. Other traits included high dry mass, good in-field root storability, and resistance to SPVD.
- The most important constraint identified by most farmers in Luwero district was the damage caused by caterpillars of sweetpotato butterfly (*Acraea* spp.) especially in the dry season, and in Kabale it was *Alternaria* blight. Other constraints included scarcity of planting materials especially after the dry season, low yielding cultivar, vermin and low soil fertility.

### **6.2.2 Stability and performance of selected genotypes**

Germplasm evaluation was conducted at the National Crops Resources Research Institute (NaCRRI) at Namulonge and Kachwekano Zonal Agricultural Research and Development Institute (KAZARDI) over three seasons using 30 existing genotypes, which included landraces and improved cultivars from the National Sweetpotato Program. The objectives were to determine the: resistance to *Alternaria* blight, and performance for other agronomic traits; stability of *Alternaria* blight resistance, TRY, and other important traits; and yield gain after application of fungicide treatment to control *Alternaria* blight in the selected sweetpotato genotypes. The additive main effects and multiplicative interaction (AMMI) stability value (ASV) (Purchase et al., 2000) which quantifies the stability of genotypes across

environments, was used as a component of the genotype selection index (GSI) (Farshadfar, 2008) to determine both the stability and mean performance of the genotypes across environments. The principal findings were:

- Higher *Alternaria* blight severity, based on area under disease progress curve (AUDPC), was recorded at Kachwekano than at Namulonge.
- Landrace, Shock had lower AUDPC values across seasons and sites and spray treatments (fungicide versus *Alternaria* blight inoculation) than the resistant check, Tanzania. The most stable genotypes with below average mean AUDPC values and therefore more resistant were: Magabali, BND145L, NASPOT 8, Namusoga, Tanzania and NKA259L.
- NASPOT 8 was selected by the GSI as the best genotype combining stability and performance for *Alternaria* blight resistance, TRY and HI. The other two most outstanding genotypes were Namusoga and BND145L.
- The best performing and, therefore, most desirable genotypes (in terms of yield stability and high yield) were: NASPOT 7, NASPOT 8, NASPOT 11, NASPOT 10 O, BND145L, Bwanjule, NKA103M, NASPOT 3 and NASPOT 1; all from the National Sweetpotato program.
- Kachwekano (2011B) was identified as the most stable environment for high *Alternaria* blight pressure with an above average mean AUDPC value whereas Namulonge (2011B) was the most stable environment for low disease pressure with a below average mean AUDPC value.
- Yield gain of 39.8% was recorded by NASPOT 1 (the most susceptible genotype) when a fungicide was used. This indicated that, in the absence of a resistant genotype, fungicides can be used to reduce the impact of *Alternaria* blight.

### **6.2.3 Inheritance of *Alternaria* blight resistance and other traits**

The mode of inheritance of *Alternaria* leaf blight resistance and yield related traits was determined using a 7 x 9 North Carolina II mating design (comprising two sets of parents, viz. 4 x 5 and 3 x 4) to generate 32 families. Each of the 32 families was represented by 30 F<sub>1</sub> genotypes (full sibs) and planted at Namulonge and Kachwekano using a 5 x 7 row-column design with two replications. The findings were:

- The general combining ability (GCA) and specific combining ability (SCA) effects were significant for AUDPC, SPVD, MRN, UMRN, TRN, TRY and DM% implying that both additive and non-additive gene action were important for all these traits. However, the predominance of the GCA sum of squares (SS) for all these traits

except DM% indicated that additive gene action was more important for the expression of these traits than non-additive gene action. Conversely, the predominance of SCA SS for DM% indicated that non-additive gene action was more important than additive gene action for this trait.

- The AUDPC values ranged from 96.9 for the most resistant family (Bwanjule x NASPOT 2) to 269.7 for the most susceptible family (Kidodo x Dimbuka).
- Family Bwanjule x Dimbuka with significant, desirable negative SCA effect for AUDPC resulted from a cross between a female parent with a negative GCA effect and a male parent with a positive GCA effect. Similarly, Bwanjule x NASPOT 2 with a positive SCA effect resulted from parents with negative GCA effects.
- Female parents Silk Omupya and Bwanjule across all males produced families with the lowest AUDPC values and were therefore the best female parents for resistance to *Alternaria* blight. Similarly, male parent NASPOT 2 produced the most resistant families across all females. These parents should be used as sources of resistance to the disease.

#### **6.2.4 Adaptability and stability of selected F<sub>1</sub> genotypes**

The best 21 F<sub>1</sub> genotypes and two checks were planted at three sites, namely: NaCRRI, KAZARDI and the National Semi-Arid Resources Resource Institute (NaSARRI) and evaluated for *Alternaria* blight resistance and other agronomic traits, and stability thereof. In addition, scientists and farmers evaluated the genotypes for their preferred traits. The main findings were:

- Resistance of genotypes to *Alternaria* blight across sites was not consistent.
- Across the sites, genotypes G49, G13, G67, G14 and G65 had the lowest AUDPC values and were therefore the most resistant, whereas G14, G16, G24, G29, G49, G59 and G69 were the most stable for *Alternaria* blight with below average AUDPC values.
- Genotypes G14, G49 and G67 were more stable for low *Alternaria* blight than Tanzania (resistant check) and genotypes G13, G24 and G67 were higher yielding and more stable than NASPOT 1 which was the higher yielding of the two checks.
- There were significant, positive Spearman's rank correlation coefficients between scientists and farmers' ranking of genotypes at Kachwekano and between scientists and farmers' ranking of genotypes at Namulonge for traits assessed at harvest and for cooking quality traits.

### **6.3 Implications for sweetpotato breeding**

Farmers in south western Uganda, where Kachwekano is located, predominantly plant landraces and have generally not embraced any of the improved cultivars. In addition, unlike the central region, where Namulonge is located and where yield was ranked as the most important trait, the Kabale farmers ranked sweetness (taste) as the top trait. It may be true that the improved cultivars do not meet the taste preferences of the farmers in Kabale but, at the same time, the Kabale area lacks well organised seed distribution channels. The National Sweetpotato Programme carries out on-station trials every season at Kachwekano (KAZARDI) but has not involved farmers during the evaluation stages of these trials which has evidently led to the lack of acceptance and wide dissemination of the new releases. Therefore, there is a need for scientists to involve farmers in the evaluation of on-station trials especially at harvest. The farmers can then select some of the promising genotypes for planting in their own lands or plots. To further improve acceptance and dissemination of new genotypes, the farmers could carry out on-farm trials which would provide another avenue for the distribution of new genotypes.

Established genotypes resistant to *Alternaria* blight were identified. Shock was more resistant than Tanzania (resistant check) and can be recommended for farmers in areas with high *Alternaria* blight severity. In addition, Shock can be used as a source of resistance in breeding for *Alternaria* blight resistance.

The best established cultivars that were highly stable for high yield were identified. All these are cultivars from the National Sweetpotato Program and have gone through a thorough genotype by environment evaluation. Since they have stability for yield they should be made available to the farmers in the different parts of the country. In particular, concerted efforts should be made to make these cultivars available to farmers in the remote, rural parts of the country where dissemination of new cultivars has historically been very poor. Unless every effort is made to make disease-free planting materials of new cultivars available to farmers, programmes to breed new cultivars will not benefit farmers in these remote areas.

Established cultivars that were highly stable for both high yield and high resistance to *Alternaria* blight were identified in the germplasm evaluation trial. Overall, the best cultivar combining high stability for high yield and resistance to *Alternaria* blight were NASPOT 8, Namusoga and BND145L. These cultivars should be made available in areas where they are currently not well distributed.

Among the promising  $F_1$  genotypes, G14, G49 and G67 were the most outstanding in terms of *Alternaria* blight resistance and stability while G13, G24 and 67 were the most outstanding

for high yield and yield stability. Furthermore, genotype G49 was ranked well both for stability by GEI analysis and for scientist and farmer preferred traits by the participatory selection process. The top five F<sub>1</sub> genotypes with superior performance and stability across all the evaluated traits were G13, G14, G24, G49 and G67. These promising genotypes should be included in the national advanced yield trials and on-farm trials for further evaluation.

This work has reconfirmed what was already known about *Alternaria* severity at the different selection environments with Namulonge and Serere being stable for low *Alternaria* blight severity and Kachwekano stable for high *Alternaria* blight severity (Mwanga et al., 2007; Osiru et al., 2009). The low *Alternaria* blight severity environments, Namulonge and Serere can be used for germplasm multiplication while the high *Alternaria* blight severity environment, Kachwekano can be used for germplasm evaluation

Evaluation of sweetpotato genotypes for combined stability and mean performance presents a considerable challenge to most breeding programmes. However, the ASV and GSI indices simplify the identification of genotypes that have wide or specific adaptation and good performance and are recommended to breeders as tools to aid selection. Genotypes identified as widely adapted can be grown across several environments while the specifically adapted ones can be grown only in those environments where their potential is optimally expressed.

The genetic analysis indicated that both additive and non-additive gene action are important for the expression of the traits evaluated. For the traits where additive gene action is predominant and provides for high narrow-sense heritability estimates, performance of the progeny can be predicted based on parental performance.

That families with significant and desirable negative GCA effects for *Alternaria* blight severity were obtained from crosses between parents with negative and positive GCA effects, and that families of crosses between parents with negative GCA effects were obtained with positive SCA effects indicated that parents with positive GCA effects may be of value in the development of *Alternaria* blight resistant genotypes. Conversely, some parents with negative GCA effects may not be very useful in the development of *Alternaria* blight resistant genotypes. Therefore parents should not be eliminated from the breeding program based on GCA effects alone but only after a thorough evaluation of the performance of their progeny.

The families exhibited a wide range of AUDPC values with some families being very resistant to the disease and others very susceptible. This wide range of AUDPC values indicated that considerable variability for *Alternaria* blight resistance was expressed in the

different families and therefore it is possible to select genotypes with high *Alternaria* blight resistance from the families under consideration. From the promising F<sub>1</sub> genotypes, G14, G49 and G67 were the most *Alternaria* blight resistant and will undergo further evaluation.

Among the parents, female parents Silk Omupya and Bwanjule which produced resistant families across all male parents and male parent NASPOT 2 which produced resistant families across all female parents should be used as sources of resistance in breeding for *Alternaria* blight resistant genotypes.

The significant positive Spearman's rank correlation coefficient between scientists and farmers' ranking of genotypes at Namulonge and between scientists and farmers' rankings at Kachwekano for harvest stage traits and for cooking quality traits implies that at these stages of selection, the scientists in this study were capable of selecting genotypes with farmer preferred traits. Therefore in order to conserve financial and logistical resources, it is possible for scientists with the necessary experience and knowledge of farmer preferences to carry out the evaluation of new sweetpotato genotypes' at harvest stage and cooking quality traits without the involvement of the target farmers.

Five promising F<sub>1</sub> genotypes, G13, G14, G24, G49 and G67 with better performance than the existing cultivars have been identified. These genotypes should be multiplied and further evaluated on-farm for disease and yield stability. The genotypes that satisfy the selection criteria will be recommended for release as new cultivars.

In conclusion, storage root yield, early maturity and sweetness (taste) were the study identified as the most important farmer preferred sweetpotato traits. *Alternaria* is an important sweetpotato production constraint especially in Kabale (south western region) causing yield losses of over 50% in susceptible genotypes. Among the thirty evaluated sweetpotato genotypes, Shock (a landrace) was the most resistant to *Alternaria* blight and can be used a source of resistance when breeding for *Alternaria* blight resistance. Additive gene action was identified as being more important than the non-additive gene action in the expression of resistance to *Alternaria* blight. Most encouragingly, the breeding program has generated five genotypes that are superior in performance to the existing cultivars and should be further evaluated for cultivar potential.

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