Manipulating morphological traits of cassava to enhance host plant resistance and biological control of cassava green mite in Zambia

by

Able Chalwe

BSc. Agriculture (University of Zambia), MSc. Plant Genetic Manipulation (University of Nottingham)

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African Centre for Crop Improvement
School of Agriculture, Earth and Environmental Sciences

University of KwaZulu-Natal Republic of South Africa

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Thesis abstract

Understanding direct and indirect defense mechanisms that enhance host plant resistance (HPR) and biological control is critical for successful development of an integrated pest management (IPM) approach. Cassava green mite (CGM) (*Mononychellus tanajoa* Bondar (Acari: Tetranychidae)) is a major arthropod pest of cassava (*Manihot esculenta* Crantz) in Africa. Strategies to control CGM include HPR and biological control by use of exotic natural enemies particularly the predatory mite *Typhlodromalus aripo* DeLeon (Acari: Phytoseiidae). The success of the latter depends on continuous survival of the natural enemy which requires suitable host plants and weather conditions. Various plant morphological traits have been recognized as indirect defense mechanisms that enhance HPR to CGM, and/or attract *T. aripo* in cassava. It was envisaged that integration of HPR and classical biological control approaches through manipulation of such indirect defense traits would lead to a more sustainable management of CGM in view of anticipated climate change. Lack of information on farmers' perception of CGM and preferred varietal attributes, and gene action controlling the inheritance of CGM resistance also limits success of resistance breeding and adoption of varieties. This research was undertaken to gather information on farmers' perceptions of cassava varietal attributes and cultural practices in relation to CGM resistance, identify suitable sources of resistance and environments for future breeding; and to determine the nature of gene action controlling CGM resistance and the inheritance of plant morphological traits that enhance the ability of cassava to host and support continuous survival of natural enemies.

High fresh storage root yield (FSRY), high storage root dry mass percentage (SRDM%), earliness combined with extended underground storability, and resistance to foliar pests and diseases are the major factors that influence adoption and retention of genotypes by farmers. Moles, termites and CGM are the most widespread and most damaging pests. However, due to the non-conspicuous nature of CGM, its effects are under-estimated and are given limited attention by farmers. The majority of the farmers are familiar with CGM leaf damage symptoms but they cannot associate them with the actual pest. Participation of farmers in field training and field research activities helps them to know CGM. Crop rotation, intercropping, removal of shoot tips, selective pruning of infested shoots, and burning of cassava fields are some of the ways used by farmers to manage CGM. Farmers associate hairy broad-leaved, tall cassava genotypes and pink leaf pigmentation (anthocyanin) with low CGM damage.

There is substantial genetic variability in the Zambian cassava germplasm for CGM resistance and associated plant morphological traits such as leaf pubescence (Pbs), leaf retention (LR), stay green (SG), tip size (TS), tip compactness, and plant height (PH), stem diameter (StD),

SRDM% and FSRY. Genotypes with wide or specific adaptability for these traits have been identified, and should be recommended for general or localized production and for use as sources of desired genes in crop improvement. Genotypes L9.304/147, 92/000, TME2, 4(2)1425, I60/42 and L9.304/175 combine wide adaptability with high levels of resistance to CGM. Genotypes Kapeza, L9.304/147 and 4(2)1425 are able to produce 13-15 t ha^{-1} at 9 months after planting suggesting their potential for early bulking.

This study has shown that both additive and non-additive gene effects play a role in the expression of CGM resistance and associated plant morphological traits. The best combinations of parents for resistance against CGM were 4(2)1425 x L9.304/147 and Mweru x L9.304/147, while L9.304/147 x I92/000 displayed combined resistance to CGM and cassava mosaic disease (CMD). The resistance of cassava to CGM is positively correlated with Pbs, LR, and TS, SG, PH, StD. Overall, the study has shown that there is wide diversity in the expression of valuable indirect defense traits among genotypes, indicating that there is scope for integration of biological control and host plant resistance for CGM in Zambia. The release of genotypes that exhibit high level of intra-season and inter-season stability for enhanced expression of LR, SG, and Pbs will minimize the impact of CGM on FSRY and SRDM% that results from seasonal effects. Such genotypes should also provide habitat for and thus help to ensure the survival of *T. aripo* in cassava fields. The study has contributed to the promotion of food security through identification of early-bulking genotypes which also have good potential for extended underground storability of roots. Early-bulking, high FSRY and SRDM% and SRR resistance are farmer-preferred traits. Therefore, enhancement of such traits through plant breeding is likely to increase the adoption of new genotypes by farmers.

Declaration

I, **Able Chalwe**, declare that:

1. The research reported in this thesis, except where otherwise indicated, is my original research.
2. This thesis has not been submitted for any degree or examination at any other university.
3. This thesis does not contain other person's data, graphs or other information, unless specifically acknowledged as being sourced from other persons.
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Signed…… ……Date……..……..

Able Chalwe (Student)

As the candidate's supervisors we agree to the submission of this thesis:

Signed:……Date……..

Prof. Rob Melis (Principal supervisor)

Signed:……Date……...

Dr. Paul Shanahan (Co-supervisor)

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Dedication

I dedicate this thesis to my daughter Chikonsha Chalwe, and my late sisters Grace, Maureen, and Martha.

Table of Contents

Introduction to thesis

1. Importance of cassava

Cassava is an important tropical root crop widely grown for its storage roots that are mainly used for human consumption and industrial applications. Cassava is used in several industries because of the high quality starch that is extracted from its storage roots (Scott et al., 2000). Cassava offers the advantage of flexible harvesting date, allowing farmers to keep the storage roots underground until needed. This, coupled with the ability of the crop to grow and give reasonable yields in marginal, low fertility acidic soils under variable rain-fed conditions ranging from less than 600 mm to more than 1000 mm per year (El-Sharkawy, 2003), makes cassava a highly dependable crop. The annual production of cassava in the world is estimated at 230 million tons, of which 53% is produced in Africa (FAOSTAT, 2012), where cassava is consumed by more than 200 million people as the second major starchy staple crop after maize.

Traditionally, cassava is grown in areas between 30° N and 30° S of the equator, where annual mean temperatures range from 18 to 20°C (Hillocks, 2002). However, unlike other crops, cassava has no critical growth period, when stress may cause major crop failure (Lenis et al., 2006)**.** The lack of such critical growth stage is linked with the simultaneous development and growth of leaves and storage roots which occur in cassava (El-Sharkawy, 2003). The robustness of cassava partly lies in its tendency to close its stomata, and maintain high concentrations of carbon dioxide as well as to fold leaves and reduce leaf area growth, in response to moisture stress and extremely high temperatures, which enables it to minimize transpiration and resource use to conserve carbohydrates (Alves and Setter, 2004).

2. Origin, production, and consumption of cassava in Zambia

Cassava was first brought by Portuguese navigators from Brazil to Fernando Po where it was grown in the Gulf of Benin and around the Congo River in the 16th century (Hillocks, 2002). It is believed that cassava probably arrived in Zambia via the Congo Basin following the migration of the Bemba people from the west in the early 1700s, into the northern part of Zambia, from where it has continued to spread to the Central, Copperbelt, North-Western, and Western Provinces (Haggblade and Nyembe, 2007).

Cassava serves as a strategic hunger relief crop in times of drought. Farmers in Zambia normally respond to drought by expanding their cassava field and reducing the area under cultivation of maize (FAOSTAT, 2012). The ability of cassava to grow on marginal soils and its low fertilizer requirement make it suitable for small-scale farmers (Nweke et al., 2002). Furthermore, lower adult labor supply, caused by HIV/AIDS infection and related mortalities,

induces farm households to move out of maize into cassava which has low external input and low labour requirement (Haggblade and Nyembe, 2007).

Currently cassava is second to maize in its importance as a staple crop in Zambia. Most of the cassava produced in Zambia is used for human consumption (Figure 1). Farmers market about 8% of total cassava production, or roughly 800 000 t of cassava per year, 350,000 t as fresh cassava with the remaining 450 000 t dried into approximately 150 000 t of cassava chips which is supplied, through informal cross-border trading, to markets in the Democratic Republic of Congo and Angola for urban consumption (Haggblade and Nyembe, 2007). Cassava leaves are also consumed as a vegetable by many people throughout the country. The sale of cassava leaves provides an important source of income for women in urban markets.

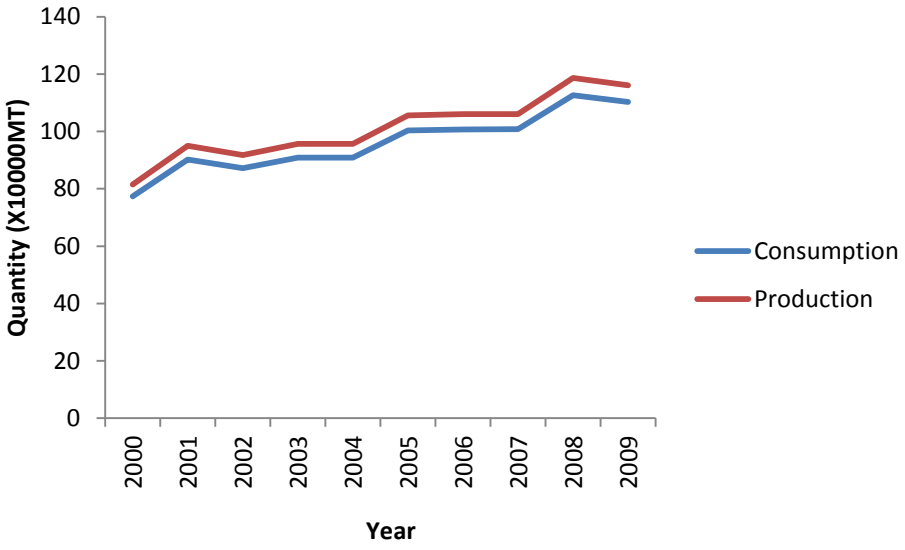

Figure 1: Production and consumption levels of cassava in Zambia, 2000-2009 (Data obtained from FAOSTAT http://faostat.fao.org/site/291)

3. History of cassava research programme in Zambia

The Root and Tuber Improvement Programme (RTIP) in Zambia was initiated in 1979 following occurrence of drought in 1978 (RTIP, 1989). Two years after the inception of RTIP, cassava mealybug (CM), *Phenucoccus manihoti* Mat.-Ferr. (Homoptera: Pseudococcidae) was reported in Luapula Province, where it caused yield losses ranging from 60 to 100% in 1981/82 (Chakupurakal et al., 1994). The seriousness of CM in Zambia, forced the government to seek external support from the International Institute of Tropical Agriculture (IITA)-led consortium. Starting in 1984, the Government of Zambia together with IITA's biological control programme

instituted trial releases of *Apoanagyrus* (*Epidinocarsis*) *lopezi* De Santis (Hymenoptera: Encyrtidae), a predator wasp which had effectively controlled outbreaks of CM in other regions of Africa (Zeddies et al., 2001). In 1986, with financial support from the International Fund for Agricultural Development, the Zambian team launched a country-wide programme of mass rearing followed by aerial and ground releases of *A. lopezi* (Yaninek and Herren, 1988; Alene et al., 2005). The RTIP also initiated a breeding programme for cassava, and managed to collect 500 landraces and 200 exotic cassava genotypes. Following this, the Swedish International Development Agency launched a ten-year programme of funding for RTIP to conduct a series of mass selection cassava trials from 1987 onwards. Subsequently, 700 accessions were systematically evaluated for yield, earliness, and resistance to cassava mosaic disease (CMD). Alongside the field screening of cassava germplasm, the releases of natural enemies also continued for four years (Alene et al., 2005).

Appreciable achievements were recorded from 1990, when the CM population had declined significantly and a pest-predator equilibrium had been established (Chakupurakal et al., 1994; Malambo et al., 1998). Furthermore, three local genotypes, namely Bangweulu, Kapumba and Nalumino were released in 1993/94, following systematic evaluation by the RTIP. These genotypes yielded 20 to 30 t ha^{-1}, compared to an average of 7 t ha^{-1} obtained from local landraces, and provided superior resistance to CMD and major pests (Chitundu and Soenarjo, 1997).

Soon after the successful containment of CM, another arthropod herbivore commonly known as cassava green mite (CGM), *Mononychellus tanajoa* Bondar (Acari: Tetranychidae), became a serious pest in Zambia and its infestation resulted in as much as 30% losses in fresh storage roots and 60% losses in dry mass (Chakupurakal et al., 1994). Consequently, collaborative efforts between IITA and the National Biological Control Unit shifted to CGM because serious outbreaks were reported from several provinces from time to time. The initial attempts to control of CGM in Zambia involved experimental releases of two species of Colombian exotic phytoseiid namely *Neoseiulus idaeus* Denmark and Muma (Acari: Phytoseiidae) and *N. anonymous* Chant and Baker (Acari: Phytoseiidae) in 1984 (Chakupurakal et al., 1997; Yaninek et al., 1993). These species of natural enemies failed to establish. An exotic predatory mite, namely*Typhlodromalus aripo* DeLeon (Acari: Phytoseiidae), was subsequently imported from South America (Bellotti et al., 1994), where it had proved to be a successful predator to CGM among other pests, and was released in Zambia in 1991 (Chakupurakal et al., 1997; Yaninek and Hanna, 2003; Alene et al., 2005).

Breeding work under RTIP also continued at Mutanda and Mansa research stations, resulting in the development of four new cultivars which were released in the 2001/2002 season, following the hybridization which commenced in 1989. The four cultivars namely Mweru, Chila,

Tanganyika and Kampolombo, combine high fresh storage root yield (FSRY), with early bulking and moderate resistance to CMD and CM. Collaboration between IITA and RTIP was strengthened following the inception of the Southern Africa Root crops Research Network (SARRNET), which has a regional mandate to facilitate exchange of cassava germplasm among network member countries. Through these efforts several elite genotypes of cassava which included CGM-resistant genotypes such as TME 4(2)1425 and TME 60142 were introduced into Zambia from IITA Hahn et al., 1989; Mahungu et al., 1994). The introduced genotypes have been evaluated for local adaptation and as gene sources for CGM resistance. Despite the efforts, CGM and CMD still remain two serious problems in much of Zambia (SARRNET, 2008).

4. Need for cassava green mite resistance breeding in north-western Zambia

Strategies to control CGM in Zambia have included host-plant resistance (HPR) and mainly biological control by use of exotic natural enemies particularly the predatory mite *T. aripo.* These two strategies unfortunately have always been implemented separately as two parallel complementary programmes. However, post-release investigations show that *T. aripo* is failing to establish, particularly in north-western Zambia. No matter which predator strain is used, *T. aripo* tends to disappear from cassava apices during the dry season (Mebelo et al., 2003). Similar results have been reported from some parts of Cameroon, and Uganda, where *T. aripo* seems to establish well only during the rainy season, and disappears from cassava plants during the dry and cold seasons (Onzo et al., 2003; Hanna et al., 2005), resulting in increased populations of CGM and associated damage in cassava fields in the dry season (Yaninek et al., 1989). Consequently, considerably high incidences of CGM of 10-100% were recorded in cassava fields in Northern and North-Western Provinces of Zambia, causing 50-75% leaf damage early in the rainy season (SARRNET, 2008).

Plant morphological traits, which attract the predatory mite to the host plant and provide them shelter or enhance the ability of the predator to find the prey, should receive more attention in cassava breeding programmes which are aimed at controlling CGM. Plant breeders need to source such traits and improve them by breeding, while the selection of traits potentially detrimental to natural enemies should be avoided whenever possible (Cortesero et al., 2000). Research has shown that *T. aripo* resides in the growing point of the plant during the day and forages on the young leaves during the night hours, while CGM prefers young leaves (Onzo et al., 2003). Therefore loss of shoot apices in the dry season induced by drought adversely affects the natural enemy, contributing to the buildup of CGM on the remaining fewer leaves. It is proposed that cassava genotypes which are tolerant to drought may also be resistant to CGM and that enhanced leaf retention and stay green in cassava may be a major factor of resistance to CGM (Nukenine et al., 1999, 2002). Genotypes which combine large compact shoot apices

with high pubescence (Pbs), especially of immature and apical leaves have been shown to protect *T. aripo*, against harsh weather conditions, supporting its continuous survival in cassava fields (Malambo et al., 1998; Mebelo et al., 2003; Zundel et al., 2009).

Recent studies have further shown that pubescent cassava genotypes tend to release volatiles that attract *T. aripo* (Onzo et al., 2012). Work by Agrawal et al. (2000) has demonstrated that the absence of leaf hairs can severely reduce abundance, distribution, reproduction, and prey consumption of predator, while presence of leaf hairs can significantly increase populations of predatory arthropods and decrease populations of phytophagous arthropods. Even in the absence of the natural enemy cassava genotypes exhibiting high Pbs tend to be more resistant to CGM and produce higher FSRY than glabrous genotypes (Byrne et al., 1982; Hahn et al., 1989; Raji et al., 2008), suggesting that Pbs could be a primary character responsible for resistance to CGM. Howvever, there is very little information on the stability cassava genotypes for such morphological traits. There is a need to know how such important traits are influenced by environment so that stable genotypes can be identified which could be used as sources of stable genes for CGM resistance breeding. Furthermore information pertaining to farmers' perceptions and knowledge of CGM needs to be captured and considered in breeding in order to accelerate adoption of new cultivars by farmers,

5. Research objectives

The main objective of the study was to develop cassava genotypes that combine resistance to CGM with enhanced expression of plant morphological traits that attract and support continued inhabitance of *T. aripo* in cassava and with farmer preferred traits.

The specific objectives were to:

1. gather traditional knowledge on desirable and non-desirable varietal attributes, as well as on plant morphological traits and cultural practices that are associated with reduced pest population and leaf damage in cassava fields;
2. gather information about farmers' perception of major cassava pests and traditional coping strategies thereof;
3. understand stability of various parental genotypes in different locations and seasons so as to identify stable sources of resistance to CGM;
4. establish the nature of gene action controlling inheritance of CGM resistance traits and associated plant morphological traits; and
5. develop new cultivars that combine resistance to CGM with other farmer-preferred traits.

The thesis is structured as follows:

Chapter 1: A review of pertinent literature

Chapter 2: Farmers' perception of cassava green mite in north-western Zambia

Chapter 3: Genotype by environment interaction effect on resistance to cassava green mite *Mononychellus tanajoa* (Bondar) (Acari: Tetranychidae) and other agronomic traits of cassava grown in north-western Zambia

Chapter 4: Intra-season and inter-season stability of resistance to cassava green mite *Mononychellus tanajoa* (Bondar) (Acari: Tetranychidae) and associated plant shoot morphological traits of cassava grown in north-western Zambia

Chapter 5: Inheritance of resistance to cassava green mite *Mononychellus tanajoa* (Bondar) (Acari: Tetranychidae) and other important agronomic traits in cassava grown in north-western Zambia

Chapter 6: General overview

Chapters 2-5 are written as discrete publication-ready papers, and consequently there will be some overlap of content and references.

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CHAPTER 1

Literature review

1.1 Introduction

Cassava (*Manihot esculenta* Crantz) is a staple food root crop for more than 600 million inhabitants in the tropics and subtropics. It is cultivated as an annual and biennial crop for its starchy roots that can be harvested at 8 to 18 months after planting (El-Sharkawy, 1993, 2004). The storage roots are mainly consumed as human food in various forms, for animal feed, as well as for starch extractions and various industrial uses (Scott, 2000; El-Sharkawy, 2004; Lebot, 2009). World annual current production exceeds 230 million tons of fresh storage roots (about 50% being produced in sub-Saharan Africa), with an average yield of 10 t ha^{-1} (FAOSTAT, 2012). It is the second most important staple crop after maize in Zambia and the rest of Africa. Cassava is a low input crop which is able to grow under marginal soil fertility in acidic soils where other crops such as maize, which demand application of purchased fertilizer and other agro-chemicals, fail (El-Sharkawy and De Tafur, 2010). For this reason most of the cassava in Africa is produced by small scale resource-limited farmers and mainly women, who may not afford purchased agro-chemicals and irrigation (Borlaug, 1983). Furthermore, cassava has the ability to tolerate a range of climatic conditions and soil types, and to grow under varying rainfall ranging from as low as 500 mm to over 1000 mm per annum. This coupled with the flexibility of cassava to be harvested at any time of the year when a farmer needs food, make it a strategic food crop which serves as a hunger relief during periods of drought for most families in Africa (Nweke et al., 2002).

However, in regions that experience mono-modal rainfall pattern, cassava takes long to mature. This long growth cycle, coupled with the frequent farmer-to-farmer exchange of stem cuttings which are used as propagation materials, expose cassava to pests and diseases. The major pests and diseases that affect cassava in many parts of Africa include cassava mosaic disease (CMD), cassava mealybug (CM), and cassava green mite (CGM). Both CGM and CM are reported to have been introduced into Africa accidentally through movement of planting materials from South America (Chakupurakal et al., 1994), and have since spread throughout the cassava-belt of Africa (Yaninek, 1988). These two pests have contributed to great losses in the yields of cassava storage roots and planting stakes. Considerable efforts and resources have been committed to the biological control of these arthropod pests in Africa through the release of exotic natural enemies, which have resulted in successful control of CM (Chakupurakal et al., 1994). Sources of resistance to CGM have been found and distributed to national cassava programmes in Africa, with technical support from the International Centre for

Tropical Agriculture (CIAT) and the International Institute of Tropical Agriculture (IITA) (Mahungu et al., 1994; Bellotti et al., 2012). Despite these efforts, CGM and CMD are continuously reported to cause serious damage in cassava fields in some countries of Africa including Zambia (SARRNET, 2008).

The literature review therefore considers CGM as a major herbivorous arthropod pest contributing to low yields of fresh storage roots (FSRY) and cassava leaves which are used as vegetable in some parts of sub-Saharan Africa. It has highlighted on some progress made so far in breeding for resistance, and biological control against CGM, and the possibility of integrating these two complementary strategies.

1.2 The origin and diffusion of cassava into Zambia

For a long time, the origin of cassava (*Manihot esculenta* Crantz subspecies *esculenta*) remained unclear, and the ancestry of cassava was not known. However, in 1982, a wild species, *Manihot flabellifolia* (Pohl), in central Brazil, was reported as the closest wild relative to cassava (Allem, 1987, 1994). Though diverse results have been obtained concerning the phylogeny of cassava (Burger et al., 2008), all the results appear to support the view that *M. flabellifolia* was the progenitor of the crop (Olsen and Schaal, 1999). Based on DNA sequence variation from a portion of the gene encoding glyceraldehyde 3-phosphate dehydrogenase (*G3pdh)*, Olsen and Schaal (2001) confirmed that the crop was derived from populations of the subspecies *flabellifolia* along the southern border of the Amazon basin. Moreover, these authors have stated that “the pattern and degree of variation in the crop versus the wild relative populations indicate that subspecies *flabellifolia* alone can account for the genetic variation observed in cassava”. Therefore the southern border of the Amazon basin stands as the centre of origin for *M. esculenta* (Olsen and Schaal, 2001).

1.3 Taxonomy of cassava

Cassava belongs to the botanical species *M. esculenta* of the family *Euphorbiaceae*, sub-family *crotonoideae*, and tribe *Manihotae*. The genus Manihot contains about 100 species of herbs, shrubs and trees among which the production of latex and cyanogenic glucosides is common (Ng and Ng, 2002). Although most of the species so far studied contain 36 chromosomes (diploid genome 2n=36), which show irregular pairing at meiosis, spontaneous polyploidy such as triploids (3n) and tetraploids (4n) of some genotypes have been reported in both wild relatives and domesticated cassava (Hahn et al., 1980). However, three nucleolar chromosomes have also been reported, which is high for true diploids, indicating that *Manihot* species are probably segmental allotetraploids, with a basic chromosome number x=9 (Jennings and Iglesias, 2002).

1.4 Major pests and diseases of cassava in Zambia

In spite of the importance of cassava as a famine and food security crop, it is constantly threatened by production constraints such as diseases and pests, lack of improved genotypes, lack of good quality planting material, frost, and severe drought stress. Diseases and pests tend to have great influence on stability of production and can cause total yield loss in some cases (Bellotti et al., 1994). Diseases that particularly affect cassava in Zambia include CMD caused by viruses of the family *Geminiviridae* (Legg et al., 2011), cassava brown streak disease caused by viruses of the family *Potyviridae* (Ogwok et al., 2012), cassava anthracnose disease (CAD) caused by *Colletotrichum gloesporioides f.sp. manihotis* (Williams et al., 2012)**,** brown leaf spot, and cassava root rot disease caused by *Cercospora henningsii* Allesch (Ayesu-Offei, 1996). The most important pests include CGM, CM, termites (*Microtermes* sp.) and rodents. From the early 80s CM was recognized as the most serious pest that almost wiped out the crop in Zambia. Concerted efforts were devoted to its management through biological control. Through collaborative efforts between IITA and CIAT, and the national biological control programme, the pest was controlled in the mid-90s (Chakupurakal et al., 1994). Soon thereafter, CGM appeared and became another serious arthropod pest that has spread throughout the country (Malambo et al., 1998).

1.4.1 Biology, origin, and ecology of cassava green mite

Cassava green mite belongs to the different taxa of spiders and ticks. The pest has a rapid multiplication potential. It completes its five-stage life cycle within 12-14 days. Though the life span of an adult CGM does not exceed 30 days, within this short period a single female can lay up to 70 eggs depending mainly on temperature and relative humidity (RH). Maximum oviposition has been recorded at 27ºC with RH ranging 50 to 70% (Hahn et al., 1989; Yaninek et al., 1989). Cassava green mite is of Neotropical origin and was first reported in Uganda in 1972, where it was accidentally introduced on cassava cuttings imported from South America. The centre of origin of CGM in South America and most of Africa share similarities in temperature and RH. This, coupled with abundance and high frequency of cassava fields in Africa, promoted rapid spread of CGM throughout the entire cassava-belt of the continent (Yaninek and Herren, 1988).

The influence of temperature and rainfall on the abundance of CGM has been comprehensively studied (Yaninek et al. 1989; Hahn et al., 1989). The populations of CGM are reported to reduce with increase in rainfall on a seasonal calendar, but peaks in mite populations are observed in the dry season and at the beginning of the wet season. Generally, CGM is a dry season pest that causes severe damage on host plants subjected to prolonged drought stress (Yaninek et al., 1989).

1.4.2 Dispersal of cassava green mite

Dispersal of CGM is generally achieved by walking, drifting passively through the air or moving involuntarily with infested plant materials (Yaninek, 1988). For as long as the suitable foliage is available on the host plant, mites often will remain on the same leaf for several generations. However, changes in leaf quality such as hardness of leaves, loss of chlorophyll due to senescence, or disease infection, and general leaf loss that result with crop age cause mites to crowd on a few healthy and active leaves (Yaninek et al., 1989). The increased competition resulting from such increasing population densities prompt the mites to disperse in search of more favourable habitats (Kennedy and Smitley, 1985; Yaninek, 1988). It is suspected that CGM dispersal from the lower mature leave towards preferred young leaves near the top is probably a positive response to light (Yaninek, 1988). Similarly the colour or shape of leaf (Hanna et al., 1997) and ultra-violet radiation (Onzo et al., 2010) have also been reported to influence abundance of mites in cassava. However, to avoid the risks associated with dispersal, some mites may remain and survive on the buds of heavily defoliated stem shoots, until new leaf buds grow. According to Yaninek (1988), the ability of CGM to survive for up to 60 day in the absence of water and nutrients on stem cuttings, and detached cassava leaves which are sold locally as vegetable, enables another mode of dispersal for the pest.

Temperature is a dominant factor affecting the growth rate and development of many arthropod populations including tetranychids. Temperatures below 14.4^{o}C result in high CGM mortality, because CGM is a specifically adapted to tropical or subtropical conditions (Yaninek et al., 1986). The mites easily get washed off from cassava leaves in heavy rains which is another cause of mortality for CGM.

1.4.3 Alternative hosts of cassava green mites

As the common name suggests, CGM is generally known to occur specifically on cassava, but it has also been reported to occur on several other plant species such as *Curcurbita pepo* L. (Cucurbitaceae), *Lycoperscum esculenta* Mill (Solonaceae) and *Sechium edule* Jacq. (Curcubitaceae) in north-eastern Brazil (Tuttle et al., 1977). De Moraes et al. (1995) also reported the presence of *M. tanajoa* on *Passiflora cincinnata* Matt (Passifloraceae), *Manihot pseudoglaziovii* Pax. et K.Hoffm. (Euphorbiaceae), *Pavonia cancellatta* Cav. (Malvaceae), *Solanum erianthum* D. Don. (Solanaceae), *Bauhinia forficate* Link. (Casalpiniaceae), *Borreria verticillata* G.F.W. Meyer (Rubiaceae), *Macroptilium mortii* Bench. (Fabaceae). However it is not known as to whether CGM feeds on such plant species, but the frequent occurrence of all stages of CGM observed on *P. cincinnata* and *M. pseudoglaziovii*, even when the mite was not abundant on cassava, indicates that these plants serve as alternative hosts, while other plants could just be random temporary hosts.

1.4.4 Cassava green mite damage on cassava plants

Cassava green mites prefer to feed on the underside of young emerging tender leaves of cassava. The damage on these leaves results from the injury caused by the needle-like stylet which CGM uses to pierce and suck leaf cell contents, causing chlorophyll depletion on cassava leaves (Bellotti, 2002). The damage symptoms resulting from heavy infestations appear in the form of defoliation starting from the growing tip of the plant and progressing downward, killing apical and lateral buds, resulting in severe dieback and candle-stick appearance of stem shoots (Bellotti, 2002). On the leaves, damage by CGM appears as stippling on the basal half of the leaf and along the veins, which later appear as “pin-pricks”. Young leaves emerge deformed and reduced in size, with a mosaic pattern resembling CMD symptoms (Nukenine et al., 2002). Environmental stress associated with drought and excessive soil fertility depletion tends to augment the level of CGM leaf damage (CGM LD). Omorusi and Ayanru (2011) observed significant reduction in CGM LD symptoms with increase in nitrogen, phosphorus and potassium element supply to CGM infested cassava plants. According to Okeke (1990) this reduction in CGM LD is attributed to the improvement in plant vigour arising from improved nutrient supply, which also translates into improved FSRY. Similarly, Agboton et al. (2006) have indicated a positive association between weed density and CGM population density (CGM PD) in Southern-Benin, suggesting that cassava genotypes which express enhanced ability to outperform weeds are likely to sustain less CGM LD.

1.4.5 Yield losses caused by cassava green mite

Cassava storage root yield losses due to CGM have been estimated to be in the range of 30 to 50% (Yaninek and Herren, 1988; Yaninek et al., 1993). Byrne et al. (1982a) reported 73% reduction in FSRY and 67% reduction in stake yield of a CGM-susceptible genotype. From this study it was also observed that harvest index (HI) is not affected by CGM infestation, suggesting that harvest index (HI) can be used with damage ratings for selecting CGM resistant and high yielding cassava genotypes. According to Cock (1978), genotypes with leaf area index (LAI) exceeding 3.0-3.5 can sustain a greater CGM LD per leaf, but their FSRY may not be affected, while higher losses in FSRY are more likely to result from CGM LD on genotypes which have LAI less than 3.0. A strong negative association has been reported between plant height and CGM LD (Egesi et al., 2007). Therefore, in order to produce genotypes that combine good FSRY and resistance to CGM, Byrne et al. (1982a) recommend use of a mixture of tolerance and other resistance components in HPR breeding.

1.5 Cassava green mite control through host plant resistance breeding

Host plant resistance has been defined as the property that enables a plant to avoid, tolerate, or recover from injury by insect populations that would cause greater damage to other plants of the same species under similar environmental conditions (Kogan, 1994). It represents the inherent

ability of crop plants to restrict, retard or overcome pest infestation and thereby improve yield and/or quality of the harvestable product (Dent, 1991). The concept of HPR has been broadly interpreted, and may not always refer to resistance properties of the plant itself. Thus a form of resistance might arise if a plant is protected from insects by having a particular phenology. Horber (1980) referred to this type of resistance as non-functional resistance. Also another form of resistance might arise if a plant is protected by natural enemies of the insect pest, which according to Price (1986) is called extrinsic resistance.

1.5.1 Breeding methods to incorporate insect resistance

There are several conventional breeding methods used to develop insect resistance including mass selection, pure-line selection, recurrent selection, pedigree breeding, bulk breeding, single-seed descent and backcross breeding (Thomas and Waage, 1996). Many programmes utilize more than one of these techniques during the development of a resistant genotype. Cassava breeding programmes mainly use mass selection and backcrossing for insect resistance (Hahn et al., 1989; Bellotti and Arias, 2001). The breeding programme at the International Crop Research Institute for the Semi-Arid Tropics has utilized mass selection, recurrent selection, and pedigree breeding techniques to develop resistance to stem borer in sorghum (*Sorghum bicolor* L.) (Nwanze et al., 1991). Pedigree breeding has been used for resistance development in rice for green leafhopper(*Nephotettix virescens* Distant), brown anthopper (*Nilaparvata lugens* Stål) and the Asian rice gall midge (*Orseolia oryzae* Wood-Mason) and in sorghum for resistance to shoot fly (*Atherigona soccata* Rondani*),* greenbug (*Schizaphis graminum* Rondani) and sorghum midge (*Stenodiplosis sorghicola* Coquillett*)* (Dent, 1991).

Mass selection: Phenotypic mass selection for insect resistance has been the major selection strategy in cassava breeding both at CIAT and IITA (Hahn et al., 1989; Mahungu et al., 1994; Jennings and Iglesias, 2002; Kawano, 2003; Ceballos et al., 2004; Cach et al., 2005). Mass selection involves selecting individual plants on the basis of superior qualities, such as resistance, after each cycle of breeding (Smith, 1989). Mass selection has also been used to increase potato resistance to the potato leafhopper (*Empoasca fabae* Harris) (Sanford and Ladd, 1983).

Backcross breeding: This method provides an effective means for improving genotypes that are deficient in one or a few characters. The method involves a recurring backcross to one of the parents (recurrent parent) of a hybrid to incorporate the desirable trait. The non-recurrent parent is the source of resistance with a higher level of resistance than that used in the previous backcross. This method is better suited for introgression of highly heritable traits (Dent, 1991).

At CIAT, backcrossing has been used to incorporate resistance to whitefly and mites into cassava (Bellotti and Arias, 2001; Bellotti and Kawano, 1980).

1.5.2 Mechanisms of resistance

According to Bynum et al. (2004), resistance can be classified by a mite's response to plant defense as antibiosis and antixenosis or by the plant's ability to withstand mite damage as tolerance. Both antixenosis and antibiosis have been observed for CGM. Byrne et al. (1982b) have reported on the ability of CGM to discriminate between susceptible and resistant genotypes and show preference for the former in its oviposition, suggesting that antixenosis is the main mechanism of resistance to CGM. Antibiosis is usually reflected through reduced fecundity, a longer development time, a shorter adult lifespan of the mite, and higher larval and nymphal mortality when CGM is feeding on resistant versus susceptible genotypes (Byrne et al., 1982b). Research by Hahn et al. (1989) at IITA indicates strong involvement of tolerance in the resistance of cassava genotypes to CGM. Plants are able to recover from mite feeding damage, without affecting the CGM population dynamics.

1.6 Cassava green mite control through biological control

Initial efforts to combat CGM in Africa involved a search for indigenous natural enemies for the pest. A complex of indigenous natural enemies was found on cassava, but it was not considered sufficiently effective to control the pest (Nyira and Mutinga, 1977). Therefore, exotic phytoseiid predators were imported from South America, where the first effective phytoseiid predators had been found (Belloti et al., 1987), which included *Neoseiulus idaeus* Denmark and Muma (Acari: Phytoseiidae) (Yaninek et al., 1991), *Typhlodromalus manihoti* Moraes (Acari: Phytoseiidae) (Yaninek et al., 1998), and later *T. aripo* DeLeon (Acari: Phytoseiidae) (Hanna et al., 2005; Yaninek and Hanna, 2003). These predators were released in the cassava belt of Africa, including Zambia (Malambo et al., 1998), but only *T. aripo* proved to be a success, and therefore, efforts to control CGM have concentrated on the use of *T. aripo* (Yaninek and Hanna, 2003). Research has shown that high population densities of *T. aripo* in cassava fields have also been associated with low severity of cassava bacterial blight (CBB), CAD and CMD (Amusa and Ojo, 2005; Onzo et al., 2005), suggesting that *T. aripo* also could be a natural enemy to other insects that act as vectors for these diseases. However, post-release studies in some parts of Zambia, Cameroon, and Uganda have shown that *T. aripo* seems to establish well during the rainy season, but disappears from cassava plants during the dry and cold seasons (Mebelo et al., 2003; Onzo et al., 2003; Hanna et al., 2005).

Post-release surveys of all the fields in Luapula and North-Western Provinces of Zambia, where the phytoseiids were released since 1992, were carried out in 1995. Observations indicated that none of the species released in previous years had established, except *T. aripo* which was

released in March 1995 at one location in Luapula Province. *Typhlodromalus aripo* were not recovered at the release sites after the cold season in June 1995. Further follow-up surveys made from January to June 1996 revealed, however, that recovery of *T. aripo* in increasing numbers from January to June in three release fields in Luapula Province and three release fields in Mwinilunga and Zambezi districts of North-Western Province. *Typhlodromalus aripo* was recovered only from the fields that received releases in October and December 1995. No recovery was made from fields that received releases just before, during or soon after the dry season between April and September. This suggests that phytoseiids should not be released during the colder period to avoid mortality. It was found that establishment was faster in fields cultivated with pubescent cassava genotypes and in genotypes with larger shoot tips (Anonymous, 1990; Malambo et al., 1998).

The rate of spread of *T. aripo* to other fields was however slow (1km y^{-1}) as compared to 12.3 km y^{-1} reported in West Africa (Yaninek et al., 1989). This slow rate of spread was probably due to wide isolation (low frequency) of fields particularly in Luapula, and due to unknown reasons in North-Western Province, which has large cassava fields. Although *T. aripo* dispersal was slow in both provinces, their increasing densities gradually reduced CGM populations in established fields within a short period (December to May) (Toko, 1996). Unfortunately, *T. aripo* disappeared again in July 1996 from all the initially established fields in Luapula and North-Western Provinces.

The disappearance is possibly attributed to the cold conditions prevailing during the cool months of the dry season between May and July and also to changes in host plant conditions such as defoliation and hardening of cassava leaves that result from the low temperatures and RH (Toko, 1996). Temperatures fall below 18°C from May to July and sometimes frost is experienced during these months, conditions that kill *T. aripo,* and any other phytoseiids, as well as the cassava plant. A high survival rate of *T. aripo* in Zambia has been observed at temperatures of around 27°C with RH slightly less than 70% from October to April.

The disappearance of *T. aripo* allowed CGM PD to increase again. Cassava green mite is still a serious pest causing considerable damage to cassava in Zambia and the need to collect *Typhlodromalus* species and other phytoseiids, as well as integration of HPR and bio-control of CGM should be emphasized.

1.7 Integration of biological control and host plant resistance breeding

Studies have revealed substantial interaction between plant traits conferring herbivore resistance and predators (Panda and Khush, 1995; Thomas and Waage, 1996). Plant breeders and biological control workers often seem to be working independently. Plant breeders have focused on selecting genotypes with enhanced defense against pests, while biological control

workers have concentrated on improving natural enemy traits, such as reproduction and host finding efficacy. There is need for integrating these two pest management practices (Cortesero et al., 2000).

1.7.1 Manipulating plant morphological traits

Plant breeders have paid little attention to indirect defense traits that influence survival of natural enemies of plant pests (Panda and Khush, 1995). Plant traits that render the plants attractive to the natural enemies of plant pests or that facilitate smooth movement and enhance the efficiency of natural enemies to search and discover the pest should be looked for in wild species and selected crop genotypes, and their expression should be improved through breeding (Cortesero et al., 2000). On the other hand, traits potentially detrimental to natural enemies should be selected against whenever possible. Agrawal et al. (2000) have demonstrated the existence of negative relationship between the presence of leaf domatia on the undersides of perennial plant species and abundance, distribution, reproduction, and prey consumption of predatory arthropods, showing how manipulation of plant traits can contribute to the reduction of phytophagous arthropod population, which would consequently result in increased crop yield.

Genotypes with large and compact shoot apices are preferred for sustenance of *T. aripo* as they protect the predatory mite from harsh weather conditions. *Typhlodromalus aripo* resides in the growing point of the plant during the day and forages on the young leaves during the night hours, while CGM prefers young leaves (Onzo et al., 2003). Therefore loss of shoot apices in the dry season induced by drought adversely affects the natural enemy, contributing to the buildup of CGM on the remaining fewer leaves. According to Nukenine et al. (1999), breeding cassava genotypes for enhanced stay green (SG) and leaf retention (LR) can improve both CGM resistance and tolerance of cassava to drought.

Even in the absence of natural enemies, cassava genotypes exhibiting high leaf pubescence (Pbs) tend to be more resistant to CGM than glabrous genotypes (Hahn et al., 1980, 1989). Research conducted at IITA in Nigeria, and in Tanzania has shown that nearly all cassava genotypes showing some degree of resistance had trichomes on the young top leaves, and that the number of trichomes per square millimeter is clearly different in the susceptible and resistant types (Hahn et al., 1989), suggesting that Pbs could be the primary character responsible for resistance to CGM.

1.7.2 Manipulating plant chemical traits

Research has shown that plants emit volatiles which can attract predators against arthropod pests. Manipulation of such plant chemical signals offers the most promising perspective for

enhancing the effectiveness of predators in the field. However, the role of such signals in the recruitment of natural enemies appears to be complex and dynamic. For this reason, Cortesero et al. (2000) recommend having a good understanding of the biology of natural enemy species so that plant attributes can be manipulated for a sustainable and balanced control of insect pests in agro-ecosystems. Recently, Onzo et al. (2012) reported that pubescent genotypes of cassava tend to emit certain volatiles that attract *T. aripo* to the apices of such genotypes.

1.8 Methodologies for mass rearing of arthropods

Methodologies have been developed for mass rearing of pests in greenhouses. At CIAT, colonies of whitefly (*Aleurotrachelus socialis* Bondar) are maintained on the susceptible genotype CMC 40 (Bellotti and Arias, 2001). Potted cassava plants containing high populations of *A. socialis* pupae and emerging adults are maintained in a fine-mesh screened chamber in a greenhouse at 28-29ºC and 70-75% RH. Twice a week, five week old potted cassava plants are exposed to whitefly adults by placing them in the infestation chamber. Adults are allowed to oviposit for 72 h after which they are removed from the plants. The plants are then removed from the chamber and placed in a separate greenhouse unit, where the immature mites are allowed to develop. Similarly, greenhouse rearing of adults of *M. tanajoa* females collected from a culture-initiated, field-collected mites has been reported (Gnanvossou et al., 2003; Onzo et al., 2005). The mites are maintained on potted cassava in a greenhouse at 26±1^{o}C and 65-85% RH for at least one month before they are used in the screening experiments.

Other than cassava leaves, maize pollen, and kidney bean (*Phaseolus vulgaris*. L.) have also been used for maintenance of phytoseiid colonies of mites such as *T. aripo*, *T. manihoti* and *Euseius fustis* Pritchard and Baker (Acari: Phytoseiidae)(Onzo et al., 2005). Edelstein et al. (2000) maintained spider mite stock culture on kidney bean plants in controlled-climate room at 25-27ºC, 60±5% RH and 16 h light.

Megevand et al. (1993) describe the cassava “tree”, which is used as a rearing unit for predatory mites. It consists of a suspended plastic sleeve filled with rockwool. Cassava cuttings are planted through the sleeve into the rockwool and a standard nutrient solution is distributed by a flexible pipe inserted in the top. When plants have reached the 15-leaf stage, the cassava “trees” are infested with CGM and covered with a screen to prevent contamination by undesirable arthropods. The infestation is done by distributing CGM-infested cassava leaf lobes containing both active stages and eggs, to all cuttings.

1.9 Screening and evaluation methods

Screening and evaluation of germplasm requires continuous maintenance of uniform pest pressure in all experimental plots. The pest pressure needs to be high enough to determine the

presence or absence of a resistance character to enable the breeder to distinguish between susceptible and resistant genotypes. This may demand repeated infestation of test materials (Gutierrez et al., 1987). Large-scale free choice evaluations are often conducted either in field plots or greenhouses to enable the breeder to eliminate susceptible plant material early in the breeding programme (Smith, 1989).

1.9.1 Laboratory screening

Laboratory experiments are normally conducted in a controlled environment in insect growth chambers to monitor the rate of fecundity of mites on plant tissues, determine the mechanism of resistance, and to investigate interaction among predator species (Gnanvossou et al., 2003). Onzo et al. (2005) investigated the interactions between predator species *T. manihoti* and *E. fustis* and their impact on CGM, in the presence or absence of maize pollen as alternative food source. The reproductive success of mites is determined by measuring oviposition rate under laboratory conditions on detached cassava leaf discs (Braun et al., 1987). Prey mite species suitability studies aimed at determining the most preferred target prey for *T. aripo* and *T. manihoti* among*M. tanajoa*, *Oligonychus gossypii* (Zacher) and *Tetranychus urticae* (Koch) (Acari: Tetranychidae) have been conducted in no-choice experiments using leaf discs (Gnanvossou et al., 2003). Similar population growth estimates have been reported on leaf disc and in the field (Yaninek et al., 1989), confirming the high convenience and efficiency attributed to the use of leaf discs in studying tetranychid biology (Helle and Overmeer, 1985).

1.9.2 Screenhouse evaluation

Screenhouse experiments have been conducted at IITA-Cotonou, Benin to screen cassava genotypes for resistance to *M. tanajoa* (Onzo et al., 2005). Cassava cuttings of test plants are planted in plastic pots filled with top soil usually collected from a fallowed field. The inoculation of plants is done by placing at least ten adult female CGM on the youngest leaves, four weeks after planting. Each plant is then caged in a cylindrical organdy bag, and regularly monitored for the development of CGM (Onzo et al., 2005). Each plant is evaluated by removing the leaves and growing point and counting all stages of mites with a stereoscope (Braun et al., 1987)

Bellotti and Arias (2001) describe a procedure for evaluation of vertical resistance of cassava to whiteflies. Selected resistant genotypes and susceptible controls are grown from stem cuttings in pots for five weeks and infested with whiteflies from the colony. Infestations are made by attaching small clip cages to cassava leaves, held in place with a rigid rod embedded in the soil. Ten whiteflies are introduced into each cage and left to oviposit for 24 h, after which the cages and adults are removed. The whiteflies infested plants are maintained in a growth chamber, where temperature (average 27^{o}C), RH (68±1%), and photoperiod (12:12h day:night) are regulated.

1.9.3 Open field evaluation

Field screening of cassava germplasm for resistance to arthropod pest is done at sites where natural populations are high and damage levels are significant so as to distinguish susceptible genotypes (Bellotti and Arias, 2001). Evaluations are done periodically throughout the growing cycle. One of the major impediments to field screening of insect pest resistance is the difficulty associated with maintenance of a uniform distribution of inoculum pressure (Gutierrez et al., 1987). Patchy and uneven distributions of arthropod pests are commonly observed in the field, which can result into wrong selections. Some of the genotypes that show little or no CGM LD under patches of low CGM populations and, therefore, low-selection pressure may actually be "escapes" (Bellotti and Arias, 2001). To avoid this problem, Bellotti and Arias recommend that, a common susceptible genotype be planted strategically throughout a screening block to measure the mite population levels, distribution and damage. The susceptible genotype also serves as a source of inoculum (spreader rows) from which mites can disperse to the test plants. Habekub et al. (2000) suggests a simpler and relatively cheaper method, which was used in infesting apple trees (*Malus domestica* Borkh.) with spider mites. The method involves collecting mite infested leaves or small twigs and weaving or fixing them end-to-end at the lowest one-third of the test plants.

1.10 Rating scale for resistance to cassava green mite

Assessment of CGM LD is normally conducted on the top five fully expanded leaves following a 1-5 scoring scale based on injury done on each genotype by a pest (Hahn et al., 1989; Yaninek et al., 1989). According to this five-point scoring scale, plants or genotypes falling in classes 1 and 2 are considered to be resistant, plants in class 3 are moderately resistant, while those in classes 4 and 5 are susceptible to CGM. Bellotti and Kawano (1980) proposed a rating system which utilizes a 0-5 and 0-10 scoring scales. The former is used as an initial screening scale to discard susceptible plants (up to 85%), while the latter is used for further evaluation of selected lines. In both scales, plants falling in classes above 3 are rejected. The scoring is made, at 3, 6, 9, and 12 months after planting, which coincides with the various seasons (Akparobi et al., 1998).

1.11 Genetic variation and genotype x environment interaction studies in cassava

Genotype by environment interaction (GEI) refers to the variation in response among genotypes, when evaluated in different environments (Fox et al., 1997). Multi-location trials help to reveal GEI, which enables plant breeders to identify superior genotypes and locations that best represent production environments. According to Crossa (1990), multi-location trials have three main objectives as:i) accurate estimation and prediction of yield based on limited data; ii)

determination and prediction of yield stability and the pattern of response of genotypes or agronomic treatments across environment; and iii) providing reliable guidelines for selecting the best genotypes for planting in future years and at new sites.

Cassava varieties often demonstrate specific adaptation due to their high sensitivity to the GEI that occurs in both short-term and long-term crop performance trials, and is a major concern in plant breeding because it reduces progress from selection (Eberhart and Russell, 1966). This makes cultivar recommendation difficult because the choice of superior cultivars changes with locations. It is possible to have little relation between a breeder's selection environments in one year and those experienced in the next, suggesting a need to test for many crop cycles, and or many locations. This kind of diversity in environments permits identification of extreme environmental conditions that guarantee selection pressure from important stresses (Fox et al., 1997). Therefore the importance of GEI lies in guiding the breeder in deciding whether to aim for wide or specific adaptation, whether to conduct early generation selection in stressed or stress-free environments, and whether to test a large number or fewer genotypes in multi-location trials.

In conducting GEI studies it is important that a breeder understands the optimal requirements for field experimentation. Dixon and Nukenine (2000) determined the optimal number of replications, locations, or years for GEI studies in cassava. The authors suggest that the best option therefore, is to use a minimum number of replication, or locations that will not jeopardize precision. Depending on the combination of number of replications and years, the critical point is generally attained when the number of location is between three and five for all the yield trials, representing the optimum number of locations required in cassava yield trials. Fewer than three locations will result in inaccurate selection for any of the yield traits, whereas more than five locations will only increase costs without any significant gain in precision. Having very few replications generally is not advisable. Therefore, three to four replications in each of three to four locations and two to three years should suffice for cassava yield evaluation (Dixon and Nukenine, 2000).

1.11.1 Statistics for analysis of stability of cassava genotypes

Various statistics have been used to assess stability of genotypes of crops. These statistics include use of variance component of a genotype x location interactions, estimated for each of the possible pairs of genotypes tested, as proposed by Plaisted and Peterson (1959). This method takes into account the average of the estimates for all combinations using a common genotype. Other statistics involve the use of the "ecovalence" stability index which is the contribution of a genotype to the GEI sum of squares (Lin et al., 1986), and an unbiased estimate of stability, developed by Shukla (1972), which partitions the GEI sum of squares into

components attributable to variance. Unlike other early methods, Shukla's method allows for the removal of the linear effects of a covariate from the GEI (Lin et al., 1986).

Until the development of the additive main effects and multiplicative interaction (AMMI), the regression-based stability index of Finlay and Wilkinson (1963) was the most widely used method of stability analysis. In this method, genotypes with low regression coefficient (*b* value) are considered stable and absolute phenotypic stability is expressed *b* = 0. Unstable genotypes are those with high *b* value. The approach was refined by Eberhart and Russel (1966) who regressed mean yield on an environmental index. Eberhart and Russel define a stable genotype as one with a high mean yield, *b* = 1.0 and $s_d^2 = 0$.

Comparison of various stability indices has been done for cassava stability assessment by Ngeve (1994), who reported similarities in stability results following use of Eberhart and Russell (1966), Perkins and Jinks (1968), Shukla (1972), and Francis and Kennenberg (1978). The AMMI model which combines regular analysis of variance for additive main effects with principal component analysis for multiplicative structure within the interaction (Crossa et al., 2002), has been widely used in cassava to study the pattern of response of genotype, environment, and GEI, and to identify genotypes with broad or specific adaptation to target agro-ecologies or environments for various traits (Benesi et al., 2004; Dixon et al., 2002; Ntawuruhunga, 2001). A significant feature of AMMI analysis like many other multiplicative models is that they account for a large proportion of the pattern related to the treatment design in the first few dimensions. Based on AMMI, Purchase et al. (2000) also proposed a stability statistic termed AMMI stability value (ASV), which is commonly being used to study stability in cassava. Considering that genotypes which combine stability with high yields are preferred by farmers, Farshadfar (2008) therefore proposed the genotype selection index (GSI) which integrates both stability value and yield into single selection criterion.

1.12 Summary

This review has shown that more research is needed in-spite of the important progress made so far in breeding cassava for resistance to mites or insects. Many publications currently available in this area of cassava research have focused on biological control. Literally no breeding work has been down in Zambia to incorporate heritable host plant resistance in cassava to green mite. There is need to source for resistance from both local and introduced genotypes of cassava in Zambia in order to develop CGM-resistant genotypes which are locally adapted and stable. The fact that *T. aripo* was recovered on certain cultivars in Zambezi and Nchelenge districts suggests the need to study the effect of GEI on the abundance of CGM*,* as well as the survival and establishment of *T. aripo* in Zambia.

Progress in genetic improvement of cassava has been considerably hindered due to the heterozygous genetic nature of the crop. Cassava scientific research is still in its infancy and there is limited knowledge on the inheritance of traits of agronomic relevance in cassava. Most of the important traits in cassava are polygenic. Detection of polygenes for a trait requires evaluation of breeding materials over a range of environmental conditions in order to cater for differences due to genotype by environment interaction. Breeding for resistance to arthropod pests requires presence and even distribution of the target pest, which may not be always the case under field conditions. The research becomes expensive in that screening has to be done over a large number of environments, and seasons, also making investment in controlled environment equipment inevitable for rearing of insects and screening of crop plants.

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CHAPTER 2

Farmers' awareness of cassava green mite and preferred traits of cassava cultivars in north-western Zambia

Abstract

Farmers are the custodians of valuable indigenous knowledge concerning wild and domesticated plants and over the years farmers have discovered various means of coping with plant pests in their farm lands. To obtain information on farmer's perception of the distribution and importance of major cassava pests and traditional coping strategies thereof, a farmer participatory study was undertaken. Through individual interviews and focus group discussions the study helped to gather traditional knowledge on plant attributes that are associated with reduced pest population and/or damage in cassava fields, with a view to identify traits that can be promoted through breeding. Termites, moles and cassava green mites (CGM) were recognized as the most prevalent pests that contribute to low yields and abandonment of certain cassava cultivars by farmers. Apparently farmers depend on traditional cultural practices such as de-topping, selective pruning, intercropping, and burning of cassava fields to reduce CGM, mealybug and termites in their fields. These methods interfer with the survival of natural enemies of CGM. For successful development of an integrated pest management aimed at controlling CGM, farmers need to be sensitized about the importance of CGM and the benefit of natural enemies, as well as the role of plant morphological traits serving as direct or indirect defense against CGM.Plant canopy size and other related attributes such as number of branches, and leaf retention, were perceived to have a negative relationship with CGM damage. Farmers desire cultivars which combined the following traits: earliness, high storage root yield and storage root dry mass percentage, resistance to CGM, moles, termites and storage root rots. Cultivars which lack in most of these traits have been abandoned by farmers. Therefore, there is a need to look for genetic sources for these farmer-desired traits and incorporate them into new cultivars through plant breeding

2.1 Introduction

Cassava is a robust and reliable crop which tolerates a wide range of climatic conditions and is able to grow under marginal soil fertility. Its production is largely concentrated among the small scale, resource-limited farmers who have no access to credit facilities, and cannot afford expensive agro-chemicals to control pests and diseases. Normally there is no break in the production cycle of cassava; farmers have to plant a new field of cassava every rainy season to have a continuous supply of food. This continuous production coupled with the long growth cycle of cassava creates a continuum of cassava pests and diseases. Under such farming conditions cassava green mite (CGM) (*Mononychellus tanajoa* Bondar (Acari: Tetranychidae)) becomes the key herbivorous arthropod pest (Omorusi et al., 2011), causing significant yield losses (Byrne et al., 1982; Yaninek and Herren, 1988). National activities aimed at controlling CGM through resistance breeding and biological control have been carried out as independent units and without active participation of farmers. Impact assessment studies have shown that most of the integrated pest management (IPM) programmes in which scientists have controlled the development and use of knowledge are not sustainable and often have impacted negatively on agricultural communities, including farmers (Dlott et al., 1994). Consequently, despite the release (Malambo et al., 1998; Mebelo et al., 2003), the pest has continued to devastate cassava production in Zambia (SARRNET, 2008). It is suggested that agricultural research and development programmes which target the poor become more effective when they take farmers' indigenous knowledge-based systems into account (Friis-Hansen and Sthapit, 2000). Participation of farmers in IPM research is thought to empower local farmers by enhancing local management capacity, increasing confidence in their own abilities (Van Den Berg and Jiggins, 2007). This kind of empowerment increases the sense of ownership among farmers for the developed technology and the likelihood of that technology being embraced (Dlott et al., 1994). Knowledge and perception of farmers is necessary for the development of appropriate pest control management strategies in line with farmers' needs (Ojwang et al., 2009).

Farmers are continuously innovating in order to cope with the ever-changing environmental, ecological, policy, and market situations, and over the years they have become the custodians of traditional knowledge on many aspects of crop production including pests and coping strategies (Sleper and Poehlman, 2006). In the longer term this will be translated into increased rates of adoption and retention of new technologies, and ultimately into a greater and more accelerated reduction in food insecurity and poverty (Weltzien et al., 2000).

Use of participatory approaches in host plant resistance breeding has enabled researchers to respond more precisely and efficiently to the needs and preferences of resource-poor farmers (Ojwang et al., 2009). In Nigeria, participatory rural appraisal (PRA) was carried out to identify farmers' preferences, which included enhanced shelf life, high storage root yield, low level of

hydrogen cyanide in cassava processed products, pests and disease resistance, and early maturity (Agwu and Anyaeche, 2007). Manu-Aduening et al. (2007) used PRA to describe the characteristics needed for cassava varieties in Ghana and reported that farmers preferred cassava varieties that had early growth and vigour to suppress weeds, early maturity, high yield, good cooking quality and suitability for intercropping. Kamau et al. (2011) used focus group discussions in the semi-arid region of eastern Kenya to identify farmers' preferences for cassava varieties, which included early maturity, high dry mass content and long, straight, round and sweet roots. Using PRA as an integral part of conventional breeding is likely to speed up the rate of development and adoption of cassava varieties (Kapinga et al., 1997; Fukuda and Saad, 2001).

Against this background, the current study was conducted in north-western Zambia to achieve the following objectives: i) gather information on farmers' perception of the distribution and importance of major cassava pests and traditional coping strategies thereof; ii) gather traditional knowledge on plant attributes that are associated with reduced pest population and or damage in cassava fields, with a view to identifying traits that can be improved through conventional breeding; and iii) gather information on desirable and non-desirable cassava varietal attributes in relation to various uses of cassava.

2.2 Materials and methods

2.2.1 Study sites

Individual and focus group interviews were conducted with 120 farmers in two districts namely Solwezi (60 farmers) and Mwinilunga (60 farmers) in Zambia (Figure 2.1). The farmers in Mwinilunga have a long history of growing cassava as a staple crop. Consequently large cassava fields with a wide diversity of cassava cultivars, and highly experienced cassava growers are prevalent in Mwinilunga (Chakupurakal et al., 1994). The district has a long history of on-farm research activities which has over the years afforded a good number of local farmers exposure to improved technologies and cultural practices. There is a long history of releases of exotic biological predatory mites and parasitoidsto control CGM and cassava mealybug (CM) *(Phenacoccus manihoti* Matile-Ferrero (Homoptera: Pseudococcidae)), respectively in Mwinilunga (Malambo et al., 1998). However the natural enemies for CGM have not established well in the district (Mebelo et al., 2003).

Sorghum (*Sorghum bicolor* (L.) Moench) is traditionally grown in Solwezi district, where people have recently migrated from areas where cassava is grown. Therefore, cassava is a relatively new crop in Solwezi where farmers grow cassava mainly for the sale of storage roots and leaves.

A PRA study was conducted in six agricultural camps in each of the two districts. In Mwinilunga farmers were interviewed in Sailunga, Nyangombi, Kawiko, Kanyama, Kampemba, and Lwau agricultural camps (Figure 2.1). In Solwezi, the camps included Mutoma, Lamba, Kisasa, Kayonge, Meheba, and Manyama. The survey team included a plant breeder, a social economist, one agricultural extension officer, and one field research assistant from the Root and Tuber Improvement Programme.

2.2.2 Individual interviews

A loosely structured questionnaire was used to obtain the required information. From each of the above named agricultural camps, an extension officer who was familiar with the local language was trained on the techniques of administering the questionnaire. The questionnaire was administered to about 10 farmers who were randomly selected along a transect in each camp (King, 2000). Cross-checking was done in the field by the researcher to ensure that information collected was accurate. An inventory of abandoned cultivars was compiled in each locality, and information about desirable and non-desirable traits attributed to each cultivar was collected and reasons for abandonment of certain cultivars were also obtained.

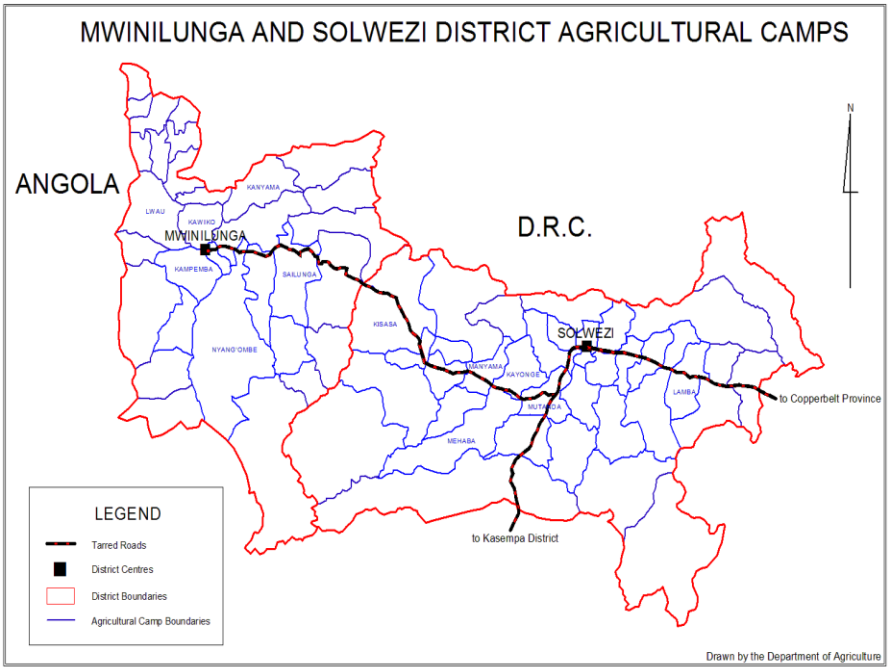


Figure 2.1 Agricultural camps sampled in the Mwinilunga and Solwezi districts for the participatory survey

2.2.3 Focus group discussion

A sub-sample consisting of 60 farmers, of which 30 were women and 30 men, was randomly selected from the 120 previously interviewed cassava growers and they were gathered together

for focus group discussions. These farmers were then sub-divided into 10 groups of six members each. Women were allowed to form their own groups to allow free expression of ideas between gender groups. Each group was assigned one trained extension officer who served as a guide. Farmers were asked to describe symptoms of damage caused by pests affecting cassava, and to provide a list of plant attributes that were considered to confer some level of plant resistance, as well as the traditional cultural practices that are used to manage such pests in their respective localities. Well-labelled live infested plants or plant parts as well as photographs of major pests and associated damage symptoms were provided as a guide to assist farmers in matching their descriptions with names of pests. Using preference scoring, farmers were asked to rank the pests in their order of importance (Figure 2.2). Similarly the effectiveness of various plant attributes and traditional cultural practices used in minimizing pest population and crop damage were also ranked by farmers.

Figure 2.2 Farmers conducting preference scoring and ranking of desirable attributes of cultivars and uses of cassava at Mutanda research station, Zambia.

2.2.4 Data analysis

Data collected were subjected to descriptive statistics analysis using SPSS version 10, statistical software.

2.3 Results

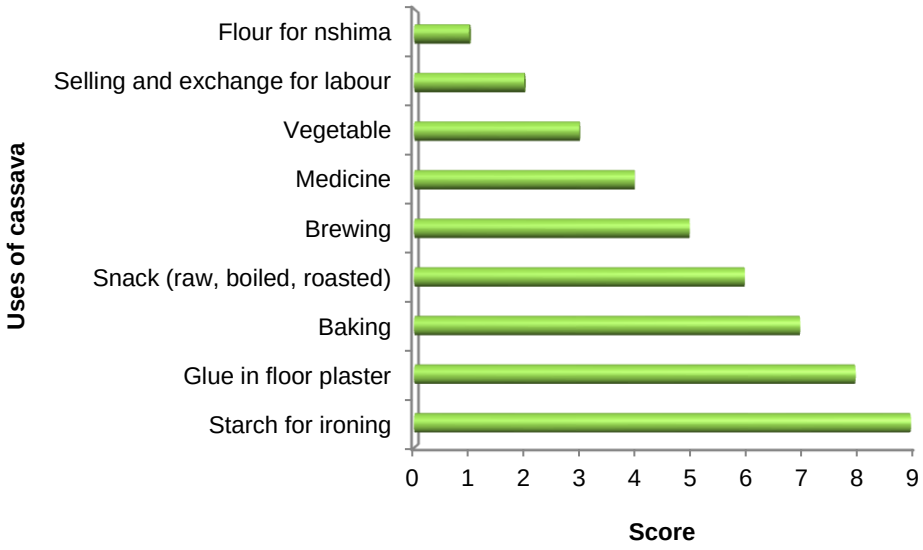
Over a period of 20 years, all the farmers interviewed (100%) have abandoned the landrace Kundamanga (Table 2.1). Ninety percent of the farmers said they have abandoned the cultivar Chamala. The cultivars Bunganabutu and Kapumba, though still planted by some farmers, have been abandoned by 80% of the farmers. The cultivar Bangwele has been abandoned by 50% of the respondents in Mwinilunga (Table 2.1). Reasons for abandonment of cultivars included poor fresh storage root yield (FSRY), low storage root dry mass (SRDM) and high storage root fibre content (SRF), susceptibility to moles, insect damage, and storage root rot (SRR) or poor underground storability (UGS), and susceptibility to frost and hail storm damage among others (Table 2.1).

Table 2.1 Cassava cultivars abandoned by farmers in Mwinilunga and Solwezi districts, Zambia

District	Abandoned cultivars	% farmers abandoning	Reasons for Abandonment
Mwinilunga	Neti,	90	Attracts insects and easily damaged by frost and hail storm
	Bunguta	60	Few and small storage roots
	Loja	45	Prone to theft and monkey damage
	Kapumba	80	Prone to moles damage, and root rots
	Nyauseya	50	Prone to root rots
Solwezi	Bunganabutu	80	Very prone to mole damage, plus low storage root yield
	Kapumba	80	Highly prone to mole damage, storage roots highly fibrous, and prone to frost damage and theft
	Tangala	75	Prone to frost and insect damage
	Chamala	90	Very poor growth and storage root yield
	Kundamanga	100	Few leaves and prone to insect damage
	Bangwele	50	Too bitter, susceptible to diseases, yellow flour

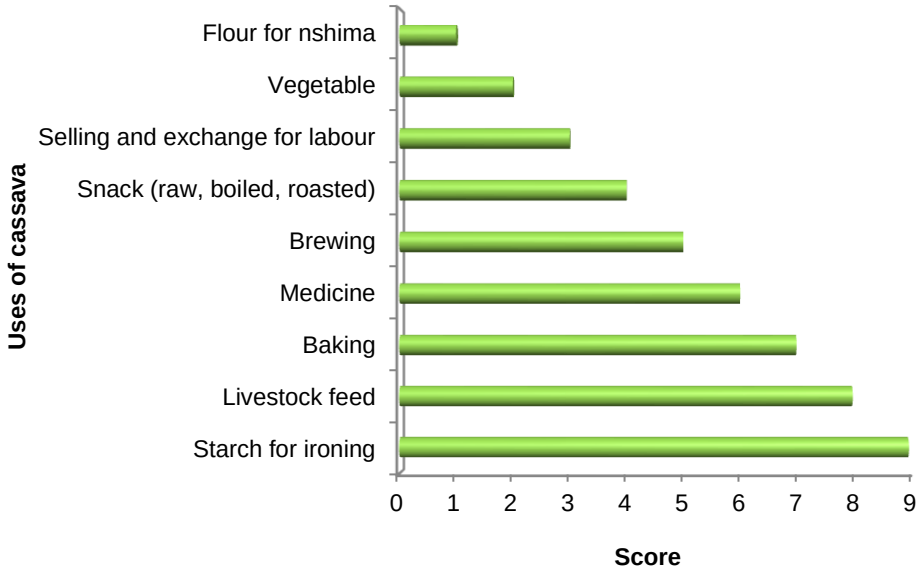
2.3.1 Ranking the uses of cassava

Cassava is mostly consumed in the form of flour which is used to make nshima (thick porridge which is eaten with sauce). Leaves are also consumed as a green vegetable both in Mwinilunga and Solwezi (Figures 2.3 and 2.4). Cassava is considered a good source of income for local farmers. Fresh and dry cassava storage roots as well as cassava flour are sold for money or exchanged with farm labour which is used to either maintain or expand fields planted to cassava or other crops such as maize. Cassava was said to have some medicinal properties and is used as a natural remedy for diarrhoea and skin diseases. The other use for cassava which was mentioned by male farmers only was for brewing local beer called Kachasu, and soft drink called Munkoyo. This use was ranked fifth by farmers in Mwinilunga and Solwezi.



Score 1 = most important, 10 = least important

Figure 2.3 Ranking of uses of cassava by farmers in Mwinilunga district, Zambia



Score 1 = most important, 9 = least important

Figure 2.4 Ranking of uses of cassava by farmers in Solwezi district, Zambia

2.3.2 Ranking the uses of cassava and desirable varietal attributes

The process of extracting cassava flour involves soaking of cassava storage roots in water, drying and milling. The soaking and fermentation help to get rid of the bitter taste and cyanide. Therefore, for the purpose of extracting cassava flour, farmers do not bother about the taste of

storage roots as both bitter and sweet cassava can be used. However, cultivars which combine high FSRY with high SRDM and resistance to SRR are most preferred for nshima. Cassava flour is sometimes mixed with clay and water to plaster mud brick houses in villages. For this purpose SRDM/starch content is the most important. Therefore cultivars which combine high FSRY with high SRDM are most preferred. For use of cassava in brewing, farmers like cultivars with high SRDM, high FSRY and extended UGS.

The SRDM is the most important attribute of cassava cultivars preferred by farmers for most uses of cassava. Cultivars which are tolerant to frost, pests and diseases are preferred as a leafy vegetable which is another source of income for farmers in the North-Western Province of Zambia (Tables 2.2 and 2.3).

Table 2.2 Ranking of uses of cassava and associated varietal attributes by farmers in Mwinilunga, Zambia

	Desirable varietal attribute							
Uses	**High FSRY**	**High SRDM**	**Good UGS**	**Early bulking**	**Sweet roots**	**High yield of planting material**	**Frost/hail storm tolerance**	**Pest/ disease resistance**
Nshima	2	1	4	3	ns	9	7	8
Baking	5	1	2	5	3	ns	ns	Ns
Glue/plaster	9	3	ns	ns	ns	ns	7	4
Brewing	4	2	5	ns	ns	ns	ns	Ns
Source of income	1	2	3	3	ns	2	ns	2
Starch for ironing	7	1	9	6	ns	ns	ns	8
Making glue	3	1	2	ns	ns	ns	ns	Ns
Vegetable	ns	ns	ns	ns	ns	1	2	3
Medicine	ns	8	9	7	ns	ns	ns	Ns

SRDM = storage root dry mass; FSRY = fresh storage root yield; UGS = underground storability;Score = ranking of the strength of association between varietal attribute and uses scored on 1-9 scale, where 1 = highest positive association, and 9 = lowest positive association; ns = no association; Source of income = income generated through selling of fresh and dry storage roots, planting materials and exchange for labour.

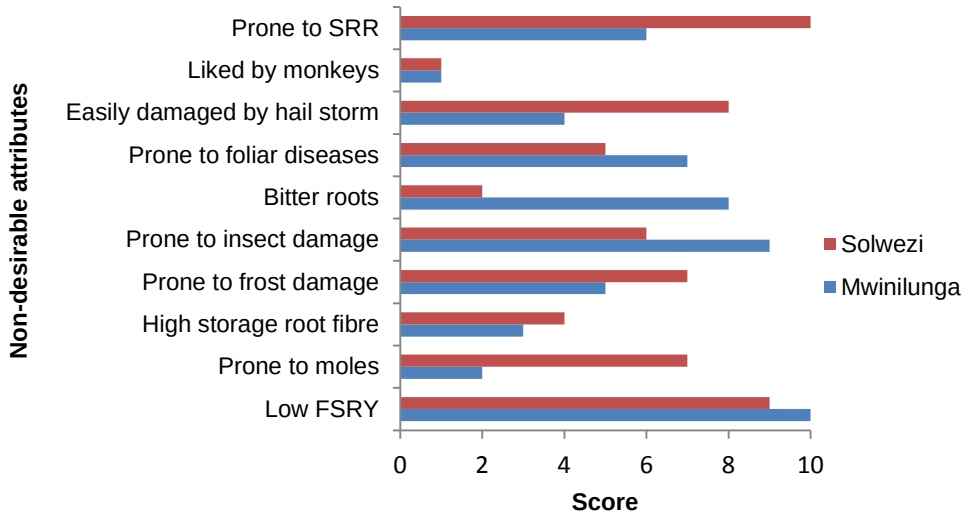
Table 2.3 Ranking by farmers of uses of cassava and associated varietal attributes in Solwezi, Zambia

Uses	Desirable attributes						
	High FSRY	**High SRDM**	**Early bulking**	**Purple inner root skin**	**Sweet roots**	**High yield of planting material**	**Pest/disease resistance**
Nshima	1	2	3	ns	ns	ns	Ns
Baking	3	2	ns	4	1	ns	Ns
Brewing	1	3	2	ns	ns	ns	Ns
Source of income	5	5	ns	5	5	ns	Ns
Livestock feed	5	ns	2	ns	5	8	5
Snack	5	5	3	2	10	ns	Ns
Vegetable	ns	ns	4	ns	ns	15	6
Medicine	12	8	5	ns	ns	ns	Ns

FSRY = fresh storage root yield, SRDM = storage root dry mass; Score = ranking of the strength of association between varietal attribute and uses scored on 1-9 scale, where 1 = highest positive association, and 9 = lowest positive association, while ns = no association; Source of income = income generated through selling of fresh and dry storage roots, planting materials, and exchange for labour.

2.3.3 Ranking of negative varietal attributes

In Mwinilunga, farmers scored susceptibility to SRR, low FSRY, and susceptibility to hail storm, moles, frost and insect damage in that order as the major negative attributes of cassava cultivars (Figure 2.4). In Solwezi, farmers scored the tendency of certain cultivars to yield few or only small roots even after two years as the most undesirable attribute which was responsible for abandonment of most cultivars. Susceptibility of a cultivar to insect damage was scored as the second most undesirable attribute (Figure 2.4). The third negative attribute and cause for cultivar abandonment is bitterness of storage roots, while susceptibility of a cultivar to foliar diseases, and poor UGS followed as the fourth and fifth most undesirable attributes, respectively.

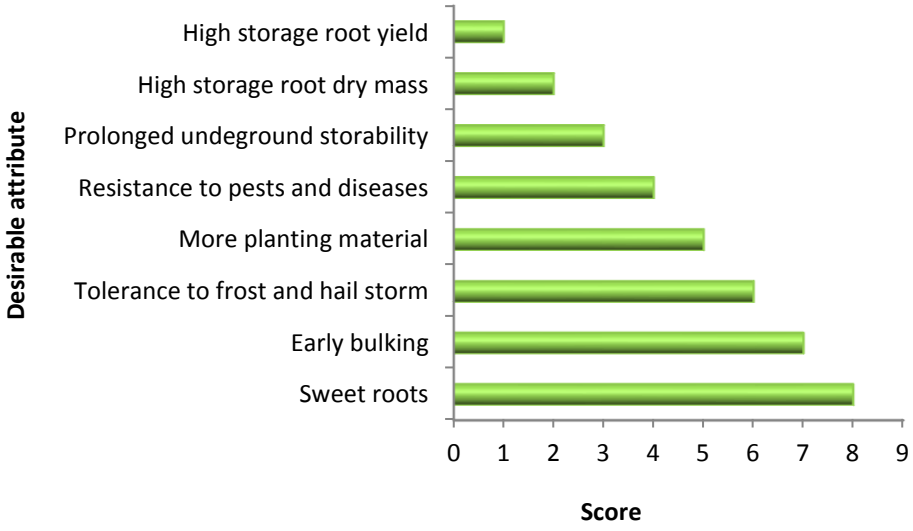


Score 1 = least non-desirable, 10 = most non-desirable

Figure 2.4 Ranking of reasons for abandonment of some cassava cultivars by farmers in Mwinilunga and Solwezi districts, Zambia

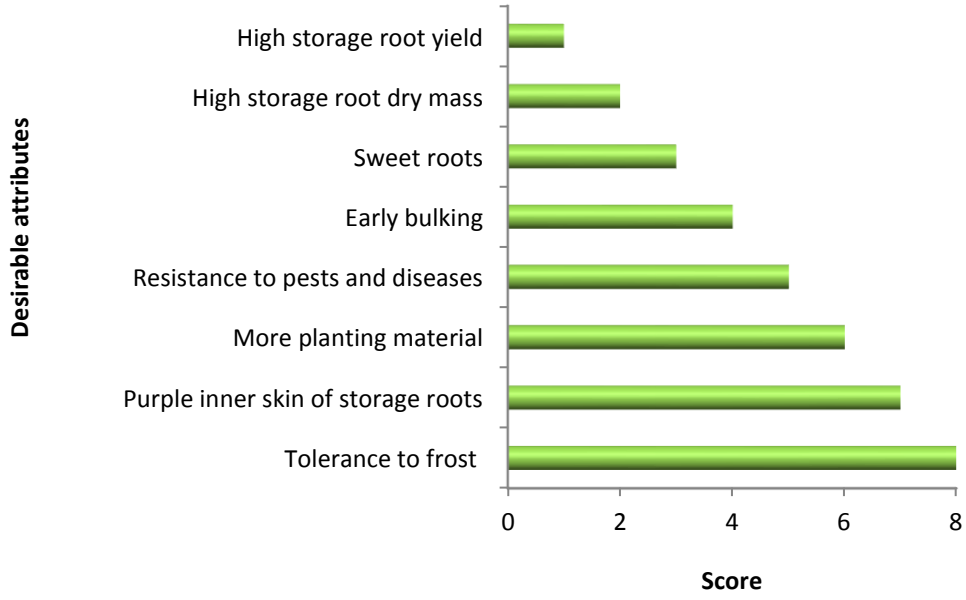
2.3.4 Ranking of desirable varietal attributes

Eight prominent positive attributes were listed for the different cultivars by farmers in Mwinilunga (Figure 2.5) and Solwezi (Figure2.6). In Mwinilunga, high FSRYwas considered the most important positive attribute (25.0%), followed by high SRDM (20.2%) prolonged UGS (17.0%), resistance to pests and diseases (15.5%), early maturity (10.4%), fast growing and more planting material (7.2%) tolerance to frost and hail storm (3.7%), and sweet taste of storage roots (1.0%). In Solwezi, high FSRYwas also considered the most important positive attribute (35.0%), followed by high SRDM (25.3%), sweetness (12.0%), early maturity (9.8%), resistance to pests and diseases (7.0%), more planting material (5.2%), purple storage root inner skin colour (3.5%), and tolerance to frost (2.5%).



Score 1 = most important, 8 = least important

Figure 2.5 Ranking of positive varietal attributes by farmers in Mwinilunga district, Zambia



Score 1 = most important, 8 = least important

Figure 2.6 Ranking of positive varietal attributes by farmers in Solwezi district, Zambia

2.3.5 Farmers' awareness about cassava green mite

Most of the farmers had no knowledge about CGM and were not able to describe or identify its damage symptoms. Nevertheless, Mutanda, Kampemba, and Kawiko camps recorded the highest number (40%) of farmers who had knowledge about CGM, followed by Sailunga and Lwau where 30 and 35% of the farmers, respectively, were knowledgeable about CGM, (Figure

2.7). None of the farmers interviewed in Lamba and Manyama camps of Solwezi district had knowledge about CGM. The farmers who had some knowledge about CGM had attained at least junior secondary level of education and had interacted with researchers either during on-farm research or farmer training. These farmers were able to recognize and describe symptoms of the pest and were even able to distinguish CGM from cassava mosaic disease (CMD) symptoms. The majority of such farmers were found in Mutanda, Kampemba, and Kawiko camps where research trials are usually conducted (Figure 2.7). However, all the farmers realized that they had seen CGM in their fields after looking at the photographs and live plant samples, based on which they were then able to estimate the extent of CGM spread and damage in their own fields.

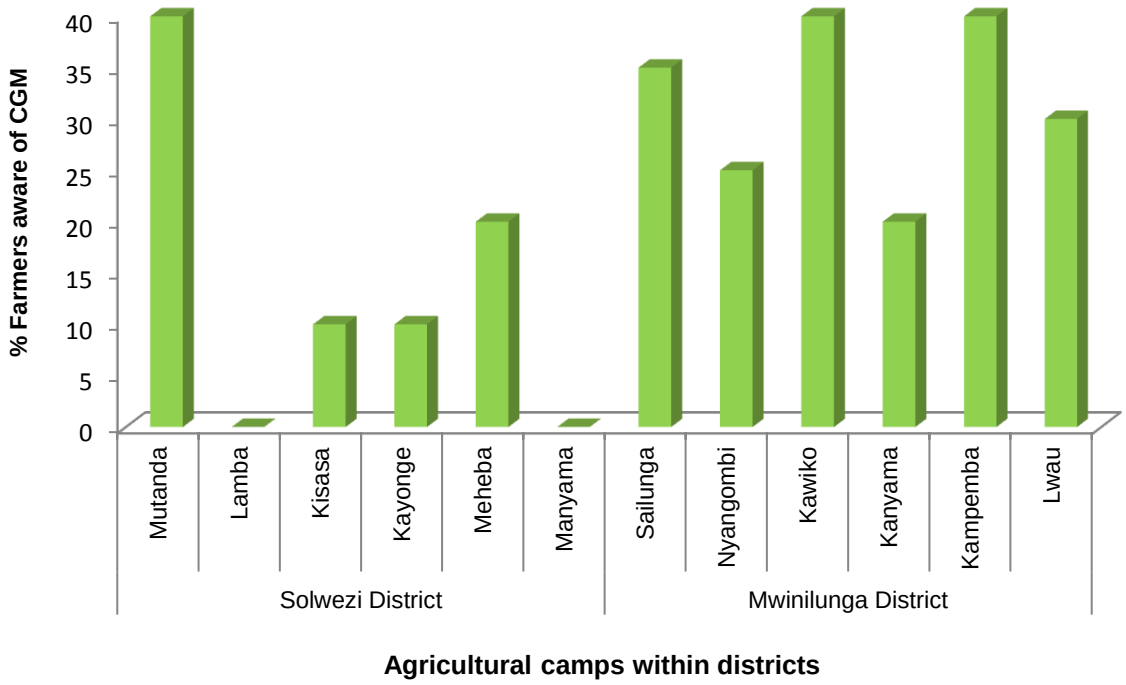


Figure 2.7 Farmers awareness about cassava green mite

2.3.6 Farmers' level of education

Most of farmers interviewed had attained primary education up to grade seven. In Mwinilunga, 45.8% of the farmers had attained primary school education, 44.2% had attained secondary school education, and 4.7% had post-secondary school formal education, while 5.3% of the farmers interviewed had no formal education at all. In Mwinilunga 54.2% of the farmers interviewed said they had attended some field training on root and tuber crops in the past, while in Solwezi only 19.2% of the farmers had attended such training (Table 2.4). In Solwezi, 67.5%

of the farmers had only attained primary school education, 17% had attained secondary school education, and 8.3% had post-secondary school formal education, while 7.2% of the farmers interviewed never had any formal education (Table 2.4).

Table 2.4 Percentage distributions of farmers according to the levels of education and field training in 12 agricultural camps in Solwezi and Mwinilunga districts of Zambia

District	Camp	% Farmers by levels of formal education attained				Training in root crops	
		No formal education	Primary school	Secondary school	Post-secondary	No field training	Trained
Solwezi	Mutanda	0	50	20	30	30	70
	Lamba	2	75	23	0	95	5
	kisasa	10	70	5	15	80	20
	Kayonge	10	80	10	0	100	0
	Meheba	20	50	25	5	80	20
	Manyama	1	80	19	0	100	0
	Mean	**7.2**	**67.5**	**17.0**	**8.3**	**80.8**	**19.2**
Mwinilunga	Sailunga	0	20	80	0	25	75
	Nyangombi	2	70	20	8	50	50
	Kawiko	5	30	65	0	30	70
	Kanyama	10	70	15	5	80	20
	Kampemba	15	35	45	5	15	85
	Lwau	0	50	40	10	75	25
	Mean	**5.3**	**45.8**	**44.2**	**4.7**	**45.8**	**54.2**

2.3.7 Distribution and importance of cassava pests in farmers' fields

Farmers were able to estimate the importance of pests experienced in their own fields. Major pests of cassava included moles, termites, CGM, scale insects (*Aonidomytilus albus* Ckll), and CM. Data obtained from focus group discussions indicate that CGM and termites (*Microtermes* sp)are the most widely distributed pests. Farmers attributed most losses in planting materials and leaves to termites and CGM, respectively (Figure 2.8). These pest were said to be most serious in the dry season, while moles were also reported to be found in all cassava fields mostly early in the rainy season. According to the farmers, moles cause about 45% crop

damage, while termites and CGM cause 25 and 20% crop damage in cassava fields, respectively (Figure 2.9).

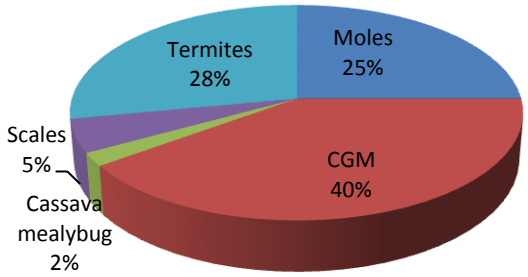


Figure 2.8 Distribution of major cassava pests in farmers' field as estimated by farmers
CGM = cassava green mite;
CM = cassava mealybug

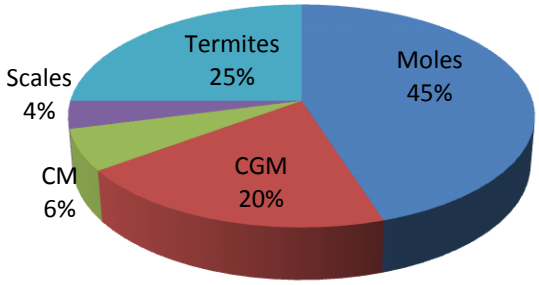


Figure 2.9 Extent of damage caused by major cassava pests in farmers' fields as estimated by farmers
CGM = cassava green mite;
CM = cassava mealybug

2.3.8 Plant attributes associated with reduced pest damage in cassava

Among the plant attributes that were mentioned by farmers as being associated with reduced pest damage, large heads (shoot apices), leaf hairiness, and extended leaf retention (LR) and stay green were highly associated with reduced damage caused by foliar pests such as CGM and CM. Canopy size and other related attributes such as number of branches, and LR, were also said to have a negative relationship with pest damage. A direct positive relationship was, however, reported between glabrous leaves and CGM leaf damage. Canopy size and LR were also said to be highly associated with reduced damage due to termites and scale insects in cassava fields. Farmers were aware of variations in response to pest damage among cultivars. Cassava cultivars that had pink or purple leaves, petiole and stems which farmers called "purple or pink cassava" was said to be not attacked by CGM, but such leaf type was not considered as a good vegetable. Bitter cassava cultivars were less preferred by termites and moles as compared to sweet ones, when grown in a mixture.

Table 2.6 Ranking of cassava plant attributes associated with reduced damage of cassava by green mite, mealybug, termites, and scale insects as ranked by farmers

Plant attribute	Pests			
	CGM	CM	Termites	Scale insects
Highly dense canopy	7	8	2	1
Highly branching	8	4	3	2
High retention of green leaves	2	1	3	3
Big and hairy shoot tips	1	2	9	7
Hairy leaves	3	3	8	7
Glabrous leaves	9	10	7	9
Leaf folding trait	4	5	5	10
Broad hairy leaves	5	9	6	5
Purple or pink cassava	6	6	10	4
Bitter roots	10	7	1	6

CGM = cassava green mite; CM = cassava mealybug; Purple or pink cassava = cassava varieties with purple or pink leaves, petioles and stems; Rank 1= highest rank, 10 = lowest rank

2.3.9 Cultural practices associated with reduced pest damage in cassava

Through a participatory process and by consensus by farmers, focus groups listed cultural practices that are associated with reduced pest population and/or damage thereof in cassava fields (Figure 2.10). De-topping of cassava tips of all plants in a field, just after the rainy season, is the most widely used traditional strategy to escape insect and frost damage in cassava fields. A total of 15.8% of the farmers interviewed said they practice selective pruning of infested plant shoots, while 13.4% intercrop cassava mainly with cereals such as maize and sorghum, and withte phrosia (*Tephrosia vogelii* Hook f.) to reduce the population of pests. A total of 11.2% of the farmers affirmed the observation that keeping cassava fields free of weeds helps to reduce pest infestation and damage, while 10.2% of the farmers also mentioned that ratooning of cassava shoots just before the on-set of the cold season helps to reduce the population of insect pests and loss of planting materials through cold injury.

Apart from use of barriers of *T.vogellii*, and milk bush (*Euphorbia tirucalli* L. (Euphorbiaceae)) planted as edge rows around the field of cassava as mentioned by 8.6% of the farmers, 2.5% of the farmers said they manage moles by setting traps underground along the tunnels, while 2.0% depende on flooding and digging out the tunnels. However, 5.3% of the farmers cited the use of fire which is primarily meant to clear weeds in cassava fields as an indirect way of destroying insect pests. They elaborated that fire is only used in old fields of cassava with the intention to completely uproot the crop shortly after burning, while 4.0% of the farmers said they do not practice any control measures against any pest in cassava fields.

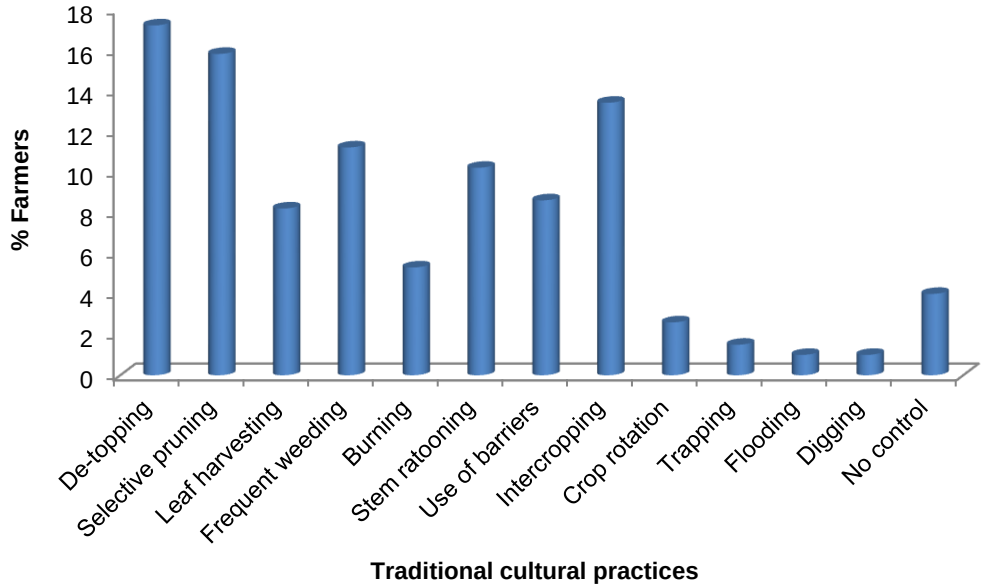


Figure 2.10 Traditional cultural practices to reduce pest damage in cassava fields as identified by farmers in Mwinilunga and Solwezi districts in Zambia

2.3.10 Ranking of the effectiveness of cultural pest management practices

Farmers believe that the effectiveness of the aforementioned cultural practices varies with the pest. Removal of cassava shoot tips and selective pruning of infested shoots were cited to be the most effective in reducing the population of both CGM and CM (Table 2.7). Crop rotation was also cited as an effective measure against CGM and termites. Selective pruning was considered to be the most effective measure against white scale insects, while low infestations of termites were normally encountered in frequently weeded fields. In this regard, farmers also said that land preparations which involve burying grass and planting cassava before trash decomposition tend to predispose cassava to termite attack which chew and girdle through planted cuttings from underground resulting in poor establishment of the crop. However, farmers clearly mentioned that the intensity of termite damage varies with location and soil type. The abundance of termite hills was said to be a direct indicator of the potential termite problem in a given area as is commonly the case in the North-Western Province. However, farmers pointed out the observation that plants that survive near a termite hill grow with vigour and give higher yields.

Burning the fields of cassava before harvest was said to be the second most effective traditional measure for reducing termites and scale insects especially for the succeeding cassava crop. The use of underground root barriers and trenches were cited as the most effective measure against moles followed by intercropping with *T. vogellii* and milk bush. Half of the farmers interviewed were knowledgeable about the negative consequences of burning

cassava fields, and said it is only used as a last resort where there is a fear of further pest population build-up in situations where the infestation is alarmingly high.

Table 2.7 Ranking of traditional cultural practices associated with reduced damage of cassava by CGM, CM, termites, scale, and moles by farmers.

Cultural practice	Pests				
	CGM	CM	Termites	Scale insects	Moles
De-topping	1	1	9	7	8
Selective pruning	2	2	8	1	8
Leaf harvesting	4	4	9	8	8
Frequent weeding	5	6	1	5	8
Burning	6	5	2	2	7
Stem rationing	7	2	11	3	8
Use of barriers	8	8	5	8	1
Intercropping	3	7	3	4	2
Crop rotation	4	6	3	5	6
Trapping	9	9	11	9	4
Flooding	9	9	7	9	3
Digging	9	9	6	9	5

CGM = cassava green mite, CM = cassava mealybug, Scale = white scale insects; Rank = ranking of the effectiveness of cultural practices for control of cassava pests scored on 1-12 scale, where 1 = most effective, and 12 = lease effective

2.4 Discussion and conclusions

The study has shown that FSRY, SRDM, earliness and resistance of cultivar to pests and diseases are the most important attributes that determine adoption and retention of new cassava cultivars by farmers in Mwinilunga and Solwezi districts. However slight variations were observed in the ranking of varietal attributes between farmers in the two districts. Farmers in Solwezi put more emphasis on factors affecting the quality of both the leaves and storage roots, while farmers in Mwinilunga are more concerned with factors affecting the physical quantity of storage roots and planting materials. The former group of farmers is interested in sweet roots which are preferred for eating as raw snacks, while the latter group of farmers normally processed cassava into flour for nshima. Farmers in Solwezi are not familiar with the processing of cassava, and because of readily available market for unprocessed cassava in the locality, farmers cannot afford to leave the storage roots in the ground beyond 16 months as is normally the case in Mwinilunga. This could explain why farmers in Mwinilunga are more concerned about SRR (poor UGS) and SRF than their counter-part in Solwezi. High incidences of SRR and SRF are mostly associated with delayed harvesting of cassava (Mskita et al., 1997). Foliar diseases and insects are a major concern to the farmers, because of their detrimental effect on the quality and quantity of planting materials and cassava leaves, which are a valuable source of income for women especially in Solwezi. The differences in ranking of varietal attributes between farmers indicate that farmers' knowledge and needs are mainly location specific and end-use dependent (Nkunika, 2002). The weights attached to various production constraints

vary with production conditions, and the cultural, and socio-economic values of the participating farmers. Therefore in order to obtain proper representation of farmers' perception of constraints, a large the sample size of participants is required (Were et al., 2012).

This study has revealed that many farmers are aware that pests and diseases are the major contributing factors to low yields of cassava in Zambia. It is also evident from the study that in Mwinilunga and to a lesser extent in Solwezi, farmers are very observant of the influence of various cultural practices on pests. However, they pay attention to larger pests which are easily seen with the naked eye, and much more attention is paid to pests that cause direct damage and thus negatively affect the quality of edible parts of the plant (Barnett and Rice, 1989). The non-conspicuous nature of CGM, however, makes it difficult for traditional farmers to clearly identify and define it. Consequently, its effect is under-estimated and limited attention is given to it by farmers. Good understanding of pest damage symptoms by farmers is crucial for an effective study of indigenous knowledge about traditional coping strategies. Supervised field tours conducted with individual farmers revealed that the co-existence of CGM and cassava mosaic disease on the same plant makes it difficult for some farmers and inexperienced extension officers to isolate symptoms of especially CGM and, therefore, the two are usually considered as one. This complication has earlier been reported by Gutierrez (1987) who stated that "for someone who is not an expert, symptoms produced by the CGM in cassava (chlorosis of young leaves followed by defoliation of young shoots) can be confused in the field with those produced by the cassava mealybug, *Phenacoccus manihoti* Matt-Ferrero, or by the African cassava mosaic virus (ACMV)".

Normally women prefer young and tender cassava leaves which are found in the top third of the plant shoot, as leaf vegetable (Ngudi et al., 2003). The competition between human and CGM for such leaves is increasing the urgency to contain CGM in Zambia. Protecting younger and tender leaves not only increases the vegetable supply but also enhances photosynthesis and hence increase production of planting materials, FSRY, SRDM (Byrne et al., 1982;Yaninek and Herren, 1988, Yaninek et al., 1993), and starch quality (Defloor et al., 1998). However, for the lack of better alternatives, farmers have resorted to de-topping, selective pruning, harvesting of tender leaves, and burning of cassava fields as ways of reducing pest populations.

One controversial issue concerning such practices lies in their interference with the survival of predatory mites and other beneficial herbivores which are natural enemies of CGM. In the Congo, the findings of the collaborative cassava study in Africa (COSCA) indicated that frequent harvesting of cassava leaves and de-topping of cassava plants is likely to lead to loss of shelter and even loss of the natural enemies (Nweke et al., 2002). Though a harvesting interval of 60 days in cassava has been suggested (Tata-Hangy, 2000), to allow for the maintenance of populations of predatory mites, farmers have reduced the harvesting interval due to increased

demand for leafy vegetables. These coping strategies are destructive in nature and have retarding effects on plant growth, leading to loss of valuable planting materials and may not help so much in controlling CGM. Though the new leaves which emerge after de-topping and burning of cassava plants in the field, look healthier and are apparently free of CGM damage, it does not take long before they become re-infested with CGM. Yaninek (1988) reports that CGM has the ability to survive on detached cuttings, and buds for up to two months, which contributes to the rapid colonization of the newly emerging young leaves. Therefore the tendency of farmers to plant tender sections of cassava stems with leaves still attached could also be responsible for transferring CGM from one planting to the next. Similarly, CGM has been reported to survive on bundles of cassava leaves that are displayed for sale as a leaf vegetable (Yaninek, 1988).

On the other hand, farmers are aware about the potential of pubescent cassava cultivars to reduce CGM damage. Leaf pubescence has also been reported to limit the movement of whiteflies (*Bemisia tabacci*) which translates to limited spread of CMD (Hahn et al., 1989). Farmers also observed that this protective effect of pubescence was more pronounced in broad-leaved cultivars which exhibited high density of hairs per unit leaf area. Similar results have been reported by Byrne et al. (1982) who observed that cultivars with leafy habit (high leaf area index) seem to sustain lower CGM leaf damage, resulting into higher FSRY for such cultivars when compared to their glabrous counterparts. Highly pubescent cultivars of cassava tended to have more tender leaves, and are considered to be more palatable and therefore preferred for vegetables by women. Enhancement of leaf pubescence in cassava will not only reduce CGM, but will improve the quality of cassava as a leaf vegetable for Zambian consumers. However there is urgent need to inform farmers about indirect and direct plant defense mechanisms and biological control initiatives for the fight against CGM to be successful.

Intercropping cassava with cereals and legumes is a popular practice among local farmers in North-Western Province. Since cassava takes more than one season to yield reasonable marketable storage roots in Zambia (RTIP, 1992), intercropping is only practicable in the first season of cassava cropping. Maize is normally provided with inorganic fertilizer which enables it to grow much faster than cassava and within four months provides some kind of a barrier to the movement of many small pests and insect vectors, the movement of which is highly influenced by wind (SARRNET, 1996). In the case of mites, pollen produced from maize for instance could provide an alternative diet on which CGM might spend much of its time consuming, sparing the cassava in the process (Edelstein et al., 2000; Gnanvossou et al., 2003). However, once maize is harvested, CGM can easily move to cassava. This could probably partly explain why there is a rapid rise in the population of CGM in cassava fields shortly following the harvest of maize, which also coincides with the beginning of the dry season (Toko, 1996).

Farmers complained that early-branching cassava varieties do not fit well in the traditional cropping pattern, which commonly involve intercropping cassava with many other crops including cereals and legumes. Early branching cultivars not only make weeding very difficult in intercropped fields, but also suffer more damage from CGM as compared to tall varieties (Egesi et al., 2007). The short distances between branching levels in short cultivars facilitate easy movement of CGM between branches and leaves within the cassava plant, in search of suitable leaves. This high branching habit also provides better protection for CGM against wind and rain effects, enabling it to continue colonizing the same host plants for a long period of time as long as suitable leaves are available, and consequently causing more leaf damage, and low FSRY (Cock et al., 1978).

Agreeing with this observation, farmers added that CGM damage tends to be worse when short cultivars were grown in weed infested fields. The reason for this could be that, the weeds tend to provide a bridge for the CGM to walk from one cassava plant to the other in search for tender leaves. This facilitates easy establishment of contacts between male and female mites, hence increasing the reproductive capacity and rate of spread of CGM (Yaninek, 1988). Research by Agboton et al. (2006) have shown a positive association between weed density and CGM population in Southern-Benin, which seems to agree with the Zambian farmers' observations. These authors have also reported reduced frequency of the natural enemy *Typhlodromalus aripo* in weedy cassava fields.

The current study therefore presents a challenge to breeders to develop fast-growing cassava cultivars that rapidly outgrow and suppress weed populations, supporting farmers' preference for cultivars that have a wider canopy and extended leaf longevity.

This study has shown that any research work towards combatting CGM in cassava will be very challenging and requires a multi-dimensional consideration of cultural, socio-economic and environmental factors. Once successful this work will go a long way to increasing the supply of a cheaper source of protein, vitamins and minerals to rural communities, as well increasing the yield of cassava, and raising the living standards of rural communities. Farmers have valuable knowledge about the biotic constraints to cassava production and they are doing a great deal within their own means to solve pest problems. However, for lack of better alternatives, farmers are using destructive methods which are potentially detrimental to beneficial predators in cassava fields and to the agro-ecosystems in general. De-topping of cassava shoots, burning cassava fields, selective pruning, intercropping, frequent weeding and right choice of cultivar are some of the key methods used by farmers to manage cassava pests including CGM in North-Western Province of Zambia. There is urgent need to sensitize farmers about CGM and the associated damage this pest causes, the importance of which has been underestimated, due to its non-conspicuous nature. Emphasis should be placed on farmer training and sensitization

about the benefits of natural enemies to CGM and the requirements for their effective presence in cassava fields. Active involvement of both educated and uneducated farmers at the planning, implementation and evaluation stages of an IPM programme for CGM is likely to contribute to its effectiveness and sustainability.

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CHAPTER 3

Genotype by environment interaction effects on resistance to cassava green mite (*Mononychellus tanajoa* Bondar (Acari: Tetranychidae)) and other agronomic traits of cassava grown in north-western Zambia

Abstract

Cassava is a food security crop that is becoming increasingly important for its potential industrial uses in Zambia. Despite the ability of cassava to grow in marginal areas, large differential genotypic responses have been reported under varying environmental conditions. Differences in pest and disease pressure contribute significantly to inconsistencies in performance of genotypes in various environments. Using a randomized complete block design, 19 cassava genotypes were evaluated in three locations for two years. The objectives of the study were to identify best genotypes that combine stability with high resistance to cassava green mite (CGM) within and across environments; identify stable genotypes with enhanced expression of plant traits that promote continuous survival of predators of CGM on cassava, and to identify locations that best represent target environment for low to no CGM damage and high expression of such traits. The expression of plant morphological traits favorable for continuous inhabitance of the phytoseiid predatory mite *Typhlodromalus aripo* on cassava, such as retention, and pubescence and stay green of leaves, were assessed. Data were also collected on the population density of CGM and associated leaf damage, storage root mass and fresh storage root yield. The additive main effects and multiplicative interaction (AMMI) analysis was used to study the genotype by environment interactions. Significant genotype by environment interaction was observed for most of the traits. The magnitude of genotype effect was greater than environment and interaction effects for all the traits. Genotypes L9.304/147, 92/000, TME2, 4(2)1425, and L9.304/175 were the most stable and most resistant to CGM across environments.

3.1 Introduction

Cassava suffers yield loss caused by pests and diseases of which cassava green mite (CGM) ((*Mononychellus tanjoa* (Bondar) (Acari: Tetranychidae)) and cassava mosaic disease (CMD) caused by viruses of the family *Geminiviridae* are the major ones (Akparobi et al., 1998). Large differential genotypic responses to these constraints have been reported under varying environmental conditions (Bokanga et al., 1994; Mkumbira et al., 2003; Aina et al., 2007; Ssemakula and Dixon, 2007). This variation in response among genotypes when evaluated in different environments is referred to as genotype x environment interaction (GEI), which commonly occurs in plant breeding programmes (Kang, 1998). The GEI are important in plant breeding and variety release (Crossa, 1990; Singh et al., 2006), as they enable plant breeders to identify superior genotypes and locations that best represent production environments (Yan et al., 2000). Most of the GEI studies conducted on cassava have focused on storage root yield (FSRY) (Dixon and Nukenine, 2000; Aina et al., 2007; Egesi et al., 2007). Only few experiments have aimed at studying the GEI effect on CGM (Bellotti et al., 2012). The major impediment to multi-location field screening of cassava genotypes for resistance to CGM has been the difficulty associated with maintenance of uniform infestation (selection pressure) throughout the experimental plots in different locations and/or years (Skovgard et al., 1993). Field screening of cassava germplasm for resistance to arthropod pests has to be done at several sites where natural populations are high and damage levels are significant so as to distinguish susceptible cultivars (Bellotti and Arias, 2001).

Work by Yaninek et al. (1989) focused on the effects of CGM on cassava yields in relation to different planting dates. Zundel et al. (2009) showed that the presence of predatory mite *Typhlodromalusaripo* in cassava was affected by habitat type effect and host plant genotype effect. Cassava apex traits such as tip size (TS) and compactness (TC), and pubescence (Pbs), matter to the abundance of *T. aripo*, as this predator is more frequently and more abundantly found on cassava genotypes with pubescent compared to genotypes with glabrous apices (Zundel et al., 2009). Even in the absence of the natural enemy, leaf retention (LR) and stay green (SG), leaf hardness, leaf folding, and increased Pbs, have been reported to promote host plant resistance against CGM (Hahn et al., 1989; Nukenine et al., 1999; Lam and Pedigo, 2001; Bynum et al., 2004; Raji et al., 2008; Onzo et al., 2010). Selecting genotypes for stability and enhanced expression of such traits would enhance the durability of host plant resistance (Belloti et al., 1994), and at the same time promote biological control of CGM in cassava fields (Zundel et al., 2009; Pratt et al., 2002), and subsequently improve FSRY (Byrne et al., 1982a; El-Sharkawy, 1992, 1993, 2003;Aina et al., 2007). Furthermore, studies of GEI for such traits might provide an explanation and a corrective measure for the reported failure of *T. aripo* to establish

well in some countries in Africa including north-western parts of Zambia and Cameroun (Mebelo et al., 2003; Onzo et al., 2003; Hanna et al., 2005).

Ultimately, farmers are interested in genotypes that combine stability with high FSRY and therefore, breeders should look for such genotypes (Farshadfar, 2008). Several stability assessment methods have been developed (Wricke, 1962; Eberhart and Russell, 1966; Perkins and Jinks, 1968; Shukla, 1972; Francis and Kannenberg, 1978; Lin and Binns, 1988), but they have not been as widely used for cassava as they have for cereals. The additive main effect and multiplicative interaction (AMMI) model which combines regular analysis of variance for additive main effects with principal component analysis for the multiplicative structure of pattern within the interaction is currently the most commonly used method for studying GEI and for grouping cassava genotypes or sites with statistically negligible cross-over interaction (Ngeve, 1994; Ntawuruhunga et al., 2001; Crossa et al., 2002; Dixon et al., 2002; Benesi et al., 2004). Against this background, multi-location trials were conducted and AMMI was used to study GEI for CGM resistance traits and other useful agronomic traits. The study was designed to achieve the following objectives: (i) to identify best genotypes that exhibit stably high resistance to CGM within and across environments; (ii) identify stable genotypes with enhanced expression of plant traits that promote continuous survival of the predatory mite *T. aripo* on cassava; (iii) identify locations that best represent target environment for low to no CGM damage and high expression of such traits; and (iv) identify stable traits across environments.

3.2 Materials and methods

3.2.1 Experimental sites and genotypes

The study was conducted in 2010 and 2011 at three sites namely Mutanda located 12°11'E and 26°24'S, at 1386 m above sea level (masl), Mwinilunga located 11°45'E and 24°23'S at 1363 masl, and Zambezi located 13^{o}30’E and 22°45’S at 914 masl (Table 3.1). At each location, the trial was planted on 15th December each year, corresponding with the begining of the rainy season which marks the traditional planting date in the area (Figure 3.1). Planting cassava at this time gives the crop four months of growth before the cold and dry season (Figure 3.2). Soil fertility status of the sites is provided in Appendix 3.1. These sites represent the major cassava growing areas of north-western Zambia.

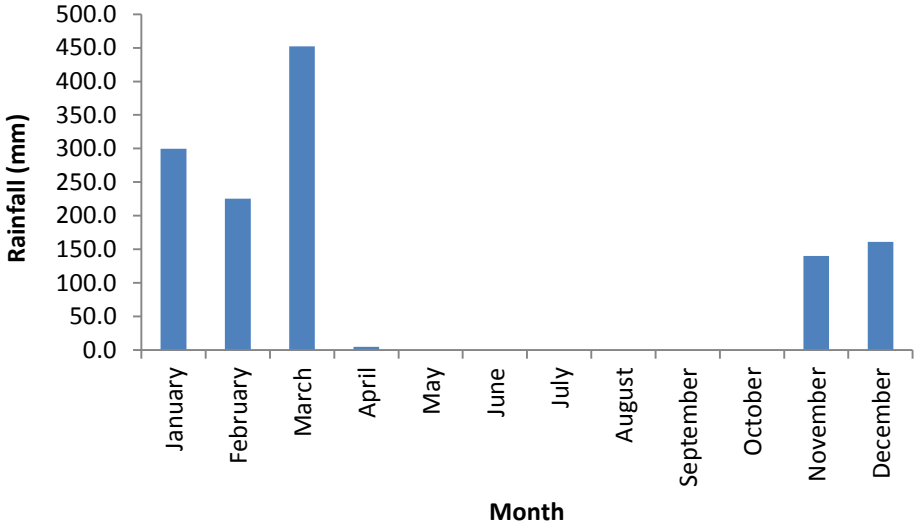

Figure 3.1 Average monthly distribution of ranfall in Solwezi, Zambia 2012.

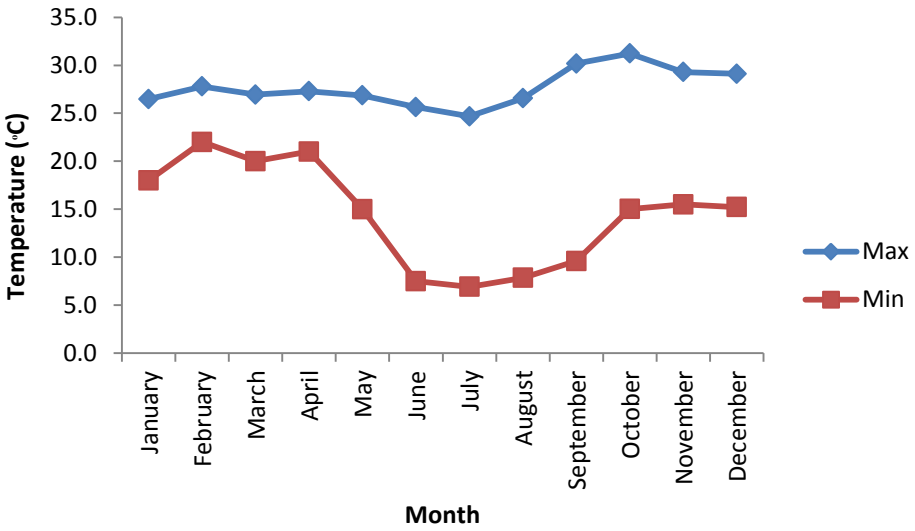

Figure 3.2 Average monthly minimum and maximum temperatures experienced in Solwezi district of Zambia, 2012.

Table 3.1 Geographical position, soil types and climatic conditions of trial locations and years

Location	Lat.	Long.	Altitude (masl)	Soil type	Rainfall (mm) Nov - Mar		Temp range (°C) Min - Max		Mean RH (%)	
					2010	2011	2010	2011	2010	2011
Mutanda	12° 11'	26° 24'	1386	Ferrasols	1200	1250	18-28	16-30	64	42
Mwinilunga	11° 45'	24° 23'	1363	Ferrasols	1100	1374	10-32	12-27	78	79
Zambezi	13° 30'	22° 45'	914	Acrisols	1400	1300	18-34	16-37	82	85

Lat.= latitude, Long. = longitude, masl = metres above sea level, Min = minimum, Max = maximum, RH= relative humidity measured as a percentage.

Nineteen cassava genotypes (described in Appendix 3.2) were evaluated. Of these genotypes, five were landraces, five were locally improved genotypes at an advanced stage of breeding, and five were introductions from the International Institute of Tropical Agriculture (IITA) in Nigeria. The remaining four were released genotypes commonly grown in Zambia and because of their outstanding agronomic performance and moderate resistance to major pests and diseases they were used as checks.

3.2.2 Experimental design and layout

The trial was laid out in a randomized complete block design with three replications. Each plot consisted of 36 plants in six-plant rows on ridges. Spacing between ridges was spaced at 1 m and also between plants within the row providing a total population of 10 000 plants ha^{-1}. No supplemental irrigation was provided to the trials.

3.2.3 Inoculation of experimental materials

The borders of each plot were planted with a CGM susceptible genotype which served as spreader rows. Two months after planting (in February each year), the borders were artificially infested with CGM obtained from a screenhouse-raised colony. Two infested leaves which had at least 20 adult mites were placed onto the intact leaves of each of the border row plants. The petiole of one infested leaf was lightly tied with a small string to the petiole of the first and second fully expanded intact leaves from the top of each of the border plants. These two leaves were then arranged in an abaxial-to-abaxial orientation and their main lobes were lightly clipped together with a plastic-insulated paper clip leaving the other leaf lobes freely open. The infester leaf and the paper clip were removed after three days. Inoculation was repeated twice during the experimental period namely soon after the cold season and at the on-set of the rainy season in August and November respectively. No fertilizers or herbicides were applied, but the trial was kept weed-free through frequent hand-weeding.

3.2.4 Data collection

The CGM population density (CGM PD) and associated leaf damage (CGM LD) were recorded as suggested by Hahn et al. (1989), using a rating system which involved estimating the proportion of leaf area covered by chlorotic spots, and the counting of adult mites on the third

fully expanded leaf from the top on each of six randomly selected plants in each plot. The damage rating was summarized based on a 1-5 score, where: 1 = no obvious symptoms; 2 = moderate damage, no reduction in leaf size, scattered chlorotic spots on young leaves, 1-2 spots cm^{-2}; 3 = severe chlorotic symptoms, light reduction in leaf size, stunted shoot, 5-10 spots cm^{-2}; 4 = severe chlorotic symptoms and leaf size of young leaves severely reduced; and 5 = tips of affected plants defoliated, resulting in a candle stick appearance of shoot tips. According to this five-point scoring scale, plants or genotypes falling within classes 1 and 2 were considered to be resistant whereas, plants in classes 3, 4, and 5 were considered to be susceptible to CGM.

Each clone was characterized visually for the degree of hairiness of apical leaves. Leaf Pbs was scored based on a 1-3 scale where 1 = glabrous; 2 = moderately pubescent; and 3 = highly pubescent. Similarly, the compactness of shoot apices (TC) was classified visually using a 1-3 scoring scale where 1 = loose; 2 = moderately compact; and 3 = compact. The size of shoot apices (TS) was also assessed visually and categorized according to a 1-3 scoring scale where: 1 = small; 2 = medium; and 3 = large. Leaf longevity was assessed by scoring for LR and SG. The LR was assessed by counting and expressing the number of nodes bearing leaves as a percentage of the total number of nodes on plant stems and branches, from 45 cm above ground level. The SG was scored visually based on a1-3 scoring scale where: 1 = poor (<50% of the leaves are live and green); 2 = moderately good (50-74% of the leaves are live and green); 3 = very good (≥75% of the leaves are live and green).

Sequential harvesting was done to identify early bulking cultivars and identify cultivars with extended underground storability. At each of the three dates of harvesting, a total of six plants were harvested from the each plot for assessment of FSRY. A sub-sample was then obtained from the bulk for storage root dry mass percentage (SRDM%) determination. The SRDM% was determined using the specific gravity method of Kawano (1980); by recording the mass of a 3 kg (air) sample of fresh storage roots in water. The SRDM% was then estimated using following formula:

$$\text{SRDM (\%)} = 158.3 \times \left(\frac{\text{Ma}}{\text{Ma}-\text{Mw}}\right) - 143$$

where M_a is the mass of storage roots in air and M_w is the mass of storage roots in water.

3.2.5 Data analysis

Data were analyzed using Genstat version 14 statistical software package (Payne et al., 2011). The additive main effect and multiplicative interaction (AMMI) analysis was performed using the model suggested by Gauch and Zobel (1996) as follows:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum \lambda_n y_{gn} \delta_{en} + \rho_{ge} + E_{ger}$$

where Y_{ger} = yield of genotype g in environment e for replicate r, μ = grand mean, α_g = genotype mean deviation (genotype means minus grand mean), β_e = environment mean deviation, n = number of principal component analysis (PCA) axes retained in the model, λ_n = singular value for PCA axis n, y_{gn} = genotype eigenvector values for PCA axis n, δ_{en} = environment eigenvector values for PCA axis n, ρ_{ge} = residuals, E_{ger} = error term.

3.2.6 Stability analysis

The AMMI stability value (ASV) proposed by Purchase et al. (2000) was used to quantify and rank genotypes according to the yield stability. There are other statistics such as Eberhardt and Russell (1966) which are widely used to measure stability, but the ASV statistic is the most suitable for AMMI which was used in this study. The ASV has been defined as the distance from the coordinate point to the origin in a two dimensional scatterplot of first interaction principal component axis (IPCA1) scores against the second interaction principal component axis (IPCA2) (Farshadfar et al., 2012). Since IPCA1 accounts for most of the GE variation, the IPCA1 scores are weighted by the ratio of IPCA1SS (from AMMI ANOVA) to IPCA2 SS in the ASV formula as follows:

$$\textbf{ASV} = \sqrt{\left[\frac{\text{SSIPCA1}}{\text{SSIPCA2}}(\text{IPCA1 score})\right]^2 + (\text{IPCA2 score})^2}$$

The lower the ASV, the more stable a genotype is. The ASV as a measure of stability was also compared with other stability statistics which included the following:

Shukla's stability variance (δ_i^2) (Shukla, 1972):

$$\boldsymbol{\delta_i^2} = \left[\frac{1}{(E-1)(G-1)(G-2)}\right] \text{x} \left[G(G-1)\sum_j(\mu_{ij} - \bar{u}_i)^2 - \sum_i\sum_j(\mu_{ij} - \bar{u}_i)^2\right],$$

Where: $\mu_{ij} = X_{ij} - \bar{X}_{.j}$; X_{ij} = observed trait value of the i[th] genotype in j[th] environment; $\bar{X}_{i.}$ = mean of all genotypes in the j[th] environment; $\bar{u}_i = \frac{\sum_j \mu_{ij}}{E}$; E= number of environments; and G= number of genotypes.

Cultivar superiority measure (*P_i*) (Lin and Binns, 1988):

$$\boldsymbol{P_i} = \sum_{j=1}^{n}\left[\frac{(X_{ij} - M_j)^2}{2E}\right]$$

Where: E = number of environments, X_{ij} = yield of the i[th] genotype in the j[th] environment, M_j = maximum response (check or otherwise) among all genotypes in the j[th] environment.

Ecovalence (Wi) (Wricke, 1962):

$$\mathbf{Wi} = \Sigma (X_{ij} - X_{i.} - X_{.j} + X..)^2$$

Where: Wi = ecovalence of the i^{th} genotype, X_{ij} = the observed phenotypic trait value of the i^{th} genotype in the j^{th} environment, $Xi_{.}$ = mean of i^{th} genotype across the entire environments, $X_{.j}$ = mean of j^{th} environment, X.= grand mean.

Environment variance (S_x^2) (Becker and Leon, 1988):

$$\mathbf{S_x^2} = \frac{\sum_i (X_{ij} - X_{i.})^2}{E-1}$$

Where:X_{ij} = yield of the i^{th} genotype in the j^{th}environment, $X_{i.}$= mean of ith cultivar across all the environments, E = number of environments. For each of the above stability indices, the genotype or environment with lowest value was considered the most stable for a given trait.

3.2.7 Genotype stability index

A stability index was calculated for each genotype based on summing the ranking of overall mean performances for each trait and the ranking for ASV for each trait. This stability index which is normally applied to yield data and is referred to as yield stability index (YSI) (Farshafar, 2008; Farshadfar et al., 2012), was also applied in this study to the mean performances of genotypes for other traits and referred to as genotype stability index (GSI). The GSI was calculated as follows:

$$GSI_i = RASV_i + RY_i,$$

Where: GSI_i = genotype stability index for the i^{th} genotype across environments for each trait; $RASV_j$ = rank of the i^{th} genotype across environments based on ASV; RY_i = rank of the i^{th} genotype based on mean performance across environments. The genotype with the lowest GSI was considered the best for a particular trait across environments. To identify superior genotypes across traits, the GSI ranks of each genotype were summed for all the traits, and the genotype with smallest rank sum (∑rank) was considered the best across traits.

3.3 Results

3.3.1 AMMI analysis

In the AMMI ANOVA the three sampling dates were also treated like addtonal environments within the locations which contributed to the large number of degrees of freedom (6 locations x 3 sampling dates x 19 genotypes x 3 replications -1 = 1025). The genotype mean squares (MS) and environment MS were highly significant (P<0.01) for CGM PD, CGM LD (Table 3.2), TC, LR, FSRY and SRDM%. For Pbs (Table 3.2), TS (Table 3.3) and SG (Table 3.4), only the

genotype MS were significant (P<0.001). For all the traits studied, the genotype sum of squares (SS) accounted for the largest proportion of both the total and treatment SS, as compared to environment and GEI SS. The GEI MS were highly significant (P<0.001) for TC, LR, SG, and SRDM% and the contributions of their respective SS to the total SS were 26.0, 10.1, 15.1, and 11.5% (Tables 3.3 and 3.4). The IPCA1 was highly significant for all the traits studied, and it explained the interaction pattern better than IPCA2 which was only significant for LR (Table 3.3) and SG (Tables 3.4). As none of the IPCAs beyond IPCA2 were significant for all the traits only the first two were considered in modeling GEI for the traits.

For CGM PD, genotype SS accounted for 44.3 and 81.3% of the total and treatment SS, respectively (Table 3.2), while environment SS had marginal respective contributions of 1.7 and 3.2% to the total and treatment SS. The GEI MS was also highly significant for CGM PD, but the GEI SS only accounted for 8.5% of the total SS. For CGM PD, IPCA1 was highly significant (P<0.001), and accounted for 70.6% of the total GEI, while IPCA 2 explained 16.2% of the GEI SS and was not significant. The residuals accounted for the remaining 13.1% of the GEI SS.

On the other hand, the environment MS were not significant for CGM LD, while genotype MS and GEI MS were significant for this trait (Table 3.2). The environment SS accounted for 24.9 and 69.0% of the total and treatment SS, respectively for CGM LD, while GEI SS contributed 8.5 and 7.4% to the total and treatment SS respectively for the trait. The IPCA1 explained 48.5% of the GEI SS, while 22.1% of GEI SS was explained by IPCA2. For this trait a comparatively larger proportion (32.0%) of GEI SS was accounted for by the residual SS.

Table 3.2 Summary of AMMI analyses for cassava green mite population density and associated leaf damage, and leaf pubescence of 19 cassava genotypes grown in six environments (three locations x two years) in Zambia

Source of variation	df	CGM PD			CGM LD (1-5)			Pbs (1-3)		
		MS	%TSS	%GEI SS	MS	%TSS	%GEI SS	MS	%TSS	%GEI SS
Total	1025	534.0			0.6			0.6		
Treatment	113	2643.0***	54.6		1.8***	36.2		1.7	37.7	
Genotype	18	13460.0***	44.3		7.9***	24.9		9.7***	31.0	
Environment	5	1920.0***	1.7		3.0	2.7		0.5	0.4	
GEI	90	519.0***	8.5		0.5**	8.5		0.4	6.3	
IPCA 1	22	1500.0***		70.6	1.0***		48.5	0.9***		54.8
IPCA 2	20	380.0		16.2	0.5		22.1	0.4		23.6
Residuals	48	128.0		13.1	0.3		32.2	0.2		21.6
Error	900	271.0			0.4			0.4		

df = degrees of freedom; SS = sums of squares; MS = mean square; GEI = genotype by environment interaction; %TSS = percentage of total SS; %GEI SS = percentage of genotype by environment interaction SS; CGM = cassava green mite; CGM PD = population counts of cassava green mites per leaf; CGM LD = level of leaf injury caused by cassava green mite scored on a 1–5 scale, where 1 = no damage, 5 = very severe damage; Pbs = pubescence which is the degree of hairiness of leaves scored on a 1–3 scale, where 1 = glabrous, and 3 = highly pubescent; IPCA = interaction principal component axis; ***significant at P<0.001; **significant at P<0.01; *significant at P<0.05

Table 3.3 Summary of AMMI analyses for shoot tip compactness and tip size, and leaf retention of 19 cassava genotypes grown in six environments (three locations x two years) in Zambia

Source of variation	df	TC (1-3)			TS (1-3)			LR (%)		
		MS	%TSS	%GEISS	MS	%TSS	%GEISS	MS	%TSS	%GEISS
Total	1025	0.5			0.5			236.7		
Treatment	113	3.4***	78.0		1.9***	40.5		615.4***	28.7	
Genotype	18	14.0***	51.0		10.5***	34.9		2167.1***	16.1	
Environment	5	0.3**	0.3		0.3	0.3		1204.9**	2.5	
GEI	90	1.4***	26.0		0.3	5.3		272.3**	10.1	
IPCA1	22	5.7***		98.3	0.6*		44.2	595.0***		53.4
IPCA2	20	0.1		1.7	0.4		30.5	366.9**		29.9
Residuals	48	0.0		0.0	0.1		24.9	85.1		16.7
Error	900	0.1			0.3			187.2		

df = degrees of freedom; MS = mean square;GEI = genotype by environment interaction;%TSS = percentage of total sum of squares; %GEI SS = percentage of genotype by environment interaction sum of squares; TC = shoot tip compactness scored on a 1–3 scale, where 1 = loose, and 3 = compact; TS = size of shoot apices scored on a 1–3 scale, where 1 = small, and 3 = large; LR = leaf retention, which is the proportion of leaves retained on a plant expressed as a percentage, IPCA = interaction principal component axis, ***significant at P<0.001, **significant at P<0.01, *significant at P<0.05

The AMMI model analysis indicated that MS due to GEI was not significant for FSRY (Table 3.4). However, MS due to the main effects were significant. Genotype SS accounted for 27.2 and 28.4% of the total and treatment SS, respectively for the trait. The SS due to the environment main effects on FSRY accounted for 14.2 and 52.2% of the total and treatment SS, respectively.

Table 3.4 Summary of AMMI analyses for stay green, storage root dry mass percentage, and fresh storage root yield of 19 cassava genotypes grown in six environments (three locations x two years) in Zambia

Source of variation	df	SG			SRDM%			FSRY		
		MS	%TSS	%GEI SS	MS	%TSS	%GEI SS	MS	%TSS	%GEI SS
Total	1025	0.7			34.7			35.6		
Treatment	113	2.7***	44.5		86.7***	27.6		88.0***	27.3	
Genotype	18	10.9***	28.5		284.2***	14.4		156.7***	7.7	
Environment	5	1.3	1.0		20.3***	1.7		1037.6***	14.2	
GEI	90	1.2***	15.1		45.4***	11.5		21.5	5.3	
IPCA1	22	3.4***		71.1	126.6***		68.2	54.2**		61.6
IPCA2	20	0.8**		16.1	28.5		14.0	19.8		20.4
Residuals	48	0.3		12.7	15.2		17.8	7.2		17.9
Error	900	0.4			28.4			28.8		

df = degrees of freedom; MS = mean square; %TSS = percentage of total sum of squares; %GEISS = percentage of genotype by environment interaction sum of squares; SG = stay green scored on a 1-3 scale, where 1= lowest, and 3 = highest'; SRDM% = storage root dry mass expressed as a percentage; FSRY= fresh storage root yield (t ha^{-1}); IPCA = interaction principal component axis; ***significant at P<0.001, **significant at P<0.01, *significant at P<0.05

3.3.2 Adaptability of genotypes

The performance of the genotypes was determined at each environment. Genotypes with the lowest mean CGM PD and CGM LD scores were considered the most resistant at a specific environment. For other traits genotypes with highest trait means in one or two environments were considered to be the best performers for a particular trait in specific environments. Genotypes which performed consistently superior in more than two out of six environments were considered to exhibit wide adaptability.

CGM density: The genotypes L9.304/147, 4(2)1425, TME2, Kapeza, and Kaleleki were ranked in that order as the top five most resistant genotypes which harboured the lowest population of mites per leaf in 2010/11 at Mutanda (Table 3.5). In the 2011/12 season, 4(2)1425, L9.304/36, L9.304/175, and I60/42 sustained the lowest CGM PD at Mutanda. The genotype 4(2)1425 also had the lowest CGM PD in both seasons at Mwinilunga (Table 3.5). At Zambezi, L9.304/175, 4(2)1425, L9.304/147, I92/000 and Kaleleki were ranked among the top five most resistant genotypes for the two seasons.

Table 3.5 Ranked means of cassava green mite population densities in 19 cassava genotypes evaluated at Mutanda, Mwinilunga and Zambezi in Zambia in 2010/11 and 2011/12 seasons.

Genotype	Mutanda				Mwinilunga				Zambezi			
	2010/11		2011/12		2010/11		2011/12		2010/11		2011/12	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
Kapeza	11.8	4	35.4	12	8.0	2	35.3	12	24.1	8	23.2	7
Mweru	64.1	18	74.7	19	80.7	19	73.7	18	61.6	19	64.6	19
M86/0016	69.4	19	60.9	18	70.3	18	56.0	17	60.6	18	60.5	18
L9.304/147	8.6	1	20.0	3	11.8	3	18.3	3	11.1	3	11.5	2
Bangweulu	22.1	9	30.5	7	16.9	6	27.9	6	25.6	11	24.4	8
Chila	31.2	14	42.9	15	40.8	15	41.6	15	31.7	15	33.4	15
Lelanyana	52.5	17	49.0	16	70.1	17	45.8	16	41.1	16	44.3	16
I60/42	37.4	15	25.3	5	50.5	16	20.5	4	22.3	7	24.5	9
Lufunda	21.9	8	39.4	14	24.4	9	38.7	14	28.3	13	28.7	13
I30040	14.8	6	36.3	13	12.4	5	35.9	13	25.3	10	24.7	10
L9.304/175	16.0	7	23.7	4	40.7	14	22.6	5	9.0	1	13.6	3
4(2)1425	9.5	2	16.1	1	7.2	1	13.3	1	10.9	2	10.2	1
Manyopola	28.8	12	33.5	10	29.1	11	30.6	8	28.2	12	28.1	12
Kampolombo	26.0	11	32.9	8	31.2	13	30.6	8	25.1	9	25.9	11
92/000	22.8	10	19.2	2	20.0	8	14.9	2	18.2	5	17.4	4
L9.304/36	30.4	13	35.4	11	30.4	12	32.5	10	30.0	14	29.8	14
Kariba	46.3	16	54.1	17	25.8	10	50.4	16	54.5	17	50.4	17
TME 2	10.5	3	33.1	9	12.0	4	33.0	11	20.3	6	20.5	6
Kaleleki	12.1	5	29.9	6	19.2	7	29.4	7	17.2	4	18.4	5
Mean	28.2		36.4		31.7		34.3		28.7		29.2	
LSD(0.05)	8.2		15.0		8.3		19.4		13.9		16.0	
F-prob.	***		***		***		***		***		***	

F-prob = F-probability measure of significance; LSD = least significant difference; *P<0.05; **P<0.01; ***P<0.001; Rank = ranking of genotypes according to their respective mean performances, with 1 = best and 19 = worst.

CGM leaf damage: The genotypes L9.304/147, 4(2)1425, L9.304/175, Kapeza, and I30040 were among the most resistant genotypes which had the least CGM LD at Mutanda in 2010/11 season (Table 3.6). In the 2011/12 season, L9.304/175, 4(2)1425, 92/000, I60/42, and L9.304/147 were the most resistant genotypes at Mutanda. Of these genotypes, 4(2)1425 was the most resistant at Mwinilunga in both seasons, and was the second most resistant genotype at Zambezi in both seasons. The genotype L9.304/175 was ranked as the second best in both seasons at Zambezi and was the second most resistant genotypes at Mwinilunga in 2011/12 season.

Table 3.6 Ranked means of leaf damage caused by cassava green mite in 19 cassava genotypes evaluated at Mutanda, Mwinilunga and Zambezi in Zambia in 2010/11 and 2011/12 seasons

Genotype	Mutanda				Mwinilunga				Zambezi			
	2010/11		2011/12		2010/11		2011/12		2010/11		2011/12	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
Kapeza	1.8	3	2.8	8	1.9	1	2.9	13	2.4	4	2.4	4
Mweru	3.2	18	3.7	18	4.0	19	3.8	19	3.4	18	3.4	18
M86/0016	3.3	19	3.4	17	3.3	17	3.4	18	3.4	18	3.4	18
L9.304/147	1.7	1	2.5	2	2.3	3	2.9	13	2.0	2	2.1	2
Bangweulu	2.3	7	2.6	5	2.4	4	2.6	5	2.4	4	2.5	6
Chila	2.6	10	2.8	8	3.0	13	2.9	13	2.7	13	2.8	13
Lelanyana	2.9	15	2.9	15	3.6	18	3.0	16	2.8	16	2.9	16
I60/42	2.6	10	2.5	2	3.0	13	2.5	4	2.4	4	2.6	10
Lufunda	2.3	7	2.6	5	2.4	4	2.7	6	2.5	8	2.5	6
I30040	2.1	5	2.7	8	2.4	4	2.8	10	2.4	4	2.4	4
L9.304/175	1.8	3	2.3	1	3.0	13	2.3	1	1.9	1	2.0	1
4(2)1425	1.7	1	2.3	8	1.9	1	2.3	1	2.0	2	2.1	2
Manyopola	2.8	14	2.7	8	2.6	9	2.7	7	2.7	13	2.8	13
Kampolombo	2.9	15	2.7	2	3.1	16	2.8	10	2.6	12	2.7	12
92/000	2.7	12	2.5	8	2.6	9	2.4	3	2.5	8	2.6	10
L9.304/36	2.7	12	2.7	8	2.8	12	2.7	7	2.7	13	2.8	13
Kariba	2.9	15	3.2	16	2.6	9	3.2	17	3.1	17	3.2	17
TME 2	2.2	6	2.7	8	2.5	8	2.8	10	2.5	8	2.5	6
Kaleleki	2.3	7	2.6	5	2.4	4	2.7	7	2.5	8	2.5	6
Mean	2.4		2.8		2.7		2.8		2.7		2.6	
LSD(0.05)	0.5		0.5		0.5		0.6		0.6		0.5	
F-prob.	***		***		***		***		***		***	

F-prob. = F-probability as a measure of level of significance; LSD = least significant difference, *P<0.05;, **P<0.01; ***P<0.001; NS = means are not significantly different at 5% level of significance; Rank = ranking of genotypes according to their respective mean performances, with 1 = best and 19 = worst.

Storage root dry mass percentage: The genotype L9.304/175 had the highest SRDM% at Mutanda and Zambezi in the 2010/11 and 2011/12 seasons respectively, while Bangweulu had highest SRDM% in the 2011/12 season both at Mutanda and Mwinilunga. Manyopola and Kapeza were ranked as best performers for SRDM% at Mwinilunga and Zambezi respectively in the 2010/11 season. The genotype L9.304/175 was ranked the second best for SRDM% in the 2011/12 season both at Mutanda and Mwinilunga. The same genotype was also ranked best for SRDM% at Zambezi in the 2010/11 season, while L9.304/147 and Bangweulu were identified as second best genotypes for SRDM% at Mutanda and Zambezi in the 2010/11 and 2011/12 seasons, respectively (Table 3.7).

Table 3.7 Ranked means of storage root dry mass percentage of 19 cassava genotypes evaluated at Mutanda, Mwinilunga and Zambezi in Zambia in 2010/11 and 2011/12 season.

Genotype	Mutanda				Mwinilunga				Zambezi			
	2010/11		2011/12		2010/11		2011/12		2010/11		2011/12	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
Kapeza	32.4	12	33.2	7	32.0	13	32.6	8	34.9	1	35.3	3
Mweru	33.0	9	32.4	11	33.8	7	32.0	11	33.4	6	34.3	7
M86/0016	33.0	9	28.5	14	36.9	3	28.6	14	27.6	16	29.9	16
L9.304/147	34.7	2	33.8	4	35.1	5	33.4	4	33.7	4	35.1	4
Bangweulu	34.6	3	37.6	1	27.5	19	36.8	1	32.7	8	35.4	2
Chila	33.7	7	34.1	3	31.6	15	33.6	3	32.2	9	34.1	8
Lelanyana	30.0	16	26.7	18	32.9	10	26.6	18	26.6	19	28.4	18
I60/42	30.6	15	29.2	13	32.5	12	28.9	13	30.5	14	31.4	14
Lufunda	33.9	6	33.0	8	34.5	6	32.2	7	33.4	5	34.6	6
I30040	32.8	11	33.5	6	32.0	14	32.9	6	34.2	3	35.0	5
L9.304/175	35.1	1	35.8	2	32.8	11	35.5	2	34.3	2	36.0	1
4(2)1425	26.9	19	27.3	16	27.8	18	26.7	17	30.5	15	30.3	15
Manyopola	34.6	3	31.1	12	37.9	1	31.1	12	31.0	13	32.8	12
Kampolombo	32.3	13	27.1	17	37.4	2	27.3	16	27.0	17	29.0	17
92/000	33.4	8	32.5	10	33.1	9	32.2	10	31.5	12	33.1	11
L9.304/36	34.5	5	32.8	9	35.2	4	32.6	9	31.8	11	33.6	9
Kariba	27.0	18	24.0	19	31.4	16	23.9	19	26.8	18	27.2	19
TME 2	32.2	14	33.7	5	28.8	17	33.1	5	31.9	10	33.6	10
Kaleleki	29.7	17	28.4	15	33.5	8	28.0	15	32.9	7	32.5	13
Mean	32.3		31.3		33.0		31.0		31.4		32.7	
LSD(0.05)	5.7		3.6		5.1		3.6		5.8		4.9	
F-prob.	NS		***		***		***		NS		***	

F-prob. = F-probability as a measure of level of significance; LSD = least significant difference; *P<0.05, **P<0.01, ***P<0.001; NS = means are not significantly different at 5% level of significance; Rank = ranking of genotypes according to their respective mean performances, with 1 = best and 19 = worst.

Fresh storage root yield: Genotypes exhibited differential responses to the environments in terms of FSRY (Table 3.8). The genotypes Kapeza, 4(2)1425, Kampolombo and TME2 were the top performers for this trait. A landrace Kapeza was the highest yielder in 2010/11 at Mutanda and Zambezi. Likewise, TME2 had the highest yield genotype in 2011/12 at Mutanda and Mwinilunga, while Kampolombo and 4(2)1425 were the best performers at Mwinilunga and Zambezi in 2010/11 and 2011/12, respectively.

Table 3.8 Ranked means fresh root yield (t ha^{-1}) of 19 cassava genotypes evaluated at Mutanda, Mwinilunga and Zambezi in Zambia in 2010/11 and 2011/12.

Genotype	Mutanda				Mwinilunga				Zambezi			
	2010/11		2011/12		2010/11		2011/12		2010/11		2011/12	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
Kapeza	18.7	1	14.8	4	13.1	16	13.5	8	22.7	1	22.9	2
Mweru	15.2	8	12.0	11	11.4	19	11.2	18	19.4	6	19.5	5
M86/0016	13.7	11	11.0	16	11.5	18	10.7	19	17.3	12	16.8	11
L9.304/147	17.5	4	14.9	3	15.5	6	14.6	3	20.4	5	19.5	6
Bangweulu	16.4	6	13.6	7	14.2	10	13.4	9	18.2	10	16.6	12
Chila	12.0	18	11.5	15	15.1	8	12.8	11	18.6	8	19.0	7
Lelanyana	12.5	17	11.0	16	13.4	14	11.7	15	16.3	16	15.5	15
I60/42	16.7	5	13.8	6	13.5	13	13.1	10	22.2	3	22.8	3
Lufunda	17.7	2	15.3	2	16.6	3	15.4	2	18.9	7	17.0	9
I30040	16.4	6	14.1	5	15.4	7	14.2	6	18.4	9	16.9	10
L9.304/175	13.3	13	11.7	13	14.0	12	12.3	14	16.7	14	15.7	14
4(2)1425	14.6	9	13.6	8	16.0	4	14.3	4	22.7	2	24.2	1
Manyopola	13.0	15	11.0	16	12.7	17	11.3	16	16.2	17	15.2	18
Kampolombo	13.0	16	12.6	10	16.9	1	14.2	5	16.9	13	15.8	13
92/000	14.3	10	13.0	9	15.7	5	13.8	7	18.0	11	17.2	8
L9.304/36	13.4	12	11.9	12	14.3	9	12.3	12	16.6	15	15.4	16
Kariba	11.1	19	10.7	19	13.3	15	11.2	17	15.8	19	15.3	17
TME 2	17.6	3	15.5	1	16.8	2	15.6	1	22.2	4	22.0	4
Kaleleki	13.0	14	11.6	14	14.2	11	12.3	13	16.0	18	14.7	19
Mean	14.7		12.8		14.4		13.1		18.6		18.0	
LSD(0.05)	4.5		3.7		4.0		4.2		7.3		5.3	
F-prob.	**		**		***		NS		NS		***	

F-prob. = F-probability as a measure of level of significance; LSD = least significant difference; *P<0.05; **P<0.01, ***P<0.001; NS = means are not significantly different at 5% level of significance; Rank = ranking of genotypes according to their respective mean performances, with 1 = best and 19 = worst.

Leaf retention: The genotype L9.304/147 was ranked best for LR in three environments namely Mutanda in 2010/11 and 2011/12, and Mwinilunga in 2011/12, while Kapeza was ranked best for the trait at Zambezi in both seasons. I30040 was the best performer at Mwinilunga in 2010/11. Kapeza was also ranked the second best performer at Mutanda in 2010/11 and 2011/12 and at Mwinilunga in 2011/12. Bangweulu, Manyopola, and L9.304/175 were ranked equally second in 2010/11at Mwinilunga, and in both seasons at Zambezi (Table 3.9).

Table 3.9 Ranked means of leaf retention percentage of 19 cassava genotypes evaluated at Mutanda, Mwinilunga and Zambezi in Zambia in 2010/11 and 2011/12

Genotype	Mutanda				Mwinilunga				Zambezi			
	2010/11		2011/12		2010/11		2011/12		2010/11		2011/12	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
Kapeza	66.7	2	69.3	2	52.2	13	73.5	2	71.3	1	76.5	1
Mweru	55.9	9	55.6	9	58.8	5	60.5	10	64.3	4	61.6	9
M86/0016	42.6	19	41.4	19	52.2	12	47.4	19	47.4	19	44.0	19
L9.304/147	67.0	1	69.6	1	57.9	6	77.8	1	52.4	14	64.8	4
Bangweulu	53.4	11	54.3	11	47.5	18	57.6	11	66.1	2	64.4	5
Chila	48.3	16	46.3	17	60.8	3	51.0	17	61.6	5	53.1	14
Lelanyana	49.0	15	49.3	14	48.9	15	54.6	15	53.4	12	53.6	13
I60/42	50.1	12	49.6	13	54.6	9	54.8	14	57.1	11	54.4	12
Lufunda	49.3	14	48.9	15	55.2	7	55.3	13	50.6	16	50.2	17
I30040	56.5	8	55.4	10	70.4	1	64.3	8	47.5	18	49.2	18
L9.304/175	64.8	3	67.3	3	53.6	11	73.3	3	61.2	6	69.2	2
4(2)1425	61.3	4	62.0	4	59.2	4	67.2	4	65.5	3	66.5	3
Manyopola	58.5	6	58.1	7	64.3	2	64.4	7	60.2	9	59.6	10
Kampolombo	50.0	13	49.8	12	54.7	8	56.5	12	49.3	17	50.2	16
92/000	55.7	10	57.0	8	49.0	14	61.7	9	61.0	7	63.1	8
L9.304/36	47.3	17	47.4	16	48.7	16	52.6	16	52.7	13	51.9	15
Kariba	44.3	18	46.1	18	34.0	19	50.0	18	52.4	15	54.4	11
TME 2	59.6	5	60.9	5	54.2	10	66.4	5	60.7	8	64.3	6
Kaleleki	57.6	7	59.5	6	47.9	17	64.7	6	58.7	10	63.8	7
Mean	54.6		55.2		53.9		60.7		57.5		58.7	
LSD(0.05)	12.9		10.2		10.8		8.5		15.6		14.0	
F-prob.	***		***		***		***		NS		***	

F-prob. = F-probability as a measure of level of significance; LSD = least significant difference; *P<0.05, **P<0.01; ***P<0.001; NS = means are not significantly different at 5% level of significance; Rank = ranking of genotypes according to their respective mean performances, with 1 = best and 19 = worst.

Leaf pubescence: The genotype 4(2)1425 was ranked as the best performer for Pbs in both seasons at Mutanda and Mwinilunga and second best in the other two environments (Table 3.10). Kaleleki and L9.304/147 were also ranked as best performers for Pbs but specifically at Zambezi in 2010/11 and 2011/12, respectively. Besides 4(2)1425, the genotype L9.304/147 was also consistently ranked as the second best performer for Pbs at Mutanda in both seasons, and at Mwinilunga in 2011/12. Kapeza was also ranked second at Mwinilunga in 2010/12.

Table 3.10 Ranked means of leaf pubescence scores of 19 cassava genotypes evaluated at Mutanda, Mwinilunga and Zambezi in Zambia in 2010 and 2011

Genotype	Mutanda				Mwinilunga				Zambezi			
	2010/11		2011/12		2010/11		2011/12		2010/11		2011/12	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
Kapeza	2.7	3	2.6	2	2.8	2	2.4	3	2.3	5	2.2	8
Mweru	1.5	16	1.4	18	1.5	18	1.4	18	1.0	19	1.8	14
M86/0016	1.3	19	1.3	19	1.3	19	1.3	19	1.2	18	1.7	15
L9.304/147	2.8	1	2.6	2	2.8	2	2.5	2	2.1	9	2.8	1
Bangweulu	1.6	14	1.8	13	1.6	15	1.8	11	2.2	8	2.0	11
Chila	2.1	10	2.0	10	2.2	10	1.9	10	1.8	12	1.9	13
Lelanyana	1.5	16	1.6	16	1.6	15	1.5	16	1.8	12	1.5	17
I60/42	1.8	12	1.9	11	1.9	12	1.8	11	2.3	5	1.5	17
Lufunda	2.2	8	2.1	9	2.3	8	2.0	9	1.8	12	2.0	11
I30040	2.4	4	2.3	7	2.5	4	2.2	6	2.0	10	2.5	4
L9.304/175	2.4	4	2.5	4	2.4	5	2.4	3	2.7	3	2.6	3
4(2)1425	2.8	1	2.8	1	2.9	1	2.7	1	2.8	2	2.7	2
Manyopola	1.6	14	1.6	16	1.7	14	1.5	16	1.8	12	1.4	19
Kampolombo	1.5	16	1.7	15	1.6	15	1.6	15	2.0	10	1.7	15
92/000	2.3	6	2.4	6	2.4	5	2.2	6	2.5	4	2.2	8
L9.304/36	1.9	11	1.9	11	2.0	11	1.8	11	1.8	12	2.1	10
Kariba	1.8	12	1.8	13	1.9	12	1.8	11	1.5	17	2.3	6
TME 2	2.2	8	2.3	7	2.3	8	2.2	6	2.3	5	2.5	4
Kaleleki	2.3	6	2.5	4	2.4	5	2.4	3	2.9	1	2.3	6
Mean	2.0		2.0		2.1		2.0		2.0		2.1	
LSD(0.05)	0.6		0.5		0.6		0.6		0.5		0.6	
F-prob.	***		***		***		***		***		***	

F-prob. = F-probability as a measure of level of significance; LSD = least significant difference; *P<0.05; **P<0.01; ***P<0.001; NS = means are not significantly different at 5% level of significance;Pubescence assessed on 1-3 scale, where 1= glabrous, and 3 = highly pubescent;Rank = ranking of genotypes according to their respective mean performances, with 1 = best and 19 = worst.

Stay green: Genotypes responded differently to six different environments in their ability to stay green (Table 3.11). The genotype I30040 was the best performing genotype in both seasons at Mutanda, and in 2012 at Mwinilunga. Also Kapeza was identified as the best performing genotype in both seasons at Zambezi, while genotype I30040 was the best performing genotype at Mwinilunga in 2010/11 season. In 2010/11 and 201/12 seasons, TME 2 was the second best performer at Mutanda and Mwinilunga, while Kapeza, Mweru, L9.304/175 and Kaleleki were identified as the second best performing genotypes at Mutanda in 2011/12, Mwinilunga in 2010/11, and at Zambezi in 2010/11, and Zambezi in 2011/12, respectively.

To identify superior genotypes across the six environments, the ranks of each genotype were summed across environments for each trait. The genotype with the lowest rank sum (∑rank) was the best for that particular trait across environments (Table 3.12). Accordingly, at 25% selection intensity, the best five genotypes, that had good level of resistance based on recording lowest CGM PD were Kapeza, 4(2)1425, L9.304/147, 92/000, and L9.304/175 in that order. On the basis of the extent of CGM LD, the most resistant genotypes were in that order of resistance: 4(2)1425, L9.304/175, L9.304/147, Kapeza, and I30040.

Genotypes with the highest mean FSRY across environments were Kapeza, Mweru, TME2, Lufunda, and L9.304/147, while those with the lowest FSRY were Kariba, Manyopola, M86/0016, Lelanyana, and Kaleleki. The best performers for mean SRDM% across environments were L9.304/175, Bangweulu, L9.304/147, Kapeza, and I30040, while Kariba, Lelanyana, Kampolombo, 4(2)1425 and Mweru were the worst. The best performers for mean LR across environments were Kapeza, L9.304/147 and L9.304/175, 4(2)1425, and TME2 in that order. The most pubescent genotypes across environments were 4(2)1425, L9.304/147, Kapeza, I30040, and Kaleleki. Genotypes, L9.304/175, TME2, Kapeza, combined best performance for mean LR with best performance for mean SG across environments. On the other hand, genotypes M86/0016, Kariba, L9.304/36 were the worst performers for SG (Table 3.12).

Table 3.11 Ranked means of stay green scores* of 19 cassava genotypes evaluated at Mutanda, Mwinilunga and Zambezi in Zambia in 2010/11 and 2011/12.

Genotype	Mutanda				Mwinilunga				Zambezi			
	2010/11		2011/12		2010/11		2011/12		2010/11		2011/12	
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
Kapeza	2.4	2	2.9	2	1.1	18	2.5	4	2.8	1	3.0	1
Mweru	1.9	10	1.8	12	2.6	2	2.0	9	2.0	10	2.1	10
M86/0016	1.1	19	1.3	18	1.5	16	1.6	17	1.0	19	1.0	19
L9.304/147	2.0	7	2.3	7	2.3	5	2.6	3	1.9	11	1.9	12
Bangweulu	2.0	7	2.0	9	1.7	12	1.9	13	2.2	7	2.4	6
Chila	1.7	13	1.9	11	1.6	14	2.0	9	1.8	13	1.8	13
Lelanyana	1.9	10	2.0	10	2.0	9	2.0	9	2.1	9	2.2	9
I60/42	1.4	15	1.3	17	2.1	6	1.6	17	1.3	16	1.4	16
Lufunda	1.4	15	1.5	15	2.0	9	1.8	15	1.2	18	1.2	18
I30040	1.7	13	1.6	13	2.9	1	2.2	8	1.5	14	1.5	15
L9.304/175	2.7	1	3.3	1	1.6	14	3.1	1	2.8	1	2.8	3
4(2)1425	2.0	7	2.1	8	1.7	12	2.0	9	2.2	7	2.4	6
Manyopola	1.8	12	1.6	13	2.6	2	1.9	13	1.9	11	2.1	10
Kampolombo	2.3	6	2.5	4	1.8	11	2.3	6	2.6	4	2.8	4
92/000	2.4	2	2.5	4	2.1	6	2.4	5	2.6	4	2.8	4
L9.304/36	1.2	17	1.5	15	1.2	17	1.7	16	1.3	16	1.3	17
Kariba	1.2	17	1.3	18	1.0	19	1.2	19	1.5	14	1.7	14
TME 2	2.4	2	2.8	3	2.4	4	2.9	2	2.4	6	2.4	6
Kaleleki	2.4	2	2.4	6	2.1	6	2.3	6	2.7	3	2.9	2
Mean	1.9		2.0		1.9		2.1		2.0		2.1	
LSD(0.05)	0.6		0.5		0.7		0.6		0.6		0.6	
F-prob.	***		***		***		***		***		***	

F-prob. = F-probability as a measure of level of significance; LSD = least significant difference; *P<0.05; **P<0.01; ***P<0.001; NS = means are not significantly different at 5% level of significance; Stay green* assessed on 1-3 scale, where 1 = lowest, 3 = highest; Rank = ranking of genotypes according to the mean trait yields with 1 = best and 19 = worst.

The 2010/11 season at Mutanda and both seasons at Zambezi had significantly ($P<0.001$) below-average CGM PD and were consequently regarded as low pest pressure environments. On the other hand, the 2011/12 season at Mutanda had significantly ($P<0.001$) the highest CGM PD and was therefore regarded as a high pest pressure environment. The 2010/11 and 2011/12 seasons at Mwinilunga were respectively characterized as moderate pest pressure environment with average CGM PD and a moderately high pest pressure environment with above-average CGM PD. However, there was no significant ($P>0.05$) difference between the mean CGM PD recorded in the 2010/11 and 2011/12 season at Mwinilunga. A similar trend was observed for CGM LD among the environments. The 2010/11 season both at Mwinilunga and Zambezi had below-average CGM LD and were characterized as low pest pressure environments, while Mutanda in both seasons and Zambezi particularly in the 2011/12 season, were characterized as high pest pressure environment with above-average CGM LD.

There were no significant differences among genotypes in their expression of Pbs across environments. However, both seasons at Zambezi and the 2011/12 season at Mwinilunga had above-average mean LR and were consequently regarded as most favourable environments for expression of LR. The 2011/12 season at Mwinilunga and Zambezi also had above-average mean SG and was equally regarded as the most favorable environment for SG expression. Significantly ($P<0.001$) the highest FSRY were recorded in both seasons at Zambezi (Table 3.12), which was therefore regarded as the highest yielding environment.

Table 3.12 Overall ranked means of traits for 19 cassava genotypes evaluated in three locations in 2010/11 and 2011/12 in Zambia

Genotype	CGM PD		CGM LD		Pbs		LR		SG		FSRY		SRDM		
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Rank sum
Kapeza	23.0	7	2.4	4	2.5	3	68.2	1	2.5	3	22.7	1	34.0	4	23
Mweru	69.9	19	3.6	19	1.4	18	59.4	7	2.1	8	19.4	2	33.2	8	81
M86/0016	62.9	18	3.4	18	1.4	19	45.8	19	1.3	19	13.0	17	29.2	15	125
L9.304/147	13.5	2	2.2	2	2.6	2	64.9	2	2.2	7	16.7	5	34.2	3	23
Bangweulu	24.5	9	2.5	6	1.8	14	57.2	10	2.1	9	15.2	9	34.8	2	59
Chila	37.0	15	2.8	15	2.0	10	53.5	12	1.8	14	14.2	12	33.3	7	85
Lelanyana	50.5	17	3.0	16	1.6	17	51.6	16	2.0	11	13.0	16	27.5	18	111
I60/42	30.1	12	2.6	11	1.9	12	53.4	13	1.5	15	16.1	7	30.3	14	84
Lufunda	30.2	13	2.5	8	2.1	9	51.6	15	1.5	15	16.8	4	33.6	6	70
I30040	24.9	8	2.5	5	2.3	6	57.2	10	1.9	13	15.7	8	33.9	5	55
L9.304/175	21.0	4	2.2	2	2.5	4	64.9	2	2.7	1	13.7	14	35.1	1	28
4(2)1425	11.2	1	2.1	1	2.8	1	63.6	4	2.1	9	16.4	6	29.0	16	38
Manyopola	29.7	11	2.7	12	1.6	16	60.8	6	2.0	12	12.9	18	32.0	12	87
Kampolombo	28.6	10	2.7	14	1.7	15	51.8	14	2.4	6	14.8	11	28.3	17	87
92/000	18.8	3	2.6	10	2.3	6	57.9	9	2.5	4	15.0	10	32.4	11	53
L9.304/36	31.4	14	2.7	13	1.9	11	50.1	17	1.4	17	13.8	13	32.8	9	94
Kariba	46.9	16	3.0	17	1.8	13	46.8	18	1.3	18	12.4	19	26.1	19	120
TME 2	21.6	6	2.5	8	2.3	8	61.0	5	2.6	2	17.6	3	32.7	10	42
Kaleleki	21.0	5	2.5	6	2.5	5	58.7	8	2.5	4	13.5	15	31.1	13	56
Mean	31.4		2.6		2.0		56.8		2.0		15.4		31.8		
[a]LSD($_{0.05}$)	6.2		0.2		0.2		5.18		0.2		2.03		2.0		
F-prob.	***		***		***		***		***		***		***		

Environment		Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Rank sum
Mutanda	2010/11	28.2	1	2.4	1	2.0	3	54.6	5	1.9	6	14.7	3	32.3	3	22
	2011/12	36.4	6	2.8	5	2.0	3	55.1	4	2.0	3	12.8	6	31.3	5	32
Mwinilunga	2010/11	31.7	4	2.7	4	2.1	1	53.9	6	2.0	5	14.4	4	33.0	1	25
	2011/12	34.3	5	2.8	6	2.0	6	60.7	1	2.1	1	13.1	5	31.0	6	30
Zambezi	2010/11	28.7	2	2.6	2	2.0	3	57.5	3	2.0	4	18.6	1	31.4	4	19
	2011/12	29.2	3	2.6	3	2.1	2	58.7	2	2.1	2	18.0	2	32.7	2	16
Mean		31.4		2.6		2.1		56.8		2.0		15.3		32.0		
[b]LSD($_{0.05}$)		3.6		0.1		0.1		2.9		0.1		1.1		1.1		
F-prob.		***		***		NS		***		**		***		***		

CGM PD= population counts of cassava green mites per leaf; CGM LD = level of leaf injury caused by cassava green mite scored on a 1–5 scale, where 1 = no damage symptoms, and 5 = very severe damage; Pbs = pubescence which is the degree of hairiness of leaves scored on a 1–3 scale,where 1 = glabrous, and 3 = highly pubescent; LR = proportion of leaves retained on a plant measured as a percentage; SG = stay green scored on a 1-3 scale, where 1 = lowest, and 3 = highest; FSRY= fresh storage root yield (t ha^{-1}); SRDM% = storage root dry mass expressed as a percentage; F-prob. = F-probability, LSD = least significant difference; *P<0.05; **P<0.01; ***P<0.001; NS = means are not significantly different at 5% level of significance; Rank sum = sum of ranks of environmental means across traits;[a]LSD($_{0.05}$) = for comparison of genotype means;[b]LSD($_{0.05}$) = for comparison of environmental means.

3.3.3 AMMI stability analysis

Stability of genotypes: The genotypes with the lowest ASV score were considered to be the most stable (Table 3.13). Therefore, at 25% selection intensity, the genotypes L9.304/36, Manyopola, Chila, Kampolombo, and L9.304/147 were the most stable for CGM PD, while genotypes I60/42, Lelanyana, Kapeza, Kariba, and L9.304/175 were least stable. The most stable genotypes for CGM LD were identified as Bangweulu, M86/0016, L9.304/36, Chila, and Kaleleki in that order, while genotypes L9.304/175, Kapeza, Lelanyana, Kariba, and I60/42 were the least stable for the trait (Table 3.13). Genotypes L9.304/175, TME2, Manyopola, L9.304/36, and Lelanyana were the most stable for FSRY, while Lufunda, L9.304/147, Mweru, 92/000, and L9.304/36 were the most stable genotypes for SRDM% (Table 3.13). The most stable genotypes for LR were Lelanyana, Kariba, L9.304/36, Mweru, and TME2. The most stable for SG were Lelanyana, Chila, L9.304/36, TME2, and 4(2)1425, while Kapeza, I30040, L9.304/175, Lufunda, and Manyopola were identified as the least stable genotypes for the trait.

Stability of traits: Of the seven traits studied, CGM LD, FSRY and Pbs had low ASV scores, while CGM PD gave the highest ASV score (Table 3.13).

Table 3.13 AMMI stability values and ranks for 19 cassava genotypes evaluated in three locations in 2010/11 and 2011/12 in Zambia

Genotype	CGM PD		CGM LD		Pbs		LR		SG		FSRY		SRDM		Rank sum
	ASV	Rank	ASV	Rank	ASV	Rank	ASV	Rank	ASV	Rank	ASV	Rank	ASV	Rank	
Kapeza	11.80	17	1.27	18	0.53	9	4.36	18	3.80	19	0.91	17	3.49	10	108
Mweru	5.42	10	0.59	13	0.98	17	1.20	4	1.70	13	0.56	11	0.66	3	71
M86/0016	7.89	12	0.23	2	0.62	10	3.00	13	1.26	11	0.37	8	7.23	17	73
L9.304/147	1.84	5	0.44	9	1.10	18	3.46	15	1.10	9	0.50	10	0.38	2	68
Bangweulu	4.46	9	0.21	1	0.81	14	3.10	14	0.96	6	0.79	15	10.5	19	78
Chila	1.53	3	0.28	4	0.37	4	3.65	17	0.25	2	1.19	18	3.66	11	59
Lelanyana	13.20	18	1.05	17	0.52	8	0.30	1	0.18	1	0.23	5	4.72	13	63
I60/42	15.60	19	0.84	15	1.10	18	1.44	6	1.88	14	0.47	9	1.28	6	87
Lufunda	5.48	11	0.31	6	0.50	7	2.17	10	1.95	16	0.81	16	0.27	1	67
I30040	9.97	14	0.39	8	0.63	12	5.97	19	3.30	18	0.59	12	3.45	9	92
L9.304/175	10.90	15	1.13	19	0.39	5	2.89	12	2.75	17	0.16	1	4.31	12	81
4(2)1425	2.07	6	0.54	12	0.21	1	0.57	2	0.94	5	1.36	19	2.50	7	52
Manyopola	0.75	2	0.45	10	0.62	10	2.10	8	1.90	15	0.20	3	5.30	15	63
Kampolombo	1.55	4	0.59	13	0.71	13	2.11	9	1.58	12	0.75	14	8.86	18	83
92/000	3.68	8	0.48	11	0.36	3	2.07	7	1.04	7	0.28	7	0.87	4	47
L9.304/36	0.66	1	0.24	3	0.39	5	0.63	3	0.30	3	0.21	4	1.19	5	24
Kariba	11.80	16	0.92	16	0.93	15	3.53	16	1.05	8	0.61	13	5.04	14	98
TME 2	8.67	13	0.36	7	0.22	2	1.30	5	0.34	4	0.18	2	6.12	16	49
Kaleleki	3.56	7	0.29	5	0.93	15	2.57	11	1.12	10	0.25	6	2.53	8	62
Mean	6.36		0.56		0.63		2.44		1.44		0.55		3.81		
Rank	7		2		3		5		4		1		6		

CGM PD = population counts of cassava green mites per leaf; CGM LD = level of leaf injury caused by cassava green mite scored on a 1–5 scale, where 1 = no leaf damage symptoms, and 5 = very severe damage symptoms; Pbs = pubescence which is the degree of hairiness of leaves scored on a 1–3 scale,where 1 = glabrous, and 3 = highly pubescent; LR = proportion of leaves retained on a plant measured as a percentage; SG = stay green scored on a 1-3 scale, with 1 = lowest, and 3 = highest; FSRY= fresh storage root yield (t ha^{-1}); SRDM% = storage root dry mass percentage, Rank sum = sum of ASV ranks across traits, with lowest = most stable, and highest = least stable across environments.

3.3.4 Comparison of stability statistics

There were similarities and dissimilarities in the ranking of the stability of the genotypes for the various traits based on the five stability indices used.

CGM Density: Stability variance and environmental variance ranked the genotype Manyopola as the most stable for CGM PD. Mweru and Kampolombo were ranked as most stable for the trait by cultivar superiority (P_i) and Wi-ecovalence (Wi), respectively (Table 3.14). L9.304/36 was ranked as the most stable genotype for CGM PD by ASV and overall across the indices (Table3.14). The stability ranking of 47.4% of the genotypes based on ASV was identical to the overall ranking across the five indices for CGM PD. Stability variance (δi^2) and environmental variance (S_x^2) each ranked 26.3% of the genotypes similarly to overall ranking. Ranking by Wi matched the overall ranking for 10.5% of the genotypes, while P_i ranked all the genotype differently from the overall ranking.

Table 3.14 Comparative ranking of 19 cassava genotypes by five different stability statistics for cassava green mite population density across six environments in Zambia

Genotype	Stability variance		Cultivar superiority		Wi-ecovalence		AMMI		Environmental variance		Overall	
	δ_i^2	Rank	P_i	Rank	Wi	Rank	ASV	Rank	S_x^2	Rank	Rank sum	Rank
Kapeza	25.2	15	1.2	14	0.5	15	11.8	17	1.3	18	79	17
Mweru	4.7	12	0.1	1	0.2	11	5.4	10	0.6	12	46	7
M86/0016	1.6	9	0.1	2	0.3	13	7.9	12	0.3	9	45	9
L9.304/147	0.6	6	1.6	18	0.0	3	1.8	5	0.2	6	38	5
Bangweulu	1.1	8	1.0	11	0.1	7	4.5	9	0.2	7	42	8
Chila	0.9	7	0.5	5	0.0	6	1.5	3	0.3	8	29	4
Lelanyana	35.5	16	0.2	3	0.6	17	13.2	18	1.1	15	69	13
I60/42	42.6	18	0.8	7	0.8	19	15.6	19	1.4	19	82	19
Lufunda	4.1	11	0.8	9	0.1	9	5.5	11	0.5	11	51	11
I30040	14.8	14	1.1	12	0.3	14	10.0	14	1.0	14	68	15
L9.304/175	39.4	17	1.2	13	0.5	16	10.9	15	1.2	17	78	17
4(2)1425	0.2	3	1.7	19	0.0	5	2.1	6	0.1	4	37	6
Manyopola	0.1	1	0.8	8	0.0	4	0.8	2	0.0	1	16	2
Kampolombo	0.2	5	0.8	10	0.0	1	1.6	4	0.1	5	25	3
92/000	0.1	4	1.3	17	0.1	10	3.7	8	0.1	3	42	10
L9.304/36	0.1	2	0.7	6	0.0	2	0.7	1	0.0	2	13	1
Kariba	45.8	19	0.4	4	0.6	18	11.8	16	1.2	16	73	16
TME 2	12.9	13	1.2	16	0.3	12	8.7	13	1.0	13	67	13
Kaleleki	4.0	10	1.2	15	0.1	8	3.6	7	0.5	10	50	11
% overall rank	26.3		0.0		10.5		47.4		26.3			

δ_i^2 = stability variance; P_i = cultivar superiority; Wi = ecovalence; AMMI = additive main effects and multiplicative interaction analysis; ASV=AMMI stability value; S_x^2 = environmental variance stability index; Rank = ranking of genotypes according to the stability values, with 1 = best and 19 = worst; Rank sum = sum of ranks across the stability indices, where smallest rank sum =most stable, largest rank sum= least stable; %overall rank = percentage of genotypes ranked exactly the same as their respective overall ranks

CGM leaf damage: Both ASV and Wi ranked genotype Bangweulu as the most stable, while stability variance and cultivar superiority ranked L9.304/36 and Mweru respectively as the most stable genotypes for CGM LD. Wi-ecovalence ranked 15.8% of the genotypes' stability the same as the overall rank, while ranking by ASV, Sx^2, and mean CGM LD across environment

matched the overall ranking for 5.3% of the genotypes. The ranking by δ_i^2 and,P_i were all different from the overall ranks of genotypes (Table 3.15).

Table 3.15 Comparative ranking of 19 cassava genotypes by five different stability indices for leaf damage due to cassava green mite across six environments in Zambia

Genotype	Stability variance		Cultivar superiority		Wi-ecovalence		AMMI		Environmental variance		Overall	
	δ_i^2	Rank	P_i	Rank	Wi	Rank	ASV	Rank	Sx^2	Rank	Ranksum	Rank
Kapeza	0.05	18	0.01	16	0.66	19	1.27	18	0.19	19	90	17
Mweru	0.02	15	0.00	1	0.21	13	0.59	13	0.10	16	58	10
M86/0016	0.00	2	0.00	2	0.04	5	0.23	2	0.01	2	13	1
L9.304/147	0.02	16	0.01	18	0.19	11	0.44	9	0.10	17	71	15
Bangweulu	0.00	5	0.01	13	0.02	1	0.21	1	0.02	5	25	4
Chila	0.00	7	0.00	5	0.03	2	0.28	4	0.02	7	25	2
Lelanyana	0.03	17	0.00	3	0.40	17	1.05	17	0.09	15	69	15
I60/42	0.01	13	0.01	9	0.27	15	0.84	15	0.05	11	63	14
Lufunda	0.00	8	0.01	12	0.03	4	0.31	6	0.02	8	38	5
I30040	0.01	12	0.01	15	0.08	8	0.39	8	0.06	13	56	11
L9.304/175	0.07	19	0.01	17	0.57	18	1.13	19	0.17	18	91	18
4(2)1425	0.00	11	0.01	19	0.11	9	0.54	12	0.05	12	63	13
Manyopola	0.00	4	0.00	8	0.20	12	0.45	10	0.01	3	37	7
Kampolombo	0.00	10	0.00	6	0.13	10	0.59	13	0.04	9	48	9
92/000	0.00	3	0.01	10	0.21	14	0.48	11	0.01	4	42	8
L9.304/36	0.00	1	0.00	7	0.06	7	0.24	3	0.00	1	19	2
Kariba	0.01	14	0.00	4	0.37	16	0.92	16	0.06	14	64	12
TME 2	0.00	9	0.01	11	0.05	6	0.36	7	0.04	10	43	6
Kaleleki	0.00	6	0.01	14	0.03	3	0.29	5	0.02	6	34	5
%Overall rank	0.0		0.0		15.8		5.3		5.3			

δ_i^2 = stability variance; P_i = cultivar superiority; Wi = ecovalence; AMMI = additive main effects and multiplicative interaction analysis; ASV = AMMI stability value; S_x^2 = environmental variance stability index; Rank = ranking of genotypes according to the stability values, with 1 = best and 19 = worst;Ranksum = sum of ranks across the stability indices, where smallest rank sum = most stable, largest rank sum= least stable; %overall rank =percentage of genotypes ranked exactly the same as their respective overall ranks

Fresh storage root yield: Based onto the stability variance, the most stable genotype was Lufunda, while cultivar superiority ranked TME 2 as the most stable genotype. Wi-ecovalence and ASV ranked Manyopola and L9.304/175 as most stable genotypes, respectively. The P_i ranked 10.5% of the genotypes the same as the overall ranking. Stability of variance and ASVeach ranked 15.8% of the genotypes the same as the overall ranking, while 10.5% of the genotypes were ranked the same by P_i and the overall ranking. On the other hand, the ranking of the genotypes based on Wi were different to the overall ranking (Table 3.16).

Table 3.16 Comparative ranking of 19 cassava genotypes by four different stability indices for fresh storage root yield in six environments in Zambia

Genotype	Stability variance		Cultivar superiority		Wi-ecovalence		AMMI		Overall	
	δ_i^2	Rank	P_i	Rank	Wi	Rank	ASV	Rank	Rank Sum	Rank
Kapeza	0.50	17	0.00	2	0.03	19	0.91	17	55	17
Mweru	0.29	16	0.01	10	0.02	15	0.56	11	52	16
M86/0016	0.10	13	0.02	15	0.00	6	0.37	8	42	12
L9.304/147	0.05	12	0.00	5	0.00	2	0.50	10	29	3
Bangweulu	0.02	6	0.01	8	0.01	10	0.79	15	39	11
Chila	0.15	15	0.01	11	0.01	13	1.19	18	57	18
Lelanyana	0.03	10	0.02	17	0.00	3	0.23	5	35	8
I60/42	0.52	18	0.00	4	0.02	17	0.47	9	48	14
Lufunda	0.01	1	0.01	6	0.01	14	0.81	16	37	10
I30040	0.01	3	0.01	7	0.01	11	0.59	12	33	7
L9.304/175	0.02	7	0.01	13	0.00	5	0.16	1	26	2
4(2)1425	0.68	19	0.00	3	0.03	18	1.36	19	59	19
Manyopola	0.03	9	0.02	18	0.00	1	0.20	3	31	4
Kampolombo	0.02	4	0.01	12	0.02	16	0.75	14	46	13
92/000	0.02	8	0.01	9	0.00	7	0.28	7	31	4
L9.304/36	0.02	5	0.01	14	0.00	9	0.21	4	32	6
Kariba	0.04	11	0.02	19	0.00	8	0.61	13	51	15
TME 2	0.12	14	0.00	1	0.00	4	0.18	2	21	1
Kaleleki	0.01	2	0.02	16	0.00	12	0.25	6	36	9
%Overall rank	15.8		10.5		0.0		15.8			

CGM = cassava green mite, AMMI = additive main effects and multiplicative interaction analysis, ASV=AMMI stability value, P_i = cultivar superiority, δ_i^2 = stability variance no covariate, Wi = ecovalence, $\bar{X}_{i.}$ = mean yield or mean trait value, Ranksum = sum of rank across the stability indices, where smallest rank sum = best, %overall rank = percentage of genotypes ranked exactly the same as their respective overall ranks, Rank = ranking of genotypes according to the stability values with 1 = best and 19 = worst

Storage root dry mass percentage: The genotype L9.304/147 was ranked as the most stable by the S_x^2, $P_{i,}$ and Wi, and it was ranked second most stable by ASV. This genotype also had best overall rank (Table 3.17). However, ASV ranked genotype Lufunda as the most stable which was also ranked second by Wi and the overall ranking. Ranking of the genotypes' stability for SRDM% by Wi matched that of the overall ranking for 31.6% of the genotype. The ASV and δ_i^2 respectively ranked 21.0% and 26.3% of the genotypes' stability respectively the same as the overall ranking, while ranking by mean SRDM% matched with the overall rank for 10.5% of the genotypes (Table 3.17).

Table 3.17 Comparative ranking of nineteen cassava genotypes by four different stability indices for storage root dry mass across six environments in Zambia

Genotype	Stability variance		Cultivar superiority		Wi-ecovalence		AMMI		Overall	
	δ^2	Rank	Pi	Rank	wi	Rank	ASV	Rank	Ranksum	Rank
Kapeza	0.01	9	0.01	8	0.01	9	3.49	10	36	9
Mweru	0.00	4	0.01	5	0.00	3	0.66	3	15	3
M86/0016	0.36	17	0.02	15	0.04	17	7.23	17	66	16
L9.304/147	0.00	1	0.00	1	0.00	1	0.38	2	5	1
Bangweulu	0.46	18	0.01	11	0.09	19	10.48	19	67	17
Chila	0.00	5	0.01	7	0.01	8	3.66	11	31	7
Lelanyana	0.09	14	0.03	17	0.02	12	4.72	13	56	13
I60/42	0.01	10	0.02	13	0.00	5	1.28	6	34	9
Lufunda	0.00	3	0.00	3	0.00	2	0.27	1	9	2
I30040	0.00	6	0.01	6	0.01	7	3.45	9	28	6
L9.304/175	0.00	8	0.00	2	0.01	10	4.31	12	32	8
4(2)1425	0.01	11	0.03	18	0.02	11	2.50	7	47	10
Manyopola	0.13	15	0.01	10	0.02	15	5.30	15	55	12
Kampolombo	0.70	19	0.02	16	0.06	18	8.86	18	71	18
92/000	0.00	2	0.01	9	0.00	4	0.87	4	19	4
L9.304/36	0.00	7	0.00	4	0.00	6	1.19	5	22	5
Kariba	0.13	16	0.05	19	0.02	14	5.04	14	63	15
TME 2	0.03	12	0.01	12	0.03	16	6.12	16	56	13
Kaleleki	0.04	13	0.02	14	0.02	13	2.53	8	48	11
%Overall rank‡	21.0		15.8		31.6		26.30			

δ_i^2 = stability variance; P_i = cultivar superiority; Wi = ecovalence; AMMI = additive main effects and multiplicative interaction analysis; ASV = AMMI stability value; S_x^2 = environmental variance stability index; Rank = ranking of genotypes according to the stability values, with 1 = best and 19 = worst; Ranksum = sum of ranks across the stability indices, where smallest rank sum = most stable, largest rank sum= least stable; %overall rank = percentage of genotypes ranked exactly the same as their respective overall ranks

Leaf retention: Lelanyana was ranked as the most stable genotype for LR by Wi and ASV but ranked second most stable according to the overall ranking. The second most stable genotype 4(2)1425 as ranked by all stability statistics exceptδ_i^2, was ranked as the most stable genotype for LR according to the overall ranking (Table 3.18). Ranking by ASV had the highest proportion of genotypes (31.6%) ranked the same as the overall ranking, followed by Wi and P_i which, respectively had 21.0 and 10.5% of the genotype's ranking, matching the overall ranking (Table 3.18).

Table 3.18 Comparative ranking of nineteen cassava genotypes by four different stability indices for leaf retention across six environments in Zambia

Genotype	Stability variance		Cultivar superiority		Wi-ecovalence		AMMI		Overall	
	δ_i^2	Rank	P_i	Rank	Wi	Rank	ASV	Rank	Rank sum	Rank
Kapeza	16.03	19	0.03	1	0.23	16	4.36	18	54	15
Mweru	0.21	8	0.09	7	0.04	5	1.20	4	24	3
M86/0016	0.48	9	0.36	19	0.12	12	3.00	13	53	13
L9.304/147	12.28	18	0.05	4	0.34	18	3.46	15	55	16
Bangweulu	4.10	14	0.13	10	0.16	15	3.10	14	53	13
Chila	2.33	12	0.20	13	0.24	17	3.65	17	59	17
Lelanyana	0.05	2	0.21	15	0.00	1	0.30	1	19	2
I60/42	0.12	5	0.18	12	0.04	6	1.44	6	29	7
Lufunda	0.10	4	0.22	16	0.06	9	2.17	10	39	9
I30040	10.10	17	0.15	11	0.48	19	5.97	19	66	19
L9.304/175	4.87	15	0.04	3	0.14	13	2.89	12	43	11
4(2)1425	0.14	7	0.04	2	0.00	2	0.57	2	13	1
Manyopola	0.09	3	0.07	6	0.05	8	2.10	8	25	6
Kampolombo	0.14	6	0.21	14	0.06	10	2.11	9	39	9
92/000	1.63	11	0.11	9	0.05	7	2.07	7	34	8
L9.304/36	0.05	1	0.24	17	0.01	3	0.63	3	24	3
Kariba	7.13	16	0.33	18	0.16	14	3.53	16	64	18
TME 2	0.70	10	0.06	5	0.02	4	1.30	5	24	3
Kaleleki	3.47	13	0.10	8	0.08	11	2.57	11	43	11
%Overall rank	5.2		10.5		21.0		31.6			

δ_i^2 = stability variance; P_i = cultivar superiority; Wi = ecovalence; AMMI = additive main effects and multiplicative interaction analysis; ASV=AMMI stability value; Rank = ranking of genotypes according to the stability values, with 1 = best and 19 = worst; Ranksum = sum of ranks across the stability indices, where smallest rank sum = most stable, largest rank sum= least stable; %overall rank = percentage of genotypes ranked exactly the same as their respective overall ranks

Leaf pubescence: The four statistics including mean trait yield ranked genotype 4(2)1425 as the most stable genotype for Pbs (Table 3.19). Stability variance, Wi, and ASV ranked 92/000 as the second most stable genotype but it was not ranked so by the overall ranking. Both P_i and overall ranking ranked L9.304/147 as the second most stable genotype. Stability of variance and the overall ranking ranked 36.8% of the genotypes the same, while P_i and ASV, respectively ranked 21.0 and 15.8% of the genotypes the same as the overall ranking. Wi-ecovalence and the overall ranking ranked 10.5% of the genotypes the same, while only 5.3% of the genotypes ranked on the basis of mean Pbs across environments had the same rank as the overall ranking.

Table 3.19 Comparative ranking of nineteen cassava genotypes by four different stability statistics for leaf pubescence across six environments in Zambia

Genotype	Stability variance		Cultivar superiority		Wi-ecovalence		AMMI		Overall	
	δ_i^2	Rank	P_i	Rank	Wi	Rank	ASV	Rank	Ranksum	Rank
Kapeza	0.00	12	0.07	4	0.26	14	0.53	9	39	10
Mweru	0.01	14	1.00	18	0.28	15	0.98	17	64	18
M86/0016	0.00	13	1.09	19	0.15	11	0.62	10	53	14
L9.304/147	0.02	19	0.05	2	0.33	18	1.10	18	57	15
Bangweulu	0.01	16	0.51	14	0.29	17	0.81	14	61	16
Chila	0.00	6	0.38	10	0.08	7	0.37	4	27	6
Lelanyana	0.00	7	0.76	17	0.08	6	0.52	8	38	9
I60/42	0.01	17	0.46	12	0.35	19	1.10	18	66	19
Lufunda	0.00	10	0.29	9	0.15	10	0.50	7	36	7
I30040	0.00	9	0.13	7	0.11	8	0.63	12	36	7
L9.304/175	0.00	3	0.06	3	0.07	5	0.39	5	16	3
4(2)1425	0.00	1	0.00	1	0.02	1	0.21	1	4	1
Manyopola	0.00	8	0.74	16	0.12	9	0.62	10	43	11
Kampolombo	0.00	11	0.65	15	0.15	12	0.71	13	51	13
92/000	0.00	2	0.12	6	0.04	2	0.36	3	13	2
L9.304/36	0.00	5	0.40	11	0.05	4	0.39	5	25	5
Kariba	0.01	18	0.50	13	0.028	16	0.93	15	62	17
TME 2	0.00	4	0.14	8	0.04	3	0.22	2	17	4
Kaleleki	0.01	15	0.08	5	0.24	13	0.93	15	48	12
%Overall rank	36.8		21.0		10.5		15.8			

δ_i^2 = stability variance; P_i = cultivar superiority; Wi = ecovalence; AMMI = additive main effects and multiplicative interaction analysis; ASV=AMMI stability value; Rank = ranking of genotypes according to the stability values, with 1 = best and 19 = worst; Ranksum = sum of ranks across the stability indices, where smallest rank sum = most stable, largest rank sum= least stable; %overall rank = percentage of genotypes ranked exactly the same as their respective overall ranks

Stay green: Equivalence in ranking the most stable genotype for SG were only apparent for δ_i^2 and ASV, both of which ranked Kariba as the most stable genotype. The rest of the statistics ranked different genotypes as the most stable. Cultivar superiority and Wi ranked Kaleleki and I60/42 respectively as the most stable genotypes for SG, while on the basis of mean SG across environments, L9.304/147 was ranked as the most stable genotype. The Wi ranking matched the overall ranking for 21.0% of the genotypes, while 15.8% of the genotypes ranked by δ_i^2 matched the overall ranking. Ranking by P_i, AMMI, and mean SG across environments matched the overall ranking for 5.3% of the genotypes (Table 3.20).

Table 3.20 Comparative ranking nineteen cassava genotypes by four different stabilitystatistics for stay green across six environments in Zambia

Genotype	Stability variance		Cultivar superiority		Wi-ecovalence		AMMI		Overall	
	δ_i^2	Rank	P_i	Rank	Wi	Rank	ASV	Rank	Rank sum	Rank
Kapeza	0.75	19	0.27	6	2.11	19	3.80	19	63	18
Mweru	0.02	12	0.43	11	0.50	13	1.70	13	49	13
M86/0016	0.00	5	1.43	10	0.31	10	1.26	11	36	9
L9.304/147	0.01	10	0.32	7	0.36	11	1.10	9	37	10
Bangweulu	0.01	7	0.42	9	0.22	7	0.96	6	29	7
Chila	0.00	2	0.67	14	0.03	1	0.25	2	19	3
Lelanyana	0.00	1	0.43	12	0.04	2	0.18	1	16	2
I60/42	0.02	14	1.06	16	0.53	14	1.88	14	58	15
Lufunda	0.02	13	1.06	17	0.64	15	1.95	16	61	17
I30040	0.21	18	0.70	15	1.60	18	3.30	18	69	19
L9.304/175	0.36	17	0.14	3	1.44	17	2.75	17	54	14
4(2)1425	0.01	6	0.41	8	0.17	5	0.94	5	24	4
Manyopola	0.04	16	0.53	13	0.71	16	1.90	15	60	16
Kampolombo	0.03	15	0.20	5	0.40	12	1.58	12	44	11
92/000	0.01	8	0.14	4	0.21	6	1.04	7	25	5
L9.304/36	0.00	3	1.23	18	0.11	3	0.30	3	27	6
Kariba	0.01	9	1.34	19	0.27	8	1.05	8	44	11
TME 2	0.00	4	0.08	2	0.14	4	0.34	4	14	1
Kaleleki	0.01	11	0.15	1	0.29	9	1.12	10	31	8
%Overall rank	15.8		5.3		21.0		5.3			

δ_i^2 = stability variance; P_i = cultivar superiority; Wi = ecovalence; AMMI = additive main effects and multiplicative interaction analysis; ASV = AMMI stability value; Rank = ranking of genotypes according to the stability values, with 1 = best and 19 = worst; Ranksum = sum of ranks across the stability indices, where smallest rank sum = most stable, largest rank sum= least stable; %overall rank =percentage of genotypes ranked exactly the same as their respective overall ranks

3.3.5 Correlation of stability statistics

Spearman's correlation of the rank orders indicated that ASV ranking was significantly ($P<0.001$) and positively correlated to the other stability statistics except *Pi* and the overall mean for CGM PD, CGM LD, LR, Pbs, and SG (Table 3.21). For SRDM%, ASV ranking was also slightly correlated with P_i ($r=0.540$), but highly correlated with δ_i^2 ($r= 0.863$), and Wi ($r = 0.944$). There was highly significant ($P<0.001$) correlation between ASV and overall ranking for all the seven traits that were studied. The *Pi* was also highly correlated to the mean trait value (trait mean) for each of the seven traits (Table 3.21).

Table 3.21 Spearman's rank correlation coefficients for five statistics used to measure stability of 19 cassava genotypes for resistance to cassava green mite, leaf pubescence, leaf retention, storage root dry mass, and fresh storage root yield across six environments in Zambia

Trait		Stability statistics					
		ASV	P_i	δ_i^2	Wi	$\bar{X}_{i.}$	Overall rank
CGM PD	P_i	-0.15					
	δ_i^2	0.92***	-0.24				
	Wi	0.95***	-0.26	0.91***			
	$\bar{X}_{i.}$	0.15	-0.98***	0.23	0.23		
	OR	0.96***	-0.05	0.95***	0.93***	0.04	
	Sx^2	0.91***	-0.19	0.98***	0.88***	0.18	0.96***
CGM LD	P_i	0.07					
	δ_i^2	0.80***	0.24				
	Wi	0.93***	0.01	0.68**			
	$\bar{X}_{i.}$	-0.06	-0.99***	-0.25	0.01		
	OR	0.89***	0.34	0.94***	0.82***	0.93	
	Sx^2	0.75***	0.31	0.98***	0.64**	-0.31	-0.34***
Pbs	P_i	0.31					
	δ_i^2	0.93***	0.27				
	Wi	0.92***	0.26	0.97***			
	$\bar{X}_{i.}$	0.30	0.99***	0.26	0.25		
	OR	0.93***	0.54*	0.93***	0.93***	0.53*	
LR	P_i	-0.01					
	δ_i^2	0.80***	-0.40				
	Wi	0.98***	-0.06	0.81***			
	$\bar{X}_{i.}$	-0.10	0.99***	-0.47	-0.17		
	OR	0.98***	0.12	0.78***	0.96***	0.02*	
SG	P_i	-0.02					
	δ_i^2	0.95***	-0.10				
	Wi	0.99***	-0.02	0.95***			
	$\bar{X}_{i.}$	-0.13	0.89***	-0.28	-0.15		
	OR	0.95***	0.26	0.91***	0.95***	0.10	
FSRY	P_i	-0.37					
	δ_i^2	0.22	-0.38				
	Wi	0.71***	-0.43	0.21			
	$\bar{X}_{i.}$	-0.39	0.91***	-0.31	-0.49*		
	OR	0.80***	-0.09	0.47*	.786***	-0.15	
SRDM	P_i	0.54*					
	δ_i^2	0.86***	0.77***				
	Wi	0.94***	0.67**	0.94***			
	$\bar{X}_{i.}$	0.24	0.85***	0.53*	0.37		
	OR	0.92***	0.78***	0.98***	0.96***	0.50*	

CGM = cassava green mite;CGM PD = population counts of cassava green mites per leaf;CGM PD= population counts of cassava green mites per leaf; CGM LD = level of leaf injury caused by cassava green mite scored on a 1–5 scale, where 1 = no leaf damage symptoms, and 5 = very severe damage symptoms; Pbs = pubescence which is the degree of hairiness of leaves scored on a 1–3 scale, where 1 = glabrous, and 3 = highly pubescent; LR = proportion of leaves retained on a plant measured as a percentage; SG = stay green scored on a 1-3 scale, with 1 = lowest, and 3 = highest; SRDM% = percentage storage root dry mass; FSRY= fresh storage root yield (t ha^{-1}); ASV=AMMI stability value; P_i = cultivar superiority; δ_i^2 = Stability variance no covariate; Wi = ecovalence; $\bar{X}_{i.}$ = mean yield or mean trait value; Overall rank = overall rank of four or five stability indices; S_x^2 = environment variance.

Significant, positive correlations were also recorded between cultivar superiority and overall rank for Pbs and SRDM%. In the case of SRDM%, P_i was positively correlated with all the other statistics. Stability variance was also highly correlated with Wi and overall ranking for all the seven traits. Highly significant (P<0.001) correlations was also evident between δ_i^2 and $S_x^2$for CGM PD and CGM LD (r =0.979 and r =0.984, respectively). The ASV, δ_i^2, and Wi had strong positive correlations with the overall rank for all seven traits (Table 3.21). In addition, a

significantly positive high correlation was observed between S_x^2 and overall ranking for CGM PD and CGM LD.

3.3.6 Selection indices for genotypes

The genotype stability index (GSI), which incorporates both the rank of ASV (as an indication of stability) and the rank of the overall trait mean (as an indication of performance) of genotypes in a single selection criterion, was employed to identify such desirable genotypes for each trait (Table 3.22). A genotype with the lowest GSI is considered the most stable with the best overall performance for a given trait. Accordingly, genotypes L9.304/147, 4(2)1425, 92/000, Kaleleki, and Manyopola combined high stability with reduced attractiveness to CGM. Bangweulu, L9.304/147 and Kaleleki, I30040 and 4(2)1425 were the most stable and most resistant with regard to CGM LD. In terms of SRDM% (Table 3.22), genotypes L9.304/147, Lufunda, Mweru, L9.304/175, and L9.304/36 had lowest GSI scores. Genotypes TME2, Mweru, L9.304/147 and L9.304/175 had lowest GSI scores for FSRY. Smallest GSI scores for LR were recorded for genotypes 4(2)1425, TME2, Mweru, L9.304/1751 and Manyopola. Genotypes TME2, 92/000, Lelanyana, 4(2)1425 and Kaleleki had lowest GSI scores for SG, while 4(2)1425, L9.304/175 and 92/000, TME2, and Kapeza had smallest GSI scores for Pbs.

Genotypes with least overall GSI rank were most stable and best performers across traits. Accordingly, genotypes L9.304/147, 92/000, 4(2)1425 and TME2 and L9.304/175 were the most stable and best performers in all the traits across environments.

Table 3.22 Genotype and environment selection indices for 19 cassava genotypes evaluated in three locations in 2010/11 and 2011/12 in Zambia

Genotype	CGM PD		CGM LD		Pbs		LR		SG		FSRY		SRDM%		Overall	
	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	Rank sum	I Rank
Kapeza	24	13	22	13	12	5	19	9	22	13	18	8	14	5	66	8
Mweru	29	15	32	17	36	19	11	3	21	12	13	2	11	3	71	11
M86/0016	30	16	20	10	29	17	32	18	30	17	25	15	32	17	110	18
L9.304/147	7	1	11	2	21	11	17	7	16	7	15	3	5	1	32	1
Bangweulu	18	8	7	1	28	14	24	14	15	5	24	14	21	11	67	9
Chila	18	8	19	9	14	6	29	16	16	7	30	18	18	9	73	12
Lelanyana	35	19	33	18	25	12	17	7	12	3	21	11	31	16	86	15
I60/42	31	17	26	15	31	18	19	9	29	16	16	5	20	10	90	16
Lufunda	24	13	14	6	16	7	25	15	31	18	20	9	7	2	70	10
I30040	22	12	13	4	18	9	29	16	31	18	20	9	14	5	73	12
L9.304/175	19	10	21	11	9	2	14	4	18	9	15	3	13	4	43	5
4(2)1425	7	1	13	4	2	1	6	1	14	4	25	15	23	13	39	3
Manyopola	13	5	22	13	26	13	14	4	27	15	21	11	27	15	76	14
Kampolombo	14	6	27	16	28	14	23	13	18	9	25	15	35	19	92	17
92/000	11	3	21	11	9	2	16	6	11	2	17	6	15	8	38	2
L9.304/36	15	7	16	8	16	7	20	12	20	11	17	6	14	5	56	7
Kariba	32	18	33	18	28	14	34	19	26	14	32	19	33	18	120	19
TME 2	19	10	15	7	10	4	10	2	6	1	5	1	26	14	39	3
Kaleleki	12	4	11	2	20	10	19	9	14	4	21	11	21	11	51	6

CGM PD= population counts of cassava green mites per leaf; CGM LD = level of leaf injury caused by cassava green mite scored on a 1–5 scale, where 1 = no leaf damage symptoms, and 5 = very severe damage symptoms; Pbs = pubescence which is the degree of hairiness of leaves scored on a 1–3 scale, where 1 = glabrous, and 3 = highly pubescent; LR = proportion of leaves retained on a plant measured as a percentage; SG = stay green scored on a 1-3 scale, with 1 = lowest, and 3 = highest; FSRY= fresh storage root yield (t ha^{-1}); SRDM% = storage root dry mass expressed as a percentage; GSI = genotype stability index; Ranksum = sum of ranks of genotype stability indices across traits, where genotype with smallest rank sum = best, and genotype with largest rank sum= worst

3.4 Discussion and conclusions

The AMMI analysis indicated that the large differences among genotypes caused most of the variations in CGM PD, CGM LD, TS, TC, LR, SG, FSRY, and SRDM%. The magnitude of GEI SS for each of these traits was smaller than that of genotypes, indicating that there were minor differences in the genotype responses across environments for all the traits studied. The IPCA 1 and IPCA 2 were significant for the model, while further IPCAs were not significant (P>0.05) and captured mostly noise, thus being less helpful. These findings are in agreement with Gauch (2006) who reported that the IPCA 1 and higher components in AMMI capture interaction exclusively in a monotonic sequence that decreases from the first and largest component to the last and smallest component. Therefore, according to Fikere et al. (2009), the interaction of genotypes in the field is best explained by the first two interaction principal component axes. However, sometimes the first two IPCAs tend to rank genotypes differently giving negative and positive values. The use of ASV is therefore, advocated (Farshadfar, 2008; Fikere et al., 2009), as it gives a balanced measure between the first two IPCAs. However, success has also been reported even with the use of a larger number of IPCAs (Sivapalan et al., 2000), signifying the need for prior predictive assessment of the model to determine the number of useful IPCAs to be retained in the model (Yan and Rajan, 2002).

The Spearman's rank correlation calculated between pairs of computed stability parameter ASV, δ^2,Wi, S_x^2, *Pi*, and the overall mean of each trait indicated that the ASV is highly correlated with δ^2, Wi, and S_x^2 for CGM PD, CGM LD,LR, Pbs, SG, SRDM%, and FSRY. This indicates that there would be no advantage in using more than one of these indices at the same time (Benesi et al., 2004). The current study has indicated existence of a strong relationship between ASV and other stability indices in detecting the stable cassava genotypes for the seven traits that were studied. However, these results show that the ranking of genotypes' stability by each of the six stability parameters varies with traits. Based on the equivalence of ranking of genotypes' stability, the higher the proportion of genotypes ranked the same as the overall rank, the more suitable the index is for a particular trait. According to this criterion, the ASV was best suited to ranking of stability for CGM PD, FSRY, SRDM%, and LR. Stability variance was best suited for FSRY, SRDM%, and Pbs. The Wi-ecovalence was found to be best suited for CGM LD, SG and SRDM%, while cultivar superiority was suitable for Pbs. The CGM PD was sensitive to environmental fluctuations, and therefore could be less amenable to selection. The environmental variance statistic measured CGM PD better than CGM LD. The environmental variance statistic is a static stability measure which is recommended for pest or disease resistance-related traits, for which constantly low resistance levels are desired despite changes in the environment (Becker and Leon, 1988).

Farmers are more interested in genotypes that perform consistently better across seasons (Fikere et al., 2009), indicating preference for widely adapted genotypes (Zhang et al., 2006; Singh et al., 2007), and likewise, breeders would like to consider both yield and stability of performance simultaneously to reduce the effect of GEI and to make selection of genotypes more precise and refined (Farshadfar, 2008). Though more resources may be required in breeding for specific environments, the merits of genotypes with local adaptation should also be recognized (Annicchiarico, 2002; Fikere et al., 2009). In the current study, none of the genotypes investigated was ranked best for stability in all the seven traits studied, but widely adapted genotypes for specific traits were identified. A number of other genotypes with high trait mean value, but specifically adapted to particular environments for specific traits were also identified.

Genotypes having wide adaptation are defined as those that in representative multi-locational trials produce yields substantially above the environmental means and then are among a few top-ranking ones at a majority of locations across the production area which is characterized by substantial variation in environmental conditions (Braun et al., 1996; Rodriguez et al., 2008). Such genotypes produce relatively high and stable yields within the area (Singh et al., 2007; Yang et al, 2009). Genotypes having specific adaptation are defined as these that produced yields substantially above the environmental means and then are among a few top-ranking ones in a range of a sub-region (macro-environment) within the target region, usually of limited environmental variation (Gauch and Zobel, 1997) or in at least one environment within the target area (Annicchiarico et al., 2010). Usually, genotypes with wide adaptation have fairly high yield potential and stress tolerance, whereas specifically-adapted ones have top levels of either yield potential or stress tolerance (Singh et al., 2007; Trethowan and Crossa, 2007).

In this study, a genotype that ranked among the top five in one or two environments was considered to be specifically adapted to either or both environments, while a genotype ranked among the top five in more than two out of six environments, was considered to be widely adapted. Environments were characterized based on the differences between the respective environmental means, which were detected based on the least significant difference. For CGM PD four categories of environments were established as high pest pressure environments, moderately low pest pressure environments, moderately high and low pest pressure environments. In terms of specific adaptability, genotypes Kapeza, M86/0016, I60/42, Manyopola, and TME2 had very small IPCA1 scores and ASV scores and were therefore considered to be adapted to moderately high pest pressure environments. Kapeza and TME2 also presented specific adaptability to low pest pressure environments, suggesting that these genotypes be recommended for both low and moderately high pest pressure environments.

Similarly I60/42 was specifically adapted to both high and moderately high pest pressure environments. M86/0016 and Manyopola were specifically adapted to Mwinilunga in the 2010/11 season which was characterized as a moderately high pest pressure environment, but not to Mwinilunga in 2011/12 season. It may appear that four of the six environments were similar in their pest pressure and could effectively be grouped as one, thereby establishing three categories: high, moderately high and low pest pressure environments. However, the inconsistencies of certain genotypes in their specific adaptability between seasons for the same location are an indication of important dissimilarities between such locations across seasons. Mutanda displayed greatest inter-season instability for CGM PD and therefore cannot be relied upon for evaluation of germplasm over seasons. Zambezi site displayed best inter-season stability for moderately low CGM PD and CGM LD, and high FSRY.

For CGM LD, environments were grouped into three categories as moderately high pest pressure, moderately low pest pressure, and low pest pressure environments. The genotypes I60/42 and 92/000 exhibited specific adaptability to the 2011/12 season at both Mutanda and Mwinilunga, which were associated with moderately high CGM LD. A landrace Kaleleki also presented specific adaptability to the 2010/11 season at Mwinilunga which like the 2011/12 season at Mutanda and Mwinilunga, was associated with moderately high levels of CGM LD, but it was not specifically adapted to either of the latter two environments. These results seem to indicate that I60/42, 92/000 and Kaleleki might have some resistance mechanisms that limit CGM population growth once infested or makes them less attractive to CGM. Further research is required to determine the nature of the mechanism underlying the resistance, an understanding of which will inform future breeding for resistance to CGM. The few earlier studies on mite resistance mechanisms indicated that CGM is able to discriminate and exhibit preference for susceptible against resistant genotypes for oviposition (example Byrne et al., 1982b), suggesting that CGM-resistant genotypes present antixenosis as the major mechanism of resistance.

None of the genotypes had a mean score of four or five which is a high to very high CGM leaf damage. Similarly, none of the genotypes exhibited total immunity to CGM. This may suggest narrow genetic differences between the genotypes for CGM resistance or simply that the particular set of genotypes evaluated in the study had generally high levels of tolerance to CGM, a possible existence of quantitative resistance mechanism. This in turn indicates the availability of relatively good sources of tolerance to CGM within the existing cassava germplasm in Zambia. These results seem to agree with Bellotti et al. (2012) who indicated non-availability of immunity in *Manihot esculenta* germplasm.

These findings seem to be consistent with those by Kawano et al. (1987) who reported significant GEI for SRDM%, which, however, was of smaller magnitude than that of the

genotype main effect, suggesting that the final selection of genotype for SRDM% should be done at each location for maximization of potential gain. Furthermore, Benesi et al. (2004) reported lack of significance of GEI effect, but higher contribution of genotype than environment main effect to the total variation in SRDM% of cassava genotypes, while Chavez et al. (2005) consistently observed more rapid deterioration in some genotypes than others under different environments. Taken together, these observations suggest that the larger part of total phenotypic variation observed in SRDM% is attributed to the genetic difference, and only to a lesser extent, due to environmental conditions.

For FSRY, environments were grouped into four categories as high yielding environments (both seasons at Zambezi), moderately high yielding environments (2010/11 season at Mutanda and Mwinilunga), moderately low yielding environment (2011/12 season at Mwinilunga), and low yielding environment (2011/12 season at Mutanda). Two genotypes namely Kapeza and Kampolombo exhibited specific adaptability for FSRY; the former to high and moderately high yielding environments, and the latter to both moderately high and low yielding environments, Mutanda but two different seasons. This suggests that since Kampolombo was insensitive to seasonal effects, it could be recommended for production in both or either of the environments.

Three major environments were identified as high LR environment (2011/12 season at Mwinilunga), moderately high LR environments (both seasons at Zambezi, and 2011/12 season at Mutanda), and moderately low LR environments (2010/11 season at Mutanda and Mwinilunga). Genotypes Mweru and Chila were adapted to moderately high and moderately low LR environments which actually represent different locations but same season. These results imply that Mweru and Chila are insensitive to locational effects for LR, but are likely to be more responsive to seasonal effects. Genotypes I30040 and Manyopola are specifically adapted to moderately low LR environments. Although leaf shedding is reported to be a survival mechanism for cassava in times of drought (El-Sharkawy 1993), genetic variations have been reported in this trait among cassava genotypes in reaction to moisture stress (Lenis et al., 2006). Genotypes that respond to drought by folding or rolling their leaves instead of shedding off their leaves exhibit prolonged photosynthetic activity even in times of drought in addition to reducing leaf conductance and rate of transpiration (El-Sharkawy 1993).

Genotypes which combine extended LR with extended photosynthetic activity of the leaves are desirable because leaf longevity is an important character determining storage root yield in cassava (Methews and Hunt, 1994). Cassava genotypes that respond to drought by folding or rolling instead of shedding off their leaves are likely to exhibit extended photosynthetic activity even in times of drought. Research by El-Sharkawy et al. (1992) has shown that, during water stress, cassava leaves retain as much as 50% of their original photosynthetic activity. Also, depending on the genotype, after recovering from stress, the mature leaves can recuperate their

photosynthetic activity to levels comparable with those of unstressed leaves (El-Sharkawy, 1993).

It is also proposed that the genetic potential of cassava to retain as many green leaves as possible may be a major factor in tolerance to CGM (Nukenine et al., 1999). Therefore, environments were also categorized for SG as low SG environment (2010/11 season at Mutanda), moderately low SG environment (2011/12 season at Mutanda), and moderately high SG environments (both seasons at Mwinilunga and Zambezi). Four genotypes Mweru, L9.304/147, I30040, and Manyopola exhibited specific adaptability to moderately high SG environment (2010/11 season at Mwinilunga). In addition, L9.304/147 also exhibited specific adaptability to the 2011/12 season at Mwinilunga which was another moderately high SG environment, suggesting that warm and relatively more humid environments, are favorable conditions for expression of this trait.

The lack of significance of environment and the GEIMS for Pbs indicates that the phenotypic variations that were observed in the expression of this trait were mainly due to genetic differences among the genotypes. Since the GEI MS was non-significant, each of the genotypes is expected to respond similarly to the environments, but the fact that genotype MS were significant, implies that the genotypes' performances for Pbs were not the same. None of the genotypes evaluated could be characterized as highly pubescent or glabrous, but all of them had moderately hairy leaves, suggesting the need for further improvement of the trait. Increased Pbs especially of apical leaves of cassava tend to provide better shelter and hence promote continuous inhabitance of the phytoseiid predatory mite *T. aripo*, which has proved to be the most powerful natural enemy of CGM so far in Africa (Zundel et al., 2009). Even in the absence of natural enemies, highly pubescent genotypes resist CGM better than glabrous cassava genotype (Byrne et al., 1982b; Hahn et al., 1989). Considering the high heritability estimates reported for this trait (Hahn et al., 1989), it should therefore be easy to incorporate the trait into high yielding cultivars to improve resistance of cassava to CGM and enhance sustenance of *T, aripo.*

There is need to source for highly pubescent parents that should be included in the hybridization programme for Zambia. The observed high environmental stability for SG and LR qualifies Zambezi as the best site for future releases of *T. aripo* in North-Western Province. The genotypes will be evaluated in the presence of *T. aripo* in the 2012/13 and 2013/14 seasons, in order to confirm their suitability for integrated management of CGM.

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Appendix 3.1: Soil nutrient analysis of three sites used for G x E trials

Location	Year	pH	P	Al	Ca	Mg	K	Na	CEC	Zn	Cu	N	C
			Meq $100g^{-1}$ soil							Ppm	ppm	%	%
Mutanda	2010	4.2	12	2.5	0.32	0.20	0.17	0.02	3.8	18.0	5.0	0.8	0.89
	2011	4.3	8	1.9	0.68	0.19	0.21	0.02	2.5	15.0	0.9	0.9	1.17
Mwinilunga	2010	4.2	6	1.8	0.32	0.83	0.38	0.03	11.2	18.7	5.0	0.1	1.70
	2011	4.1	3	2.6	0.26	0.85	0.32	0.02	11.0	16.2	3.0	0.2	0.64
Zambezi	2010	5.8	4	-	0.25	0.22	0.50	0.03	9.5	20.0	1.5	0.9	1.50
	2011	5.6	3	-	0.31	0.25	0.42	0.03	8.9	24.0	1.9	1.0	2.00

Appendix 3.2: Description of the nineteen cultivars used in the study

Genotype		
Code	Name	Source
G1	Kapeza	Landrace
G2	Mweru	RTIP Zambia
G3	M86/0016	RTIP Zambia
G4	L9.304/147	RTIP Zambia
G5	Bangweulu	RTIP Zambia
G6	Chila	RTIP Zambia
G7	Lelanyana	Landrace
G8	I60/42	IITA Nigeria
G9	Lufunda	Landrace
G10	I30040	IITA Nigeria
G11	L9.304/175	RTIP Zambia
G12	14(2)1425	IITA, Nigeria
G13	Manyopola	Landrace
G14	Kampolombo	RTIP Zambia
G15	92/000	IITA
G16	L9.304/36	RTIP Zambia
G17	Kariba	RTIP Zambia
G18	TME 2	IITA
G19	Kaleleki	Landrace

CGM = cassava green mite, CMD = cassava mosaic disease, RTIP = Root and Tuber Improvement Programme; IITA =International Institute of Tropical Agriculture

Appendix 3.3: Scores of the first and second Interaction principal component axes for 19 cassava genotypes

Genotypes		CGM density		CGM damage		FSRY (t ha^{-1})		SRDM%		Pbs (1-3)		LR (%)		SG (1-3)	
		IPCA 1	IPCA 2	IPCA 1	IPCA 2	IPCA 1	IPCA 2	IPCA 1	IPCA 2	IPCA 1	IPCA 2	IPCA 1	IPCA 2	IPCA 1	IPCA 2
Kapeza		2.71	0.75	0.59	-0.3	-1.5	-0.76	0.7	-0.76	0.07	-0.51	2.44	-0.10	0.86	-0.08
Mweru		-1.19	1.59	-0.23	-0.34	-1.09	-0.43	0.12	-0.36	0.42	0.15	-0.29	1.08	-0.38	0.26
M86/0016		-1.76	-1.88	0.06	0.19	-0.41	-0.34	-1.5	0.79	0.24	0.26	-1.64	0.65	-0.28	-0.26
L9.304/147		0.42	0.28	0.10	-0.40	-0.07	-0.50	0.08	0.04	0.47	-0.11	0.36	-3.41	-0.23	-0.39
Bangweulu		1.01	-0.86	0.10	0.04	0.34	-0.78	2.14	1.11	-0.30	0.41	1.48	1.62	0.21	0.26
Chila		-0.28	0.96	-0.13	-0.01	-0.13	1.19	0.74	0.46	0.12	-0.25	-1.62	2.25	0.05	-0.12
Lelanyana		-3.04	0.33	-0.51	0.03	0.37	0.19	-0.96	0.37	-0.22	0.04	-0.01	0.30	-0.02	0.16
I60/42		-3.59	-0.98	-0.4	0.18	-1.42	-0.04	-0.25	-0.34	-0.47	-0.18	-0.64	0.89	-0.42	0.06
Lufunda		1.25	0.81	0.15	0.01	0.83	-0.76	0.05	-0.13	0.15	-0.35	-1.22	-0.11	-0.44	-0.24
I30040		2.29	0.68	0.16	-0.19	0.55	-0.56	0.70	-0.41	0.27	-0.05	-3.20	-1.75	-0.74	-0.09
L9.304/175		-2.47	2.13	-0.51	-0.37	0.47	0.04	0.88	0.29	-0.14	0.19	1.39	-1.48	0.61	-0.53
14(2)1425		0.44	-0.74	0.26	-0.08	-1.21	1.30	0.45	-1.19	-0.08	-0.10	0.30	0.20	0.21	0.19
Manyopola		-0.08	-0.67	0.08	0.41	0.29	-0.17	-1.08	0.39	-0.26	-0.18	-1.18	-0.03	-0.42	0.39
Kampolombo		-0.36	0.05	-0.28	0.02	1.14	0.65	-1.81	0.64	-0.30	0.15	-1.15	-0.49	0.35	0.17
92/000		-0.74	-1.79	-0.12	0.41	0.51	0.22	0.16	0.34	-0.15	-0.07	1.15	0.26	0.23	0.21
L9.304/36		-0.01	-0.66	-0.04	0.22	0.62	0.03	-0.22	0.47	0.16	0.12	-0.21	0.51	-0.02	-0.28
Kariba		2.65	-2.50	0.43	0.27	0.38	0.60	-1.03	-0.56	0.38	0.25	1.95	0.65	0.23	0.30
TME 2		1.98	1.19	0.16	-0.12	-0.43	0.11	1.25	0.27	0.04	0.2	0.68	-0.45	-0.03	-0.31
Kaleleki		0.76	1.31	0.14	0.03	0.76	-0.01	-0.4	-1.4	-0.4	0.03	1.41	-0.58	0.25	0.29
-----Environment--															
Mutanda	2010/11	-2.06	-3.22	-0.17	0.7	-0.1	-1.95	-0.62	1.26	0.27	-0.41	0.21	-1.2	0.1	0.001
	2011/12	2.31	1.60	0.37	-0.37	0.55	-0.65	1.53	0.8	-0.06	-0.13	1.01	-1.76	0.44	-0.52
Mwinilunga	2010/11	-6.17	2.00	-1.07	-0.32	1.83	1.18	-3.52	-0.08	0.21	-0.46	-5.37	0.66	-1.45	0.27
	2011/12	2.75	2.64	0.39	-0.49	1.19	0.28	1.27	0.91	0.001	0.07	0.43	-2.58	-0.14	-0.71
Zambezi	2010/11	1.97	-2.03	0.28	0.18	-1.28	0.19	0.66	-2.05	-1.00	0.22	1.09	4.02	0.46	0.33
	2011/12	1.20	-1.00	0.20	0.30	-2.19	0.95	0.67	-0.83	0.58	0.71	2.63	0.87	0.59	0.63

IPCA = interaction principal component; CGM = cassava green mite; CGM density = population counts of cassava green mites per leaf; CGM damage = level of leaf injury cause by cassava green mite scored on a 1–5 scale; FSRY = fresh storage root yield (t ha^{-1}); SRDM% = storage root dry mass expressed as a percentage; Pbs = pubescence which is the degree of hairiness of leaves scored on a 1–3 scale; LR = proportion of leaves retained on a plant expressed as a percentage; SG = stay green scored on a 1-3 scale

CHAPTER 4

Intra-season and inter-season stability of resistance against green mite *Mononychellus tanajoa* (Bondar) (Acari: Tetranychidae), and associated plant shoot morphological traits of cassava

Abstract

Cassava genotypes that combine earliness with prolonged underground storability are most preferred for food security under subsistence farming. However, the long growth cycle of cassava coupled with the delayed harvesting by local farmers in Zambia exposes the crop to cassava green mite (CGM) attack which contributes to instability in yield performances of cassava. Various plant morphological traits have been recognized as direct or indirect defense mechanisms that enhance host plant resistance (HPR) to CGM. However, little research has been done to understand the stability of such traits despite their potential impact on the durability of HPR. With this background, field trials, involving sequential harvesting of cassava at 9, 12, and 15 months after planting (MAP) were conducted for two seasons. The objectives of the study were to establish the intra-season and inter-season stability of genotypes for resistance to CGM, and to understand the optimal bulking period of different cassava genotypes in order to identify early-bulking CGM-resistant genotypes, as well as to identify clones with good underground storability. The genotype stability index was computed for each genotype for CGM population density and leaf damage, fresh storage root yield (FSRY) and storage root dry mass percentage (SRDM%), storage root rot (SRR), and plant shoot morphological traits related to CGM resistance, across sampling dates and seasons. There were highly significant differences among genotypes at different sampling dates for all the traits studied. Genotypes Mweru and L9.304/175 exhibited high intra-season and inter-season stability for low incidence of SRR combined with high SRDM%. The level of injury caused by CGM on Mweru did not affect its FSRY, SRDM%, and resistance to SRR. Genotypes L9.304/147, L9.304/175, 4(2)1425, I60/42 exhibited the highest levels of intra-season and inter-season stability for high CGM resistance. The most stable genotypes for earliness were Kapeza, L9.304/147, and 4(2)1425 which consistently yielded above 13 t ha^{-1} at 9 MAP across seasons.

4.0 Introduction

Cassava (*Manihot esculenta* Crantz) is the second major staple after maize (*Zea mays* L)in Zambia and it serves as a source of livelihood for more than 6 million people. Cassava offers the advantage of flexible harvesting, allowing farmers to keep the storage roots underground until needed (Nweke et al., 2002). However, the long growth cycle of many cassava genotypes is one of the constraints hampering the adoption of the crop by young farmers who would otherwise engage in cassava production as a business. In turn this indicates a clear need for early bulking cassava genotypes. Existing improved cultivars in Zambia take 14-16 months to provide reasonable yields, while most landraces take a minimum of 24 months (RTIP, 2004). However, most of the relatively early bulking improved genotypes exhibit poor underground storability; they are prone to rotting if harvesting is delayed beyond 24 months (Chalwe et al., 1998). Cassava breeders in Zambia are being challenged by the demands by the farming community for genotypes that combine earliness with acceptable underground storability. For food security, farmers normally want genotypes that bulk early but are able to remain in the ground for a long period of time without rotting. Long growing season requirements of cassava and the varying agronomic conditions in which cassava is cultivated expose the crop to numerous biotic and abiotic stresses (Bellotti et al., 1994), a combination of which can result in devastating effects on storage root yield (Aina et al., 2007). Seasonal variability of cassava pests and/or disease pressure has been widely reported (Yaninek et al., 1989; Akparobi et al., 1998; Zundel et al., 2009). During the dry season, combined attack of cassava green mite (CGM) and termites (*Microtermes* sp)coupled with lack of moisture aggravate yield losses (Yaninek and Herren, 1988; Yaninek et al., 1993;Chakupurakal et al., 1994; Toko, 1996; Nkunika, 1998; Aina et al., 2007). It is also documented that the impact of pest or disease attack varies with the genotype and growth stage at which the injury or damage is caused (Hahn and Theberge, 1985; Ogbe et al., 2003; Raji et al., 2008).

Few studies are available on how CGM is influenced by phenotypic traits such as leaf pubescence (Pbs) (Hahn et al., 1989), colour or shape of leaf (Hanna et al., 1997), size and compactness (TC) of shoot apices (TS) (Zundel et al., 2009), leaf retention (LR) and stay green (SG) (Nukenine et al., 1999), and environmental factors such as rainfall, temperature, relative humidity (Yaninek et al., 1989; Zundel et al., 2009), and ultra-violate radiation (Onzo et al., 2010). Research has shown that high Pbs protects natural enemies of CGM, particularly the phytoseiid predatory mite *Typhlodromalus aripo*, against harsh weather conditions, supporting its continuous survival in cassava fields (Mebelo et al., 2003; Zundel et al., 2009). Recent studies have shown that

pubescent cassava genotypes tend to release volatiles that attract *T. aripo* (Onzo et al., 2012). However, due to the fact that pubescent genotypes may also differ in other traits that confer resistance to mites, further study is required to determine if leaf hair density is the primary mechanism of resistance of cassava to CGM (Miyazaki et al., 2012). Moreover, little research has been done to understand the variability of the aforementioned traits, and how the interactions of genetic factors with crop age and season influence the expression of these vital indirect plant defense mechanisms (Cortesero et al., 2000; Zundel et al., 2009).

It is envisaged that selecting genotypes for high intra- and inter-season stability of enhanced CGM resistance-conferring traits (Farshadfar, 2008), would in turn enhance the durability of host plant resistance (HPR) (Belloti et al., 1994), and promote biological control by supporting continuous survival of natural enemies in cassava fields planted to improved cultivars (Pratt et al., 2002; Zundel et al., 2009). Knowledge of the stability of desirable traits across different selection stages or stages of plant growth would also enable a breeder to more accurately predict the performance of genotypes at later stages in the breeding programme and for release purposes. Therefore the breeder can make decisions at an early stage of breeding and/or without waiting for the crop to reach full maturity (Kamau et al., 2009). Against this background, genotype by environment interaction (GEI) trials were conducted in order to achieve the following objectives: i) establish the within year (season) and between years stability of genotypes for traits that enhance the resistance of cassava to CGM and the ability of cassava to host *T. aripo;* ii) understand the optimal bulking period of different cassava genotypes in order to identify early-bulking CGM-resistant cultivars; and iii) identify genotypes with good underground storability.

4.2 Materials and methods

4.2.1 Study site

The study was conducted at Kawiko which is located 11º45'E and 24º23'S at 1363 m above sea level in the Mwinilunga district of Zambia. Details of the weather conditions during the 2010/11 and 2011/12 seasons the study was conducted in, and soil nutrient analyses are presented in Table 4.1.

Table 4.1 Climatic data and soil nutrient analysis for Kawiko agricultural camp, Mwinilunga, Zambia (2010/11 and 2011/12 seasons)

Year	Climatic parameters			pH	Soil chemical elements										
	Rainfall (mm)	Temp (ºC)	RH (%)		P	Al	Ca	Mg	K	Na	CEC	Zn	Cu	N	C
	Nov-Mar	Min-Max	(mean)		Meq $100g^{-1}$ soil							ppm	ppm	%	%
2010	1374	10 - 24	72	4.2	6	1.8	0.32	0.83	0.38	0.03	11.2	18.7	5.0	0.1	1.7
2011	1200	12 - 27	75	4.1	3	2.6	0.26	0.85	0.32	0.02	11.0	16.2	3.0	0.2	0.64

Temp = temperature measured in degree Celsius (ºC); Min = minimum temperature; Max = maximum temperature; RH = average relative humidity measured as a percentage; pH = potential of hydrogen ions as a measure of soil acidity based on calcium chloride; ppm = parts per million; Meq = milli-equivalent

4.2.2 Experimental materials

Nineteen cassava genotypes (Table 4.2), which included five landraces, eight locally improved, and six introductions from the International Institute of Tropical Agriculture (IITA) in Nigeria, were evaluated.

Table 4.2 Description of the nineteen cultivars used in the study

Genotype		Source
Code	**Name**	
G1	Kapeza	Landrace
G2	Mweru	RTIP Zambia
G3	M86/0016	RTIP Zambia
G4	L9.304/147	RTIP Zambia
G5	Bangweulu	RTIP Zambia
G6	Chila	RTIP Zambia
G7	Lelanyana	Landrace
G8	I60/42	IITA Nigeria
G9	Lufunda	Landrace
G10	I30040	IITA Nigeria
G11	L9.304/175	RTIP Zambia
G12	14(2)1425	IITA, Nigeria
G13	Manyopola	Landrace
G14	Kampolombo	RTIP Zambia
G15	92/000	IITA
G16	L9.304/36	RTIP Zambia
G17	Kariba	RTIP Zambia
G18	TME 2	IITA
G19	Kaleleki	Landrace

CGM = cassava green mite; RTIP = Root and Tuber Improvement Programme; IITA =International Institute of Tropical Agriculture

4.2.3 Experimental design and layout

The experiment was laid out in a randomized complete block design with three replications. The materials were grown and evaluated over two growing seasons under rain-fed conditions. The first trial was planted on 15th December 2009 and evaluated from January 2010 to March 2011. The same genotypes were planted in the second trial on 15th December 2010 and evaluated from January 2011 to March 2012. Each

plot consisted of 36 plants spaced at 1 m between rows and 1 m within rows, equivalent to 10,000 plants ha^{-1}.

4.2.4 Inoculation of experimental materials

The borders of each plot were planted with a CGM susceptible genotype. Two months after planting (in February each year), the borders were artificially infested with CGM from a screenhouse-raised colony by attaching two infested leaves, which had at least 20 adult mites each, onto each of the border plants in every replication (Habekub et al., 2000). The petiole of each infested leaf was lightly tied with string to the petiole of the first and second fully expanded leaf from the top of each of the two plants per clone (Figure 4.1). The detached infested leaf and the attached uninfested leaf were placed with their abaxial surfaces in contact with each other. The main lobes were lightly held together with a plastic coated paper clip leaving the other leaf lobes free. The infester leaves and paper clips were removed after three days. Inoculation was repeated soon after the cold season in August. No fertilizers or herbicides were applied, but the trial was kept weed-free by frequent hand weeding.

Figure 4.1 Inoculation by attachment of CGM-infested leaves onto a test plant

4.2.5 Data collection

The CGM population density (CGM PD) and CGM leaf damage (CGM LD) were recorded as suggested by Hahn et al. (1989), using a rating system which involved estimating the proportion of leaf area covered by chlorotic spots, and the counting of adult mites on the third fully expanded leaf from the top on each of six randomly selected plants in each plot. The CGM LD was based on a 1-5 scale, where: 1 = no obvious symptoms; 2 = moderate damage, no reduction in leaf size, scattered chlorotic spots on young leaves, 1-2 spots cm^{-2}; 3 = severe chlorotic symptoms, light reduction in leaf size, stunted shoot, 5-10 spots cm^{-2}; 4 = severe chlorotic symptoms and leaf

size of young leaves severely reduced; and 5 = tips of affected plants defoliated, resulting in a candle stick appearance of shoot tips. Plants with scores of 1 and 2 were considered to be resistant, whereas plants with scores of 3 to 5 were considered to be susceptible to CGM.

Each genotype was scored for the following traits on a 1 to 3 scale: (i) Pbs; where: 1 = glabrous, 2 = moderately pubescent, and 3 = highly pubescent; (ii) TC, where: 1 = loose, 2 = moderately compact, and 3 = compact; (iii) TS, where: 1 = small, 2 = medium, and 3 = large; (iv) leaf longevity assessed by scoring for LRand SG, where for LR: 1 = poor (<50% of the leaves are retained), 2 = moderately good (50-74% of the leaves are retained), and 3 = very good (≥75% of the leaves are retained); and for SG: 1 = poor (<50% of the leaves live and green), 2 = moderately good (50-74% of the leaves are live and green), and 3 = very good (≥75% of the leaves live and green)

Three sampling (harvesting) dates were chosen, namely 9, 12, and 15 months after planting (MAP). At each sampling date, a total of six plants, one from each row, were randomly selected for data collection. These plants were then up-rooted for collection of storage root yield-related data and were inspected for storage root rot (SRR). The incidence of SRR was used as an indicator for underground storability (UGS), and was estimated as a proportion of the number of rotten storage roots out of the total number of storage roots harvested per plot (six plants) expressed as a percentage. The mass of storage roots was taken to estimate FSRY per plot, and expressed on a per hectare basis. The numbers of storage roots were also recorded. Storage root dry mass percentage (SRDM%) was determined by submerging a 3 kg sample of fresh storage roots in water and recording its mass. The SRDM% was then estimated based on the specific gravity method of Kawano (1980) using the following formula:

$$\text{SRDM (\%)} = 158.3 \times \left(\frac{\text{Ma}}{\text{Ma}-\text{Mw}}\right) - 143$$

where M_a is the mass of storage roots in air and M_w is the mass of storage roots in water.

4.2.6 Statistical analyses

Analysis of variance: Separate analyses of variance (ANOVA) were conducted using Genstat 14 (Payne et al., 2011) for each season, and sampling date with each season for the eight traits. Hartley's F-max test (Hartley, 1950) based on the ratio of the largest error MS to the smallest error MS was performed for each trait to test the homogeneity of variances across environments. The test indicated that the variance of the two

seasons and three sampling dates within seasons were homogeneous for all the traits, and therefore there was no need for standardization of sampling date, and a combined ANOVA was carried out.

Combined general analyses of variance were performed for all genotypes for each of the eight traits across seasons and sampling dates within seasons using Genstat 14. The F-tests and significance of the main effects and interactions were determined using the appropriate error term and degrees of freedom.

Genotype stability: Stability assessment was performed using Wricke (1962) ecovalence stability measure (Wi) using the formula:

$$Wi_i = \Sigma(X_{ij} - X_{i.} - X_{.j} + X..)^2$$

Where: Wi_i = ecovalence of the i^{th} genotype, X_{ij} = the observed phenotypic value of the i^{th} genotype in the j^{th}season (or sampling date), $X_{i.}$ = mean of i^{th} genotype across the the seaons (or sampling dates), $X_{.j}$ = mean of j^{th}season (or sampling date), X..= grand mean. Genotypes with the lowest Wi_i value were regarded as the most stable across sampling dates and/or seasons.

Genotype stability index: A stability index was calculated for each genotype based on combining the ranking of overall mean performances for each trait and the ranking for Wi stability score for each trait. This stability index which is normally applied to yield data and is referred to as yield stability index (YSI) (Farshadfar et al., 2012) was also applied in this study to mean performances of genotypes for other traits and referred to as genotype stability index (GSI). Instead of using the AMMI stability value as is normally the case for YSI, the GSI was calculated as the sum of ranks for Wi-ecovalence stability index and trait overall mean using the modified formula (after Farshadfar, 2008):

$$GSI_i = \sum RWi_i + \sum RY_i,$$

Where: GSI_i = genotype stability index for the i^{th} genotype across sampling dates or seasons for each trait; $\sum RWi_j$ = sum of ranks of the i^{th} genotype across sampling dates within a season or across seasons based on Wi; $\sum RY_i$ = sum of ranks of the i^{th} genotype based on mean performance across sampling dates (S-date) within a season or across seasons. The genotype with the lowest GSI was considered the best for a particular trait across sampling dates, and a genotype with lowest GSI rank sum over the two seasons was considered the best for a trait across seasons. The Wi was

choosen because it is very easy to compute and has no restrictions pertaining to the number of environments as is the case with AMMI stability variance.

4.3 Results

The ANOVA were performed for each season separately and only combined for sampling dates within each season (Table 4.3). The mean squares (MS) for genotype (G) main effects were significant (P<0.05) for all the traits measured across sampling dates (S-date) and seasons (Table 4.3). The S-date MS were significant for all the traits measured in the 2010/11 season, and only for LR, SRR, and FSRY in the 2011/12 season. The G x S-date MS were also significant for CGM LD, SG, FSRY, and SRDM% in the 2010/11 season. However, the G x S-date MS were not significant for any of the traits measured in the 2011/12 season.

Table 4.3 Analysis of 19 cassava genotypes evaluated for resistance to green mite density and associated leaf damage, leaf retention, stay green, leaf pubescence, fresh storage root yield, storage root rots, and storage root dry mass percentage at three sampling dates in Zambia

Source of Variation	Df	Mean squares							
		CGM PD	CGM LD	LR	SG	Pbs	FSRY	SRR	SRDM%
2010/11									
Genotype (G)	18	2101.9***	1.4***	433.7***	3.0***	2.2***	56.0***	500.6***	61.4*
Sampling date (S)	2	1472.4**	1.0*	2993.4***	2.0***	1.1*	3598.8***	1296.6***	75.2
G x S	36	173.1	0.5*	501.6***	0.6*	0.2	24.4***	146.7***	62.3**
Residual	112	215.8	0.3	163.1	0.4	0.3	10.9	63.9	29.5
2011/12									
Genotype (G)	18	2227.9***	1.5***	709.0***	3.4***	1.7***	81.2***	645.6***	85.9***
Sampling date (S)	2	499.1	0.1	856.6*	0.6	0.2	534.7***	461.5*	49.8
G x S	36	120.6	0.2	106.6	0.2	0.2	17.1	43.4	15.2
Residual	112	349.4	0.4	252.0	0.4	0.5	28.1	109.6	31.2

CGM PD = population counts of cassava green mites per leaf; CGM LD = level of leaf injury caused by cassava green mite scored on a 1–5 scale, where 1 = no leaf damage symptoms, and 5 = very severe damage symptoms; LR = proportion of leaves retained on a plant measured as a percentage; SG = stay green scored on a 1-3 scale, with 1 = lowest, and 3 = highest; Pbs = pubescence which is the degree of hairiness of leaves scored on a 1–3 scale, where 1 = glabrous, and 3 = highly pubescent; FSRY = fresh storage root yield in t ha^{-1}; SRR = storage root rot disease incidence expressed as a percentage, SRDM% = percentage storage root dry mass; *P≤0.05; **P≤0.01; ***P≤0.001

4.3.1 Cassava green mite population density

The G and S-date main effects were significant for CGM PD in 2010/2011 season, but their interaction was not (Table 4.3). Significantly (P<0.01) the highest CGM PD were recorded at 9 MAP as compared to later sampling dates. At 9 MAP, the genotype TME2 had the lowest CGM PD, followed by 4(2)1425, I60/42, L9.304/175 and Kaleleki. Genotype 4(2)1425 had the lowest CGM PD at 12 MAP followed by L9.304/147, Bangweulu, L9.304/175, and Kaleleki. Genotype 4(2)1425 also had the lowest CGM PD at 15 MAP followed by Kaleleki, Bangweulu, L9.304/175, and Kapeza. Across

sampling dates, the lowest CGM PD was recorded by 4(2)1425, Kaleleki, L9.304/175, L9.304/147 and TME2.

In 2011/2012 season, the G MS were significant for CGM PD, but the S-date MS and the G x S-date MS were not significant for the trait (Table 4.4). At 9 MAP, L9.304/147 had the lowest CGM PD followed by L9.304/175, 4(2)1425 and Kaleleki. The genotype L9.304/147 also had the lowest CGM PD at 12 MAP, followed by Kaleleki, Lelanyana, L9.304/175 and 4(2)1425. The same genotype L9.304/147 was ranked best for the CGM PD at 15 MAP, followed by 4(2)1425, I60/42, 92/000 and L9.304/36. Genotypes with lowest rank sum were the best across the seasons. Accordingly 4(2)1425, L9.304/147, L9.304/175, and Kalelek had lowest CGM PD and were regarded as the most resistant across seasons.

Table 4.4 Ranked mean performances of 19 cassava genotypes evaluated for population densities of cassava green mite at three sampling dates at Kawiko in Mwinilunga, Zambia in 2010/11 and 2011/12 seasons

Genotype	2010/11								2011/12								Rank sum across seasons
	9 MAP		12 MAP		15 MAP		Overall		9 MAP		12 MAP		15 MAP		Overall		
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	
Kapeza	28.3	10	25.0	14	21.7	5	25.0	9	33.3	14	13.3	6	33.3	13	26.7	11	20
Mweru	65.0	18	56.7	19	53.3	17	58.3	18	73.3	19	51.7	18	73.3	19	66.1	19	37
M86/0016	76.7	19	50.0	18	61.7	19	62.8	19	61.7	18	61.7	19	58.3	18	60.6	18	37
L9.304/147	20.0	8	10.0	2	11.7	3	13.9	4	10.0	1	6.7	1	10.0	1	8.9	1	5
Bangweulu	31.7	11	11.7	3	36.7	15	26.7	10	16.7	3	21.7	10	23.3	9	20.6	6	16
Chila	45.0	14	23.3	10	30.0	12	32.8	14	30.0	10	30.0	15	30.0	12	30.0	14	28
Lelanyana	48.3	15	31.7	16	36.7	15	38.9	16	43.3	16	10.0	3	50.0	16	44.4	16	32
I60/42	10.0	2	21.7	8	26.7	8	19.4	6	30.0	10	28.3	14	15.0	3	24.4	9	15
Lufunda	18.3	6	23.3	11	23.3	6	31.7	13	25.0	7	30.0	15	20.0	7	25.0	10	23
I30040	33.3	12	23.3	12	30.0	13	28.9	11	30.0	10	26.7	12	23.3	9	26.7	11	22
L9.304/175	11.7	4	11.7	4	15.0	4	12.8	3	10.0	2	11.7	4	23.3	9	15.0	3	6
4(2)1425	10.0	2	5.0	1	8.30	1	7.80	1	16.7	3	11.7	4	13.3	2	13.9	2	3
Manyopola	33.3	12	25.0	15	28.3	9	28.9	11	35.0	15	21.7	10	46.7	15	34.4	15	26
Kampolombo	25.0	9	21.7	9	25.0	7	23.9	8	30.0	13	19.7	9	38.3	14	29.3	13	21
92/000	18.3	6	13.3	6	31.7	14	21.1	7	18.3	6	18.0	7	16.7	4	17.7	5	12
L9.304/36	48.3	15	23.3	13	28.3	10	33.3	15	25.0	7	26.7	12	16.7	4	22.8	8	23
Kariba	58.3	17	35.0	17	58.3	18	50.6	17	55.0	17	43.3	17	53.3	17	50.6	17	34
TME 2	6.7	1	16.7	7	28.3	10	17.2	5	28.3	9	18.3	8	18.3	6	21.7	7	12
Kaleleki	11.7	4	11.7	5	10.0	2	11.1	2	16.7	3	8.3	2	21.7	8	15.6	4	6
Mean	33.2		23.2		29.7		28.7		31.0		25.8		30.8		29.2		
CV (%)	49.7		61.8		47.7		51.2		63.7		62.9		66.6		64.1		
SEM	16.5		14.3		14.8		14.7		19.7		16.2		20.5		18.7		
SED Genotype			11.7		11.4		6.9		16.7		16.1		16.7		8.8		
SED S-date					2.8								3.5				
SED G x S-date					6.9								15.3				
F-prob. Genotype	<0.001		0.009		<0.001		<0.001		0.019		0.01		0.019		<0.001		
F-prob. S-date					0.002								0.244				
F-prob. G x S-date					0.773								1.000				

MAP = months after planting; G = genotype; S-date = sampling date set at 9, 12, and 15 months after planting; G x S-date = genotype by sampling date interaction; CV = coefficient of variation measured as a percentage; SEM = standard error of means; SED = standard error of difference of means; F-prob. = level of significance for F-test

4.3.2 Leaf damage due to cassava green mite

The G and S-date main effects and the G x S-dateinteraction effects were significant ($P<0.05$) for CGM LD during the 2010/11 season (Table 4.5). Significantly ($P<0.05$) the lowest CGM LD was recorded at 9 MAP compared to later sampling dates. However, there were no significant differences in CGM LD among genotypes at 9 MAP, but highly significant differences were observed at 12 MAP ($P<0.01$) and 15 MAP ($P<0.001$). Genotypes L9.304/147, 4(2)1425 and Kaleleki recorded the lowest CGM LD (mean score 2.0) and therefore sustained theleast CGM LD at 12 MAP. Genotype 4(2)1425 together with I60/42, L9.304/175, and TME2 had the lowest CGM LD at 15 MAP. Overall, 4(2)1425 had the CGM LD across sampling dates in the 2010/11 season, followed by I60/42, Mweru and Kaleleki.

In the 2011/12 season, the S-date main effects were not significant for CGM LD. Similarly, the G x S-date interaction effects were not significant for the trait (Table 4.5). However, the G main effects were significant for the trait, but only at 9 MAP ($P<0.05$). Kapeza sustained the least injury due to CGM with a mean score of 1.0 at 9 MAP, followed by Bangweulu and 4(2)1425. Across sampling dates, genotypes L9.304/147 and L9.304/175 were the most resistant followed by 4(2)1425 and Kaleleki. Overall, 4(2)1425, L9.304/175, Kaleleki, L9.304/147, and Kapeza were the most resistant genotypes across seasons.

Table 4.5 Ranked mean performances of 19 cassava genotypes evaluated for leaf damage due to cassava green mite at three sampling dates at Kawiko in Mwinilunga, Zambia in 2010/11 and 2011/12 seasons

Genotype	2010/11								2011/12								Rank sum across seasons
	9 MAP		12 MAP		15 MAP		Overall		9 MAP		12 MAP		15 MAP		Overall		
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	
Kapeza	2.0	1	2.3	4	2.3	5	2.2	3	1.0	1	2.0	1	3.0	14	2.4	5	8
Mweru	3.3	19	3.0	15	3.0	13	3.1	17	2.3	4	2.7	6	2.3	4	3.6	19	36
M86/0016	2.7	13	3.7	19	4.3	19	3.6	19	3.7	19	3.7	18	3.3	18	3.3	18	37
L9.304/147	2.0	1	2.0	1	3.0	13	2.3	6	3.0	13	3.7	19	3.3	18	2.0	1	7
Bangweulu	2.0	1	2.7	10	2.7	9	2.4	8	2.0	2	2.0	1	2.0	1	2.6	7	15
Chila	2.7	13	2.7	10	2.7	9	2.7	13	2.3	4	2.3	4	3.0	14	2.7	11	24
Lelanyana	2.3	6	2.7	10	3.0	13	2.7	13	2.7	11	2.7	6	2.7	6	2.8	13	26
I60/42	2.0	1	2.3	4	2.0	1	2.1	2	3.0	13	2.7	6	2.7	6	2.7	11	13
Lufunda	2.3	6	2.3	4	3.0	13	2.6	9	2.7	11	2.7	6	2.7	6	2.6	7	16
I30040	2.3	6	3.0	15	2.3	5	2.6	9	2.3	4	2.7	6	2.7	6	2.4	5	14
L9.304/175	2.3	6	2.3	4	2.0	1	2.2	3	2.3	4	2.7	6	2.3	4	2.0	1	4
4(2)1425	2.0	1	2.0	1	2.0	1	2.0	1	2.0	2	2.0	1	2.0	1	2.2	3	4
Manyopola	2.7	13	2.7	10	3.0	13	2.8	15	2.3	4	2.3	4	2.0	1	2.8	13	28
Kampolombo	2.7	13	2.3	4	2.7	9	2.6	9	3.0	13	2.7	6	2.7	6	2.8	13	22
92/000	2.3	6	3.0	15	2.3	5	2.6	9	3.0	13	2.7	6	2.7	6	2.9	16	25
L9.304/36	3.0	18	2.7	10	3.0	13	2.9	16	3.0	13	2.7	6	3.0	14	2.6	7	23
Kariba	2.3	6	2.3	4	2.7	9	3.1	17	2.3	4	2.7	6	2.7	6	3.2	17	34
TME 2	2.7	13	3.0	15	1.3	1	2.3	6	3.3	18	3.3	17	3.0	14	2.6	7	13
Kaleleki	2.3	6	2.0	1	2.3	5	2.2	3	2.3	4	2.7	6	2.7	6	2.2	3	6
Mean	2.4		2.6		2.7		2.6		2.7		2.3		1.7		2.6		
CV (%)	24.1		18.7		21.7		21.6		21.6		24.2		22.2		22.4		
SEM	0.6		0.5		0.6		0.6		0.6		0.6		0.6		0.6		
SED Genotype	0.5		0.4		0.5		0.3		0.5		0.5		0.5		0.3		
SED S-date	0.1								0.1								
SED G x S-date	0.5								0.5								
F-prob. Genotype	0.33		0.008		<.001		<0.001		0.05		0.171		0.06		<0.001		
F-prob. S-date	0.04								0.73								
F-prob. G x S-date	0.03								0.99								

MAP = months after planting; G = genotype; S-date = sampling date set at 9, 12, and 15 months after planting; G x S-date = genotype by sampling date interaction; CV = coefficient of variation measured as a percentage; SEM = standard error of means; SED = standard error of difference of means; F-prob. = level of significance for F-test

4.3.3 Leaf retention

There were significant (P<0.01) differences in LR among genotypes at 8 and 12 MAP in the 2010/11 season (Table 4.6). Significantly (P<0.001) the highest LR was recorded at 4 MAP (77.4%) while the lowest LR was recorded at 8 MAP (49.2%). The genotype means for LR at 4 MAP ranged between 56.0% and 94.0%, and there were no significant differences among genotypes at this stage. Genotype 4(2)1425 had the highest LR (83.3%) while Kampolombo, L9.304/36, and 92/000 had the lowest LR (30.0%) at 8 MAP. At 12 MAP, 92/000 maintained 80.0% of its leaves and had the best LR. Across sampling dates, landrace Kapeza recorded the highest LR, with a mean of 76.7%, while M86/0016, had the lowest LR (47.8%) across sampling dates in this season (Table 4.6).

In the 2011/12 season, the highest significant (P<0.05) LR was recorded at 4 MAP (76.1%), while the lowest and non-significant LR was recorded at 8 MAP (54.2%). Genotype L9.304/175 and Kaleleki maintained the largest proportion (90.0%) of their leaves at 4 MAP, while Lufunda only retained 61.7% of its leaves. At 8 MAP Kapeza had the highest LR (80.0%) while Kampolombo had the lowest LR (33.3%). Kapeza and Kampolombo were ranked the same for LR at 12 MAP. Kapeza had the smallest overall rank sum for LR across the seasons and therefore was the best genotype for LR as it retained 81.7% of its leaves, while Lufunda had the least LR with a mean of 48.9% across the seasons (Table 4.6).

Table 4.6 Ranked mean leaf retention (%) of 19 cassava genotypes evaluated at three sampling dates at Kawiko in Mwinilunga, Zambia in 2010/11 and 2011/12 seasons

Genotype	2010/11								2011/12								Rank sum across seasons
	4 MAP		8 MAP		12 MAP		Overall		4 MAP		8 MAP		12 MAP		Overall		
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	
Kapeza	88.3	2	76.7	2	61.7	10	75.6	1	81.7	6	80.0	1	83.3	1	81.7	1	2
Mweru	86.7	3	63.3	5	60.0	12	70.0	3	65.0	16	60.0	5	68.3	4	64.4	10	13
M86/0016	61.7	18	41.7	11	46.7	17	50.0	19	63.3	18	45.0	14	50.0	18	52.8	17	36
L9.304/147	85.0	4	36.7	15	46.7	17	56.1	16	81.7	6	61.7	4	71.7	2	71.7	4	20
Bangweulu	85.0	4	66.7	4	63.3	7	71.7	2	88.3	3	58.3	7	60.0	9	68.9	6	8
Chila	83.3	6	56.7	6	61.7	10	67.2	7	73.3	10	48.3	12	51.7	16	57.8	14	21
Lelanyana	73.3	14	41.7	11	58.3	13	57.8	13	73.3	10	48.3	12	55.0	14	58.9	13	26
I60/42	65.0	16	71.7	3	48.3	15	61.7	11	68.3	15	51.7	11	60.0	9	60.0	12	23
Lufunda	65.0	16	50.0	7	63.3	7	59.4	12	61.7	19	33.3	17	51.7	16	48.9	19	31
I30040	56.7	19	50.0	7	50.0	14	52.2	18	65.0	16	41.7	16	56.7	12	54.5	16	34
L9.304/175	81.7	7	46.7	9	78.3	2	68.9	4	90.0	1	60.0	5	61.7	7	70.6	5	9
4(2)1425	71.7	15	83.3	1	50.0	14	68.3	5	86.7	4	66.7	3	70.0	3	74.5	2	7
Manyopola	80.0	10	41.7	11	65.0	6	62.2	10	85.0	5	61.7	4	60.0	9	68.9	6	16
Kampolombo	75.0	12	30.0	17	66.7	5	57.2	15	70.0	13	33.3	17	50.0	18	51.1	18	33
92/000	93.3	1	30.0	17	80.0	1	67.8	6	81.7	6	56.7	8	61.7	7	66.7	9	15
L9.304/36	80.0	10	30.0	17	63.3	7	57.8	13	70.0	13	45.0	14	56.7	12	57.2	15	28
Kariba	75.0	12	45.0	10	48.3	15	56.1	16	73.3	10	53.3	9	55.0	14	60.5	11	28
TME 2	81.7	7	41.7	11	70.0	4	64.5	8	76.7	9	71.7	2	68.3	4	72.2	3	11
Kaleleki	81.7	7	31.7	16	78.3	2	63.9	9	90.0	1	53.3	9	63.3	6	68.9	6	15
Mean	77.4		49.2		61.1		57.5		76.1		54.2		60.8		63.7		
CV (%)	20.4		33.0		14.9		22.2		19.1		29.4		27.5		27.0		
SEM	12.7		16.2		9.1		12.8		11.7		15.9		16.7		15.9		
SED Genotype	10.4		13.2		7.4		6.0		9.5		13.0		13.7		7.5		
SED S-date	2.4								3.0								
SED G x S-date	10.4								13.0								
F-prob. Genotype	0.07		0.002		<0.001		<0.001		0.04		0.08		0.69		<0.001		
F-prob. S-date	<0.001								0.037								
F-prob. G x S-date	<0.001								0.998								

MAP = months after planting; G = genotype; S-date = sampling date or dates of harvest set at 9, 12, and 15 months after planting; G x S-date = genotype by sampling date interaction; SEM = standard error of means; SED = standard error of difference; CV = coefficient of variation measured as a percentage; F-prob. = F-probability showing the level of significance.

4.3.4 Stay green

In the 2010/11 season, genotypes Kampolombo and 92/000 had the highest mean SG score of 3.0 at 4 MAP, while M86/0016 had the lowest mean SG score of 1.0 at 4 MAP (Table 4.7). Highest mean SG score of 3.0 was recorded by L9.304/175 and Kaleleki at 8 MAP (Table 4.7), while L9.304/147 had the lowest score of 1.0. Kapeza, Bangweulu, L9.304/175, Kampolombo and 92/000, had the highest score of 3.0 for SG at 12 MAP, while M86/0016 and L9.304/36 had the lowest score of 1.0 for the trait at 12 MAP. The genotype L9.304/175 had the highest SG score of 2.9 across sampling dates in 2010/11 season, while M86/0016 had the lowest SG score of 1.1 across sampling dates in the season.

In the 2011/12 season, the highest scoring genotypes with score 3.0 for SG at 4 MAP were Kapeza, Bangweulu, Kampolombo, 92/000 and Kaleleki, while the lowest SG score of 1.0 was recorded by M86/0016. Kapeza, L9.304/175, and Kaleleki were the best genotypes for SG at 8 and 12 MAP (Table 4.7). Overall, L9.304/175, Kapeza, and Kaleleki had the lowest rank sum and were therefore the best genotypes for SG across the seasons.

4.3.5 Leaf pubescence

In 2010/11 the season, the highest mean score for Pbs of 2.2 was obtained at 9 MAP as compared to the later dates (Table 4.8). Genotype 4(2)1425 and 92/000 had the highest score for Pbs at 9 MAP in 2010/11 season of 3.0. Kaleleki had the highest mean Pbs score of 3.0 both at 12 and 15 MAP. Genotypes 4(2)1425, L9.304/175, and I30040 had the highest for Pbs scores at 9, 12, and 15 MAP, respectively in 2011/12 season. The most pubescent genotype across sampling dates in the 2011/12 season was L9.304/147, while Manyopola was the least pubescent genotype across sampling dates in the season. Overall, 4(2)1425, L9.304/175, and Kaleleki had the lowest rank sums and, therefore, were the best genotypes for Pbs across the seasons (Table 4.8).

Table 4.7 Ranked mean stay green scores of 19 cassava genotypes evaluated at three sampling dates at Kawiko in Mwinilunga, Zambia in 2010/11 and 2011/12 seasons

Genotype	2010/11								2011/12								Rank sum across seasons
	4 MAP		8 MAP		12 MAP		Overall		4 MAP		8 MAP		12 MAP		Overall		
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	
Kapeza	2.7	3	2.3	8	3.0	1	2.7	5	3.0	1	3.0	1	2.7	1	3.1	1	6
Mweru	2.0	11	1.3	14	2.7	6	2.0	10	2.0	10	2.3	5	2.3	6	2.2	9	19
M86/0016	1.0	19	1.3	14	1.0	18	1.1	19	1.0	19	1.3	14	1.0	18	1.1	19	38
L9.304/147	2.0	11	1.0	19	2.7	6	1.9	11	2.0	10	1.7	12	2.0	10	1.9	12	23
Bangweulu	2.3	7	1.3	14	3.0	1	2.2	7	3.0	1	2.0	10	2.3	6	2.4	6	13
Chila	2.0	11	1.0	19	2.0	9	1.8	13	2.0	10	1.7	12	1.7	14	1.8	13	26
Lelanyana	2.0	11	2.3	8	2.0	12	2.1	9	2.3	8	2.3	5	2.0	10	2.2	9	18
I60/42	1.0	19	2.0	10	1.3	16	1.4	16	1.3	17	1.3	14	1.3	15	1.3	16	32
Lufunda	1.3	17	1.0	19	1.3	16	1.2	18	1.3	17	1.0	19	1.3	15	1.2	18	36
I30040	1.7	14	1.0	19	1.7	13	1.4	16	1.7	14	1.3	14	1.3	15	1.4	15	31
L9.304/175	2.3	7	3.0	1	3.0	1	2.9	1	2.7	6	3.0	1	2.7	1	2.8	3	4
14(2)1425	1.7	14	2.3	8	2.3	9	2.1	9	2.7	6	2.3	5	2.3	6	2.4	6	15
Manyopola	1.3	17	2.3	8	1.7	13	1.8	13	2.0	10	2.0	10	2.0	10	2.0	11	24
Kampolombo	3.0	1	2.0	10	3.0	1	2.7	5	3.0	1	2.3	5	2.7	1	2.7	5	10
92/000	3.0	1	2.3	8	3.0	1	2.8	2	3.0	1	2.7	4	2.7	1	2.8	3	5
L9.304/36	1.7	14	1.0	19	1.0	18	1.2	18	1.7	14	1.3	14	1.0	18	1.3	16	34
Kariba	1.3	17	1.7	11	1.7	13	1.6	14	1.7	14	1.3	14	2.0	10	1.7	14	28
TME 2	2.3	7	2.7	3	2.3	9	2.4	6	2.3	8	2.3	5	2.3	6	2.3	8	14
Kaleleki	2.3	7	3.0	1	2.7	6	2.7	5	3.0	1	3.0	1	2.7	1	2.9	2	7
Mean	2.0		1.8		2.2		2.0		2.2		2.0		2.0		2.1		
CV (%)	25.8		29.5		30.2		29.9		28.9		31.1		33.6		30.9		
SEM	0.6		0.5		0.7		0.6		0.6		0.6		0.7		0.6		
SED Genotype	0.5		0.4		0.5		0.3		0.5		0.5		0.6		0.3		
SED S-date	0.11								0.12								
SED G x S-date	0.49								0.55								
F-prob. Genotype	0.003		<0.001		<0.001		<0.001		<0.001		<0.001		0.021		<0.001		
F-prob. S-date	0.004								0.214								
F-prob. G x S-date	0.014								0.999								

MAP = months after planting; G= genotype; S-date = sampling dates set at 9, 12, and 15 months after planting; G x S-date = genotype by sampling date interaction; SEM = standard error of means; SED = standard error of difference; F-prob. = F-probability showing the level of significance; CV = coefficient of variation measured as a percentage.

Table 4.8 Ranked mean leaf pubescence of 19 cassava genotypes evaluated at three sampling dates at Kawiko in Mwinilunga, Zambia in 2010/11 and 2011/12 seasons

Genotype	2010/11								2011/12								Rank sum across seasons
	4 MAP		8 MAP		12 MAP		Overall		4 MAP		8 MAP		12 MAP		Overall		
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	
Kapeza	2.3	6	2.3	4	2.3	6	2.3	5	2.3	5	2.0	10	2.3	5	2.2	17	22
Mweru	1.0	18	1.0	18	1.0	18	1.0	19	2.0	10	1.7	16	1.7	13	1.8	13	32
M86/0016	1.0	18	1.3	16	1.0	18	1.1	18	1.3	18	2.0	10	1.7	13	1.7	14	32
L9.304/147	2.3	6	2.0	5	2.0	8	2.1	9	3.0	1	2.7	1	3.0	1	2.9	1	10
Bangweulu	2.7	3	2.0	5	2.0	8	2.2	8	2.0	10	2.0	10	2.0	9	2.0	10	18
Chila	2.0	12	1.7	14	1.7	12	1.8	14	2.0	10	1.7	16	2.0	9	1.9	12	26
Lelanyana	2.3	6	1.7	5	1.7	12	1.9	12	1.7	15	1.7	16	1.3	16	1.6	16	28
I60/42	2.3	6	2.0	5	2.7	2	2.3	5	1.7	15	2.0	10	1.0	19	1.6	16	21
Lufunda	2.0	12	2.0	5	1.7	12	1.9	13	2.0	10	2.3	4	1.7	13	2.0	10	23
I30040	2.3	6	2.0	5	2.0	8	2.1	9	2.3	5	2.3	4	3.0	1	2.6	3	12
L9.304/175	2.7	3	2.7	2	2.7	2	2.7	3	2.7	3	2.7	1	2.3	5	2.6	3	6
14(2)1425	3.0	1	2.7	2	2.7	2	2.8	2	3.0	1	2.3	4	2.7	3	2.7	2	4
Manyopola	2.0	12	1.7	14	1.7	12	1.8	14	1.3	18	1.3	19	1.3	16	1.3	18	32
Kampolombo	2.0	12	2.0	5	2.0	8	2.0	11	1.7	15	2.0	10	1.3	16	1.7	14	25
92/000	3.0	1	2.0	5	2.3	6	2.4	4	2.3	5	2.3	4	2.0	9	2.2	8	12
L9.304/36	2.0	12	2.0	5	1.3	16	1.8	16	2.0	10	2.0	10	2.3	5	2.1	9	25
Kariba	2.0	12	1.3	16	1.3	16	1.6	14	2.3	5	2.7	1	2.0	9	2.3	6	20
TME 2	2.3	6	2.0	5	2.7	2	2.3	5	2.7	3	2.3	4	2.7	3	2.6	3	8
Kaleleki	2.7	3	3.0	1	3.0	1	2.9	1	2.3	5	2.3	4	2.3	5	2.3	6	7
Mean	2.2		2.0		2.0		2.5		2.4		2.1		2.4		2.1		
CV (%)	31.3		28.5		31.4		28.1		32.2		36.5		30.6		32.8		
SEM	0.6		0.6		0.6		0.8		0.7		0.8		0.6		0.7		
SED Genotype	0.5		0.5		0.5		0.3		0.6		0.6		0.5		0.3		
SED S-date	0.11								0.10								
SED G x S-date	0.47								0.60								
F-prob. Genotype	0.006		0.020		0.005		<0.001		0.150		0.800		0.008		<0.001		
F-prob. S-date	0.04								0.64								
F-prob. G x S-date	0.99								1.00								

MAP = months after planting; G = genotype, S-date = sampling date or dates of harvest set at 9, 12, and 15 months after planting; G x S = genotype by sampling date interaction; SEM = standard error of means; SED = standard error of difference; CV = coefficient of variation measured as a percentage; F-prob. = F-probability showing the level of significance;

4.3.6 Fresh storage root yield

The G and S-date main effects and G x S-date interaction effects were highly significant (P<0.001) for FSRY in the 2010/11 season (Table 4.9). Significantly (P<0.001) the highest FSRY of 27.4 t ha^{-1} was obtained at 15 MAP as compared to 16.2 and 12.1 t ha^{-1} at 12 and 9 MAP, respectively. At 9 MAP, FSRY ranged from 9.6 to 15.7 t ha^{-1} with a mean of 12.1 t ha^{-1}. The highest FSRY at 9 MAP was recorded by landrace Kapeza (15.7 t ha^{-1}), which proved to be a good early bulking genotype. Other early bulking genotypes which had above-average FSRY at 9 MAP were Chila (15.5 t ha^{-1}), Lufunda (14.9 t ha^{-1}), L9.304/147 (13.8 t ha^{-1}) and 4(2)1425 (13.8 t ha^{-1}). Yields in the range of 12 to 19 t ha^{-1}, with a mean of 16.2 t ha^{-1}, were obtained at 12 MAP. Kapeza also had the highest FSRY at 12 MAP, followed by M86/0016 and 4(2)1425, which yielded 19.1 t ha^{-1} each, while lowest FSRY was recorded by Manyopola (12.1 t ha^{-1}). At 15 MAP, the FSRY ranged from 21 to 38 t ha^{-1}, with a mean of 27.0 t ha^{-1}. Generally all the genotypes had FSRY above 20 t ha^{-1}, and the significantly (P<0.001), highest FSRY (38.2 t ha^{-1}) was obtained for the genotype TME 2. The genotype Kariba had the lowest FSRY of 22.1 t ha^{-1} at 15 MAP. Overall, 4(2)1425, TME 2, Kapeza, I60/42 and L9.304/147 yielded above 20.0 t ha^{-1} and were the best across the sampling dates in 2010/11.

In 2011/12 the G and S-date main effects were highly significant (P<0.001), while the MS due to G x S-date interaction effects were not significant for FSRY (Table 4.9). However, significant mean differences in FSRY among genotypes were only evident at 9 MAP and for the means across sampling dates. At 9 MAP FSRY ranged from 11.0 to 21.7 t ha^{-1}, with a mean of 13.6 t ha^{-1}. Genotypes 4(2)1425 and TME 2 had the highest FSRY of 21.7 and 20.9 t ha^{-1}, respectively (good early bulking genotypes), while Kariba and L9.304/36 recorded the lowest FSRYof 11.6 t ha^{-1} each at 9 MAP. The genotype 4(2)1425 which had 24.2 t ha^{-1} was the best across sampling dates. Overall, 4(2)1425, Kapeza, TME 2, and I60/42 had the lowest rank sums and were the best genotypes across the seasons (Table 4.9).

Table 4.9 Ranked mean fresh storage root yield of 19 cassava genotypes evaluated at three sampling dates at Kawiko in Mwinilunga, Zambia in 2010/11 and 2011/12 season

Genotype	2010/11								2011/12								Rank sum across season
	9 MAP		12 MAP		15 MAP		Overall		9 MAP		12 MAP		15 MAP		Overall		
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	
Kapeza	15.7	1	19.2	1	31.8	4	22.3	3	18.7	4	24.7	1	26.4	4	23.3	2	5
Mweru	12.8	6	16.6	8	27.3	9	18.9	8	15.5	8	22.8	2	21.2	8	19.8	5	13
M86/0016	12.2	8	19.1	2	22.5	16	17.9	12	13.5	15	18.6	5	16.9	19	16.3	12	24
L9.304/147	13.8	4	19.0	4	31.0	5	21.3	5	18.8	3	15.5	13	22.5	7	18.9	6	11
Bangweulu	10.3	17	16.5	9	27.8	7	18.2	10	14.8	11	15.4	14	19.5	11	16.6	11	21
Chila	15.5	2	14.0	14	28.2	6	19.3	6	13.8	12	17.7	7	24.1	5	18.5	7	13
Lelanyana	12.8	6	13.3	16	21.1	18	15.7	17	12.9	16	16.9	8	17.7	15	15.8	15	33
I60/42	10.8	14	18.6	5	36.8	2	22.1	4	18.0	5	21.5	4	29.2	1	22.9	3	7
Lufunda	14.9	3	14.8	12	27.6	8	19.1	7	13.6	13	16.6	11	20.6	10	16.9	10	17
I30040	11.4	10	18.3	6	25.1	12	18.3	9	15.3	9	16.2	12	19.4	12	17.0	9	18
L9.304/175	11.5	9	14.4	13	22.5	16	16.1	16	12.9	16	14.1	15	21.1	9	16.0	13	31
14(2)1425	13.8	4	19.1	2	35.2	3	22.7	1	21.7	1	22.7	3	28.1	2	24.2	1	2
Manyopola	9.8	18	12.1	18	26.8	10	16.2	14	15.2	10	12.9	17	17.1	18	15.1	18	34
Kampolombo	9.6	19	15.6	10	24.3	13	16.5	13	16.4	6	13.3	16	18.2	14	16.0	13	28
92/000	10.8	14	16.6	8	26.3	11	17.9	11	15.6	7	12.4	18	23.8	6	17.2	8	20
L9.304/36	11.4	10	13.8	15	23.4	14	16.2	14	11.6	18	16.9	8	18.5	13	15.7	16	32
Kariba	10.5	16	13.3	16	22.1	19	15.3	18	11.6	18	17.9	6	17.2	17	15.6	17	36
TME 2	10.9	13	18.5	6	38.2	1	22.5	2	20.9	2	16.9	8	27.7	3	21.8	4	6
Kaleleki	11.2	12	15.5	11	23.2	15	16.6	12	13.6	13	11.9	19	17.3	16	14.3	19	32
Mean	12.1		16.2		27.4		18.6		15.5		17.1		21.4		18.0		
CV (%)	17.4		18.1		17.2		17.7		26.4		15.0		27.4		29.4		
SEM	1.7		2.9		4.7		0.3		4.1		2.6		5.8		5.3		
SED Genotype	1.4		2.4		3.9		1.6		3.3		2.1		4.8		2.5		
SED S-date	0.62								0.99								
SED G x S-date	2.69								4.32^{NS}								
F-prob. Genotype	<0.001		0.04		<0.001		<0.001		0.13		<0.001		0.17		<0.001		
F-prob. S-date	<0.001								<0.001								
F-prob. G x S-date	<0.001								0.955								

MAP = months after planting; G = genotype; S-date = sampling date or dates of harvest set at 9, 12,and 15 months after planting; G x S-date = genotype by sampling date interaction; SEM = standard error of means; SED = standard error of difference; CV = coefficient of variation measured as a percentage; F-prob. = F-probability showing the level of significance.

4.3.7 Storage root rots

The incidence of SRR was generally low in both seasons (Table 4.10). The incidence of SRR ranged from 0.0 to 37.2% with a mean of 6.7%, and from 0.0 to 29.4% with a mean of 7.4% in the 2010/11 and 2011/12 seasons, respectively. In the 2010/11 season, significantly ($P<0.001$) the highest incidence (11.9%) of SRR was recorded at 15 MAP as compared to 2.5 and 5.7% which was recorded at 9 and 12 MAP, respectively. However, genotypes reacted differentially to SRR at different sampling dates within seasons. The genotype Kariba recorded significantly ($P<0.001$) the highest incidence of SRR (10.8%), but no symptoms of SRR were found in 12 out of the 19 genotypes that were evaluated at 9 MAP. At 12 MAP in 2010/11 season, seven of the genotypes had significantly ($P<0.001$) high incidence of SRR, with the genotypes M86/0016 and Kariba being the most susceptible with incidences of 22.0 and 22.7%, respectively. At 15 MAP, SRR were present in 11 of the 19 genotypes evaluated with incidence ranging from 0.0 to 37.0%. Genotypes M86/0016, L9.304/147, and Kariba, were the most susceptible with respective SRR incidences of 37.2, 30.5 and 30.0%. No SRR were recorded by Mweru, Lelanyana, Kampolombo, 92/000, and Kaleleki in the 2010/11 season. Genotypes M86/0016 and Kariba were the most susceptible with 22.7 and 20.9% disease incidence, respectively across sampling dates in the season (Table 4.10).

In 2011/12 season, the G and S-date main effects were significant for SRR, but unlike the previous season, the MS due to G x S-date interaction effect was not significant for the trait. The incidence of SRR ranged from 0.0 to 29.4% with a mean of 7.4% across the season. Significantly the highest SRR incidence of 10.8% was recorded at 15 MAP compared to 5.5 and 5.8% which were recorded at 9 and 12 MAP, respectively. At 9 MAP differences between genotypes for SRR were not significant, but 11 genotypes recorded no SRR. However, highly significant differences were observed between genotypes for SRR at 12 MAP ($P<0.001$) and 15 MAP ($P<0.01$). At 12 MAP, 10 of the genotypes presented no SRR, but a 25.0% incidence of SRR was recorded by M86/0016. The same genotype had the highest incidence of SRR (29.4%) at 15 MAP, and it was considered to be the most susceptible to SRR, with an overall mean incidence of 23.0% across the season. Kapeza, Mweru, and Bangweulu had no SRR across the season (Table 4.9). Overall, genotypes Mweru, 92/000, Kaleleki, Kampolombo and Lelanyana had the lowest rank sum for SRR and were therefore considered to be the most resistant across the seasons (Table 4.9).

Table 4.10 Ranked mean incidence of root rots (%) of 19 cassava cultivars evaluated at three sampling dates at Kawiko in Mwinilunga, Zambia in 2010/11 and 2011/12 seasons

Genotype	2010/11								2011/12								Rank sum across seasons
	4 MAP		8 MAP		12 MAP		Overall		4 MAP		8 MAP		12 MAP		Overall		
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	
Kapeza	8.3	16	0.0	1	0.0	1	2.8	8	0.0	1	0.0	1	0.0	1	0. 0	1	9
Mweru	0.0	1	0.0	1	0.0	1	0.0	1	0.0	1	0.0	1	0.0	1	0.0	1	2
M86/0016	3.3	13	27.7	19	37.2	19	22.7	19	14.4	16	25.0	19	29.4	19	23.0	19	38
L9.304/147	0.0	1	4.2	13	30.5	18	11.6	14	11.1	15	4.2	14	14.4	13	9.9	13	27
Bangweulu	8.3	16	0.0	1	0.0	1	2.8	8	0.0	1	0.0	1	0.0	1	0.0	1	9
Chila	0.0	1	0.0	1	11.1	10	3.7	10	0.0	1	0.0	1	8.5	10	2.8	10	20
Lelanyana	0.0	1	0.0	1	0.0	1	0.0	1	0.0	1	1.7	12	0.0	1	0.6	5	6
I60/42	0.0	1	0.0	1	22.2	14	7.4	13	15.0	17	0.0	1	18.3	15	11.1	14	27
Lufunda	8.3	16	16.7	15	22.2	14	15.7	17	20.8	19	16.7	15	28.3	18	21.9	17	34
I30040	0.0	1	16.7	15	27.8	16	14.8	16	8.3	14	16.7	15	22.5	16	15.8	16	32
L9.304/175	0.0	1	0.0	1	4.2	9	1.4	6	0.0	1	0.0	1	1.7	6	0.6	5	11
4(2)1425	4.2	14	0.0	1	0.0	1	1.4	6	0.0	1	0.0	1	3.3	9	1.1	9	15
Manyopola	0.0	1	4.2	13	11.7	12	5.3	12	4.2	12	1.7	12	12.7	12	6.2	12	24
Kampolombo	0.0	1	0.0	1	0.0	1	0.0	1	0.0	1	0.0	1	1.7	6	0.6	5	6
92/000	0.0	1	0.0	1	0.0	1	0.0	1	0.0	1	0.8	11	0.0	1	0.3	4	5
L9.304/36	4.2	14	16.7	15	17.8	13	12.9	15	7.5	13	16.7	15	15.8	14	13.3	15	30
Kariba	10.8	19	22.0	18	30.0	17	20.9	18	18.3	18	22.0	18	27.7	17	22.7	18	36
TME 2	0.0	1	0.0	1	11.1	10	3.7	10	0.0	1	0.0	1	10.0	11	3.3	11	21
Kaleleki	0.0	1	0.0	1	0.0	1	0.0	1	0.0	1	0.0	1	1.7	6	0.6	5	6
Mean	2.5		5.7		11.9		6.7		5.5		5.8		10.8		7.4		
CV (%)	162.2		117.4		98.8		119.5		197.6		119.5		108.7		148.8		
SEM	4.0		6.7		11.7		8.0		10.4		8.0		11.2		10.4		
SED Genotype	3.3		5.4		9.6		3.8		8.5		3.8		9.2		4.9		
SED S-date				1.5									2.0				
SED G x S-date				6.5									5.8				
F-prob. Genotype	0.008		<0.001		<0.001		<0.001		0.160		<0.001		0.005		<0.001		
F-prob. S-date				<0.001									0.017				
F-prob. G x S-date				<0.001									0.999				

MAP = months after planting;G = genotype; S-date = sampling date or dates of harvest set at 9, 12, and 15 months after planting; G x S-date = genotype by sampling date interaction; SEM = standard error of means; SED = standard error of difference; CV = coefficient of variation measured as a percentage; F-prob. = F-probability for significance of F-test

4.3.8 Storage root dry mass percentage

The G main effects were significant (P<0.05) for SRDM%, while S-date main effects were not significant for the trait. The G x S-date interaction effects were highly significant (P<0.01) for SRDM%. In 2010/11 season, the difference between the genotypes were significant (P<0.05) for SRDM% at 9 and 12 MAP, but the difference between genotypes were not significant at 15 MAPfor the trait (Table 4.11). The SRDM% ranged from 21.0 to 39.0% with a mean of 31.4%. Genotypes Kapeza, L9.304/175, I30040, Lufunda, and Bangweulu had the highest SRDM% with respective means of 34.4, 34.2, 34.2, and 33.6% across sampling dates in the 2010/11 season (Table 4.11).

In 2011/12 season, only the G main effects were significant (P<0.001) for SRDM%. Across sampling dates, SRDM% ranged from 23.3 to 38.7% with a mean of 32.7%. The genotypes L9.304/147 and Kapeza had the highest SRDM% with respective means of 36.7 and 36.4%, followed by L9.304/175 (35.7%) and I30040 (35.0%), while the lowest SRDM% (25.8%) was recorded by Lelanyana.

Table 4.11 Ranked mean storage root dry mass percentageof 19 cassava cultivars evaluated at three sampling dates at Kawiko in Mwinilunga, Zambia in 2010/11 and 2011/12 seasons

Genotype	2010/11								2011/12								Rank sum across seasons
	9 MAP		12 MAP		15 MAP		Overall		9 MAP		12 MAP		15 MAP		Overall		
	Mean	Rank	Mean	Rank	Mean	Rank	Mean[2]	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	
Kapeza	35.0	6	36.7	3	31.7	10	34.4	1	34.7	9	38.0	3	36.7	2	36.4	2	3
Mweru	35.3	5	32.7	8	31.5	12	33.2	6	36.0	5	34.3	8	33.7	7	34.7	6	12
M86/0016	30.3	15	23.7	17	26.7	17	26.9	17	32.7	12	29.9	16	30.0	13	30.8	14	31
L9.304/147	38.3	1	28.3	13	30.3	13	32.3	7	36.3	3	38.7	1	35.0	4	36.7	1	5
Bangweulu	34.7	7	34.3	6	31.7	10	33.6	4	37.3	2	33.0	10	31.7	11	34.0	10	14
Chila	36.0	4	29.0	12	32.0	8	32.3	7	35.3	7	34.7	7	32.3	10	34.1	8	15
Lelanyana	26.0	17	31.6	9	26.8	16	28.1	15	30.0	17	23.5	19	24.0	19	25.8	19	34
I60/42	24.3	19	37.9	2	31.7	9	31.3	11	27.7	19	32.3	11	29.0	15	29.7	16	27
Lufunda	32.7	11	30.8	10	38.0	1	33.8	4	38.0	1	32.0	13	31.6	12	33.9	11	15
I30040	34.7	7	34.7	5	33.3	6	34.2	3	34.0	11	35.3	6	35.7	3	35.0	4	7
L9.304/175	36.3	3	33.9	7	33.0	7	34.4	1	36.0	4	36.8	4	34.3	5	35.7	3	4
14(2)1425	24.7	18	39.4	1	26.7	17	30.2	14	28.7	18	32.3	11	28.3	17	29.8	15	29
Manyopola	34.0	10	29.8	11	27.0	15	30.3	13	32.0	14	35.4	5	34.2	6	33.9	11	24
Kampolombo	32.0	14	23.4	18	27.3	14	27.2	16	30.7	16	25.7	18	28.7	16	28.3	17	33
92/000	38.3	1	21.0	19	35.7	3	31.7	9	35.7	6	34.3	8	32.3	10	34.1	8	17
L9.304/36	34.7	7	23.9	16	36.7	2	31.7	9	34.7	9	31.2	14	36.8	1	34.2	7	16
Kariba	28.0	16	25.9	15	25.7	19	26.4	18	31.3	15	26.9	16	26.5	18	28.2	18	36
TME 2	32.0	13	26.2	14	35.0	5	31.1	12	32.7	12	38.3	2	33.6	8	34.8	5	17
Kaleleki	32.7	11	34.8	4	35.3	4	33.6	4	35.3	7	30.4	15	29.1	14	31.6	13	17
Mean	32.6		30.4		31.2		31.4		33.6		32.8		31.8		32.7		
CV(%)	15.8		19.7		17.4		17.3		13.6		19.5		18.6		17.1		
SEM	5.1		6.0		5.4		5.4		4.6		6.4		5.9		5.6		
SED Genotype	4.2		4.9		4.4		2.4		3.8		5.2		4.8		2.6		
SED S-date	2.6								1.0								
SED G x S-date	4.4								4.6								
F-prob. Genotype	0.04		0.008		0.18		0.011		0.29		0.24		0.43		<0.001		
F-prob. S-date	0.082								0.207								
F-prob. G x S-date	0.002								0.992								

MAP = months after planting;G = genotype; S-date = sampling date or dates of harvest set at 9, 12, and 15 months after planting; G x S-date = genotype by sampling date interaction; SEM = standard error of means; SED = standard error of difference of means; CV(%) = coefficient of variation measured as a percentage; F-prob. = F-probability showing the level of significance.

4.3.9 Stability analysis

Genotypes which had lowest rank sum for Wi across the sampling dates for a particular trait were considered to exhibit high intra-season stability, while genotypes which had lowest rank sum for Wi across season were considered to exhibit high inter-season stability (Appendix 4.1). Genotypes with lowest GSI scores combine high stability with desirable trait means and were therefore considered to be the most stable and superior for the trait, while genotypes with high GSI scores are undesirable.

Cassava green mite population density: Genotypes 4(2)1425 and L9.304/147 had the lowest GSI overall for CGM PD and so were the most resistant and most stable across sampling dates in each of the seasons and across seasons (Table 4.12).

Cassava green mite leaf damage: Genotypes Kapeza and Bangweulu had lowest GSI for CGM LD across sampling dates in the 2010/11 season. Genotypes 4(2)1425, Bangweulu and L9.304/175 had lowest GSI for CGM LD across sampling dates in 2011/12. Overall, genotypes 4(2)1425, Bangweulu, and I60/42 were the most stable and most resistant across seasons, while Mweru and Kariba were the most susceptible and least stable genotypes across seasons (Table 4.12).

Table 4.12 Ranked genotype stability indices for cassava green mite population density and associated leaf damage of 19 cassava genotypes evaluated across three sampling dates in 2010/11 and 2011/12 seasons at Kawiko in Mwinilunga district, Zambia

Genotype	CGM PD						CGM LD					
	2010/11		2011/12		Overall		2010/11		2011/12		Overall	
	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank
Kapeza	18	8	28	15	46	14	7	1	24	15	31	5
Mweru	25	14	37	19	62	18	36	19	35	19	71	19
M86/0016	32	18	20	12	52	16	20	12	24	15	44	13
L9.304/147	7	2	6	1	13	1	13	5	18	9	31	5
Bangweulu	23	11	16	7	39	7	10	2	14	2	24	2
Chila	25	14	22	13	47	15	24	14	22	14	46	15
Lelanyana	22	10	35	18	57	17	16	8	18	9	34	9
I60/42	24	12	16	7	40	9	11	3	15	4	26	3
Lufunda	30	16	11	3	41	10	16	8	15	4	31	5
I30040	12	4	17	9	29	5	14	6	20	11	34	9
L9.304/175	10	3	19	10	29	5	16	8	14	2	30	4
4(2)1425	4	1	11	3	15	2	12	4	6	1	18	1
Manyopola	13	6	30	16	43	12	24	14	25	17	49	17
Kampolombo	13	6	26	14	39	7	25	16	15	4	40	12
92/000	19	9	9	2	28	4	14	6	17	7	31	5
L9.304/36	30	16	11	3	41	10	29	17	17	7	46	15
Kariba	33	19	31	17	64	19	34	18	26	18	60	18
TME 2	24	12	19	10	43	12	23	13	21	12	44	13
Kaleleki	12	4	15	6	27	3	16	8	21	12	37	11

CGM PD = cassava green mite population density per leaf; CGM LD = cassava green mite leaf damage scored on 1-5 scale, where 1 = no damage, and 5 = very severe damage; GSI = genotype stability index

Leaf retention: In the 2010/11 season, Bangweulu, Kapeza and Mweru combined high stability with highest LR while Kampolombo, L9.304/36, and L9.304/147 combined low stability with low LR across sampling dates (Table 4.13). In the 2011/12 season, smallest GSI scores for LR were recorded for genotypes 4(2)1425, L9.304/147, and Kariba. Genotypes 4(2)1425 and Kapeza exhibited high stability for LR combined with high mean for the trait across the two seasons, while Kampolombo and L9.304/36 combined low stability with low LR.

Stay green: Kampolombo, 92/000 and Bangweulu had lowest GSI scores for SG, while Manyopola, I60/42 and Kariba combined low stability with low SG in the 2010/11 season (Table 4.12). In the 2011/12 season, 92/000 and Bangweulu had the lowest GSI for SG, while M86/0016, Lufunda and I60/42 combined low stability with lowest means for SG across sampling dates in the season. Overall, 92/000 and Kampolombo had the lowest GSI scores and were therefore the most stable with high SG across seasons.

Leaf pubescence: Genotypes Kaleleki, L9.304/175, and 92/000 had the lowest GSI for Pbs and were therefore considered to be the most stable and the most pubescent across sampling dates in 2010/11 season, while Chila, Kariba and Bangweulu had the highest GSI scores and were considered to be the least stable and least pubescent genotypes across sampling dates in the season (Table 4.13). Genotypes 4(2)1425, l9.304/147 and L9.304/175 were the most stable and the most pubescent across sampling dates in 2011/12 season. Overall, L9.304 and 4(2)1425 had lowest GSI scores and were therefore the most stable and the most pubescent genotypes across the two seasons, while largest GSI scores were recorded for I60/42, Kampolombo, and M86/0016 which were therefore considered to be the least stable and the least pubescent genotypes across the seasons.

Table 4.13 Ranked genotype stability indices for leaf retention, stay green, and leaf pubescence of 19 cassava genotypes evaluated across three sampling dates in 2010/11 and 2011/12 seasons at Kawiko in Mwinilunga district, Zambia

Genotype	LR (%)						SG (1-3)						Pbs (1-3)					
	2010/11		2011/12		Overall		2010/11		2011/12		Overall		2010/11		2011/12		Overall	
	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank
Kapeza	6	2	19	8	25	1	17	4	13	5	30	4	10	4	26	14	36	7
Mweru	7	3	26	16	33	5	22	12	28	15	50	14	24	15	15	6	39	9
M86/0016	20	7	20	10	40	11	28	16	36	19	64	19	22	12	31	18	53	18
L9.304/147	29	17	11	2	40	11	18	6	22	12	40	9	20	11	5	2	25	5
Bangweulu	4	1	22	13	26	3	14	3	7	1	21	3	27	17	22	12	49	16
Chila	10	4	19	8	29	4	18	6	15	7	33	5	32	19	16	7	48	15
Lelanyana	20	7	21	11	41	13	18	6	17	8	35	7	25	16	20	11	45	11
I60/42	25	13	21	11	46	15	31	19	29	17	60	18	22	12	34	19	56	19
Lufunda	20	7	35	18	55	17	23	14	29	17	52	15	18	7	24	13	42	10
I30040	25	13	28	17	53	16	20	10	21	10	41	12	19	9	19	9	38	8
L9.304/175	15	5	18	7	33	5	20	10	20	9	40	9	6	2	7	3	13	1
4(2)1425	21	11	4	1	25	1	26	15	13	5	39	8	15	5	3	1	18	2
Manyopola	20	7	14	6	34	7	29	18	25	14	54	16	19	9	28	15	47	14
Kampolombo	30	18	36	19	66	19	7	2	8	3	15	2	22	12	29	17	51	17
92/000	25	13	13	4	38	9	5	1	7	1	12	1	9	3	11	4	20	4
L9.304/36	31	19	25	15	56	18	19	9	21	10	40	9	17	6	28	15	45	11
Kariba	26	16	12	3	38	9	28	16	28	15	56	17	27	17	19	9	46	13
TME 2	21	11	13	4	34	7	17	4	24	13	41	12	18	7	11	4	29	6
Kaleleki	18	6	23	14	41	13	22	12	11	4	33	5	3	1	16	7	19	3

LR = leaf retention expressed as a percentage; SG= stay green scored on 1-3 scale, where 1 = lowest, and 3 = highest; Pbs = leaf pubescence score on 1-3 scale, where 1 = glabrous, and 3 = highly pubescent; GSI = genotype stability index

Fresh storage root yield: The genotypes M86/0016, I30040, Kapeza, Mweru and Kaleleki, had lowest GSI scores for FSRY and therefore were considered the most stable and most high yielding in the 2010/11 season. For the 2011/12 season, Bangweulu, Kapeza, Mweru, Lelanyana, 92/000 and L9.304/36 recorded lowest GSI scores and were considered most stable and most high yielding, while Kampolombo, Kariba, and I30040 had highest GSI scores and were therefore least stable and lowest yielding genotypes for the season. Overall, M86/0016, Mweru, Kapeza and I30040 recorded lowest GSI scores and were the most stable and most high yielding across seasons (Table 4.14).

Storage root rot: In 2010/11 season genotypes 92/000, Kaleleki, Kampolombo, Lelanyana, and Mweru had lowest GSI scores for cassava SRR incidence, and were therefore considered the most stable genotypes with the most extended underground storability. In 2011/12 season, L9.304/175, Kampolombo, and Kaleleki had lowest GSI scores for SRR, and were the most stable genotypes with good underground storability, while M86/0016, I60/42, and I30040 werethe least stable genotypes with poor underground storability (Table 14).

Storage root dry mass percentage: The genotype L9.304/175 had the lowest GSI score for SRDM% across sampling dates in 2010/11, followed by I30040, Bangweulu, and Mweru. The lowest GSI score for SRDM% in 2011/12 season was recorded by L9.304/175, followed by L9.304/147, and Mweru, which were considered the most stable genotypes with highest SRDM%, while M86/0016, Kariba, and 4(2)1425 were the least stable genotypes with the lowest SRDM%. Genotypes, L9.304/175, L9.304/147, and Mweru had the least GSI and therefore were ranked the best for SRDM% across the seasons (Table 4.14).

Table 4.14 Ranked genotype stability indices for fresh storage root yield, storage root dry mass percentage and the incidence of root rots of 19 cassava genotypes evaluated across three sampling dates in 2010/11 and 2011/12 seasons at Kawiko in Mwinilunga district, Zambia.

Genotype	FSRY						SRR (%)						SRDM (%)					
	2010/11		2011/12		Overall		2010/11		2011/12		Overall		2010/11		2011/12		Overall	
	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank	GSI	Rank
Kapeza	17	3	19	2	36	2	21	11	11	5	32	9	12	5	18	8	30	6
Mweru	17	3	19	2	36	2	6	1	11	5	17	4	10	4	11	3	21	2
M86/0016	13	1	21	14	34	1	36	19	37	19	73	19	23	12	31	17	54	18
L9.304/147	20	10	21	14	41	11	31	17	26	15	57	16	22	11	9	2	31	7
Bangweulu	23	16	18	1	41	11	21	11	11	5	32	9	8	3	21	11	29	4
Chila	18	6	20	7	38	6	13	7	15	8	28	8	14	7	15	5	29	4
Lelanyana	21	11	19	2	40	10	6	1	20	10	26	5	28	18	22	12	50	15
I60/42	22	14	21	14	43	16	28	15	33	17	61	17	27	16	23	13	50	15
Lufunda	18	6	20	7	38	6	21	11	25	14	46	13	17	8	27	15	44	11
I30040	15	2	21	17	36	2	32	18	33	17	65	18	6	2	16	6	22	3
L9.304/175	19	9	20	7	39	9	8	6	7	1	15	3	3	1	7	1	10	1
4(2)1425	18	6	20	7	38	6	16	10	10	4	26	5	32	19	28	16	60	19
Manyopola	32	19	20	7	52	19	13	7	19	9	32	9	21	10	14	4	35	8
Kampolombo	21	11	22	18	43	16	6	1	7	1	13	1	25	14	18	8	43	9
92/000	22	14	19	2	41	11	6	1	20	10	26	5	27	16	18	8	45	13
L9.304/36	23	16	19	2	42	15	25	14	28	16	53	14	26	15	17	7	43	9
Kariba	24	18	22	18	46	18	30	16	24	13	54	15	19	9	32	19	51	17
TME 2	21	11	20	7	41	11	13	7	20	10	33	12	24	13	23	13	47	14
Kaleleki	17	3	20	7	37	5	6	1	7	1	13	1	13	6	31	17	44	11

FSRY = fresh storage root yield (t ha^{-1}); SRR = storage root rot disease incidence (%); SRDM% = percentage storage root dry mass; GSI = genotype stability index

4.4 Discussion and conclusions

The study has clearly indicated effects of seasonal variations on the performance and stability of cassava genotypes. The average daily temperatures of 28ºC and relative humidity of 72-75% experienced during the seasons seem to coincide with the optimum temperature of 27^{o}C and RH of 50-70% reported for maximum oviposition of CGM (Yaninek et al., 1986; Hahn et al., 1989; Yaninek et al., 1989). This is a probable reason for the highest CGM PD recorded at 9 MAP. Heavy rains are normally experienced in December (second sampling) while March (third sampling) coincides with the end of the rainy season. Consistent with this observation, Yaninek et al. (1989) attributed increased CGM mortality to the mites being washed of the leaves during the wet season. The minimum temperature of 10^{o}C experienced in June and July, which happened to be lower than the estimated thermal threshold for CGM of14.4ºC (Yaninek et al., 1986), is another source of mite mortality (Mebelo et al., 2003).

Locally improved genotype L9.304/147 exhibited better levels of stability for low CGM PD as compared to 4(2)1425 and I60/42, which are widely used as sources of resistance to CGM in Africa (Hahn et al., 1989; Mahungu et al., 1994). Similarly, the high stability for low CGM PD as displayed by landrace Kaleleki indicates that locally adapted sources of resistance are available. Having been grown in the locality for several years, landraces are more likely to cope with environmental stresses including crop pests and diseases common to a given locality, making them suitable candidates for inclusion as parents in a breeding programme (Raji et al., 2008).

Genotypes Kapeza and I60/42 were better ranked for CGM LD than they were for CGM PD, which suggests that, these genotypes exhibit a tolerance mechanism towards CGM. Consequently, genotypes which combine low CGM PD with low CGM LD, such as 4(2)1425, L9.304/147, and L9.304/175, are the most desirable and can be recommended for wider production, or as sources of resistance for breeding programmes.

The study revealed the presence of genetic variability in the germplasm for LR in Zambia. Six genotypes that combined high stability with high mean LR had one characteristic in common, namely a tendency to either fold or roll their leaves downward away from the sun during hot periods. According to El-Sharkawy (2003), the action of leaf folding may be a mechanism for water stress avoidance. It is also suggested that genotypes which exhibit high LR combined with enhanced SG are likely to be resistant to both CGM and drought (Nukenine et al., 1999).

In cassava, Pbs is said to be the primary trait responsible for resistance to CGM (Hahn et al., 1989; Raji et al., 2008). The Pbs, especially of immature leaves and shoot apices, has been reported to provide suitable habitat for *T. aripo* which has proved to be the most successful

natural enemy against *M. tanajoa* and whitefly (*Bemisia tabacci* Gennadius) in Africa (Yaninek and Hanna, 2003; Amusa and Ojo, 2005; Onzo et al., 2005; Onzo et al., 2010). The current study was conducted in the absence of the natural enemy, and therefore, it was not possible to confirm or otherwise these reports, but this study indicated that the trait is little influenced by seasonal effects and that there is genetic variability for this in the local Zambian germplasm. The results of the current study coupled with other reports of heritability estimates as high as 93% for this trait (Hahn et al., 1989), imply that the expression of Pbs is highly predictable and therefore it should be relatively easy to incorporate into new genotypes. Three genotypes which exhibited the highest stability combined with high level of Pbs were L9.304/175, 4(2)1425, and Kaleleki. These genotypes had high inter-season stability for low CGM PD and CGM LD, and could be used as sources of genes for CGM resistance.

In Northern, Muchinga, Luapula, and North-Western Provinces, which constitute the cassava-belt in Zambia, cassava is considered a food security crop. Farmers are interested in cassava genotypes that bulk early, but can stay in the ground for a long time without rotting. It is rare that farmers harvest the entire field of cassava at one time. This is necessitated by the fact that subsistence farmers have no means of storing freshly harvested storage roots, which normally deteriorate within 24 hours after harvest (Ceballos et al., 2006). This flexibility in harvesting cassava, as and when required for consumption is an important attribute that has made cassava one of the most important food security crops in Africa (Nweke et al., 2002). However, as environments keep changing, root rots are becoming increasingly important in many parts of Africa (Makambila, 1994; Mskita et al., 1997a; Chalwe et al., 1998), where they are reported to cause yield losses of up to 80% (Msikita et al., 2005).

Storage roots were harvested at 9, 12, and 15 MAP to identify early-bulking CGM-resistant genotypes that can be harvested earlier than 12 months, as well as to identify genotypes with good underground storability. Three genotypes, namely Kapeza, L9.304/147 and 4(2)1425 consistently yielded above 13 t ha^{-1} as early as 9 MAP in both seasons, suggesting their potential as early bulking genotypes. Though SRR were encountered at all three sampling dates, the incidence varied with genotype, implying that there is genetic variability in the cassava germplasm available in Zambia (Onyeka et al., 2005a; Onyeka et al., 2005b). However, the highest incidence of SRR symptoms both in terms of number of genotypes and number of infected plants per genotype was recorded at 15 MAP corroborating earlier reports that delayed harvesting contributes to high incidence of SRR (Mskita et al., 1997b; Chalwe et al., 1998). The current study was conducted under natural field conditions, where the infection was highly random as evidenced by high CV% for all sampling dates in both seasons. However, this study

identified at least two genotypes that combined FSRY stability and performance with stability for low or no incidence of SRR within and across the seasons, namely landrace Kaleleki and a locally improved genotype Mweru. At least two genotypes, Mweru and L9.304/175 combined stability with lowest means for SRR and SRDM%. Three genotypes M86/0016, Mweru, I30040 and Kapeza, combined stability with high mean performances for both SRDM% and FSRY. These results therefore suggest that Mweru is a strong and dependable genotype. The level of injury caused by CGM on this genotype does not seem to affect its stability for FSRY, SRDM%, and resistance to SRR.

Inconsistencies in ranking between mean FSRY and stability scores as was commonly displayed by genotypes such as 4(2)1425, TME2, I60/42, and L9.304/147 which were among the most high yielding but least stable, and Kaleleki, Lelanyana, L9.304/175, L9.304/36, which were most stable but among the lowest yielding, suggest the need to consider the overall mean performance and stability simultaneously when evaluating genotypes in multi-environment trials (Farshadfar, 2008). Mohammadi et al. (2007) have cautioned that stability on its own should not be the criterion for selection, because the most stable genotypes would not necessarily give the best trait performance. For this reason, incorporation of both stability and overall trait mean performance into a single stability index (GSI) is a recommended approach (Kang, 1991; 1993; Farshadfar, 2012). Moreover, since farmers are interested in genotypes that perform consistently better in every environment (Mohammedi and Amri, 2009), FSRY and stability should be considered simultaneously.

Though slight differences were observed in SRDM% between seasons and genotypes responded differently at each sampling date within the first season, this study indicates that genetic differences among genotypes were responsible for the variation observed in SRDM% within seasons. Genotypes L9.304/175, Mweru, and I30040 were least affected by the seasonal effects, as compared to 4(2)1425, and M86/0016. According to Ramanujam and Biradar (1987), genotypes which branch profusely like M86/0016 and 4(2)1425 have a tendency to partition most of their dry mass to the above-ground biomass (leaves and branches) at the expense of SRDM%. Although the harvest index was not determined in the study, the results at least for SRDM%, tend to corroborate those of Manrique (1990) who reported that dry mass partitioning to storage roots had little seasonal variation and increased with plant age.

Overall, the study has shown that there is wide diversity in the expression of valuable indirect defense traits among genotype, indicating that there is scope for integration of biological control and host plant resistance for CGM in Zambia. Release of genotypes that exhibit high levels of

intra-season and inter-season stability for enhanced expression of LR, SG, and Pbs will minimize the impact of CGM on FSRY and SRDM% that results from seasonal effects. Such genotypes will also provide the required habitat for *T. aripo* in cassava fields. The study has identified genotypes which have good stability across seasons within a year and across years. However, the study contributed to the promotion of food security in Zambia and elsewhere where cassava is grown through the identification of early-bulking genotypes which also have good potential for extended underground storability. Early-bulking, high FSRY and SRDM% and SRR resistance are farmer-preferred traits. Therefore, enhancement of such traits through plant breeding is likely to increase the adoption of new genotypes by farmers. However, in future research the evaluation of genotypes must extend over 36 months, which is the longest period that farmers keep the crop in the field.

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CHAPTER 5

Inheritance of resistance to cassava green mite (*Mononychellus tanajoa)* (Bondar) (Acari: Tetranychidae) and other useful agronomic traits in cassava grown in north-western Zambia

Abstract

Cassava green mite (CGM) (*Mononychellus tanajoa*) is a major arthropod pest causing significant loss in the yields of storage roots and planting materials of cassava in Zambia. Its control has been mainly based on the use of exotic predatory mites as biological control agents, which unfortunately, have not established well in Zambia due to the lack of suitable host genotypes and harsh weather conditions. The current study was aimed at breeding cassava for improvement of morphological traits that are associated with resistance to CGM, which at the same time can enable cassava genotypes to provide shelter and ensure continuous survival of natural enemies of CGM, and to determine the inheritance of these traits by assessing combining ability and therefore the type of gene action involved in their expression. Using a 5 x 5 half diallel mating design, full-sib cassava genotypes were generated out of which 300 were selected and evaluated in the field. Data were collected for CGM density (CGM PD), CGM leaf damage (CGM LD) and cassava mosaic disease severity, plant growth habit, leaf morphological traits, storage root yield and storage root dry mass percentage. Both general combining ability and specific combining ability effects were significant ($P<0.01$) for the reaction of the F_1 progeny to CGM, and for the various plant morphological traits that were measured, suggesting that both additive and non-additive gene effects play a role in the expression of the traits. High narrow-sense heritability estimates were obtained for CGM PD, CGM LD, leaf retention, and size and compactness of shoot apices. Using the farmer participatory-formulated selection index, 30 F_1 progeny which combined various farmer desired traits were identified.

5.1 Introduction

Cassava (*Manihot esculenta* Crantz) is a very important crop especially in tropical and sub-tropical Africa, Asia and Latin America where more than 500 million people depend on it for their livelihood. Cassava occupies a high position as a food security crop particularly because of its ability to withstand adverse environmental conditions such as drought and low soil fertility conditions under which other crops fail to survive (Lenis et al., 2006). However, the yields for cassava are very unstable mainly due to pests and diseases, particularly cassava green mite (CGM), cassava mosaic disease (CMD), and cassava brown streak disease, and there are very few cultivars that combine resistance to pests and diseases with good agronomic characteristics (Mahungu et al., 1994; Dixon et al., 2001).

In Zambia specifically, CGM is reported to cause a 30 to 50% reduction in fresh storage root yield (FSRY) (Chakupurakal et al., 1994). Strategies to control CGM include host-plant resistance (HPR) and biological control using exotic natural enemies (Byrne et al., 1982; Hahn et al., 1989; Yaninek and Hanna, 2003; Zundel et al., 2009; Onzo et al., 2012). Particularly in Zambia, the management of CGM has not been effective probably because HPR and biological control have been utilised separately as two parallel or complementary pest management strategies. However, the failure of the natural enemies of CGM to establish well in north-western Zambia (Mebelo et al., 2003), and some parts of Africa (Onzo et al., 2003; Hanna et al., 2005) probably due to unsuitable climate and/or lack of suitable host cassava cultivars (Malambo et al., 1998; Zundel et al., 2009), necessitates the integration of the two approaches in order to achieve more sustainable and effective management of CGM.

There is inadequate information about the inheritance of host-based genetic resistance to CGM and associated indirect defense mechanisms despite the importance of cassava as a food crop. Compared to cereal crops, there are very few published articles regarding the inheritance of agronomic traits in cassava (Calle et al., 2005; Jaramillo et al., 2005; Perez et al., 2005; Kamau et al., 2010; Were et al., 2012), which makes attempts to improve these traits through breeding difficult and consequently slows progress.

This study was therefore conducted to achieve the following objectives: i) evaluate and select for those plant morphological traits that confer resistance to CGM and those which may not be mutually exclusive, that support continuous inhabitance of natural enemies, particularly *Typhlodromalus aripo*, on cassava; and ii) study the combining abilities and therefore gene action controlling inheritance of CGM resistance and associated indirect defense traits.

5.2 Materials and methods

5.2.1 Site description

Crosses were made in the field (2009/10), and the seedling stage (2010/11) and clonal stage trials (2011/12) were conducted at Mutanda research station, situated at latitude 12º11'S and longitude 26º24'E with an elevation of 1386 m above sea level. Zambia is divided into three agro-ecological zones or regions which are differentiated based on the length of growing season at 70% probability, mean monthly temperature, amount of sunshine in the rainy season, and occurrence of frost in the dry season (SCRB, 2001). Mutanda experiences a mono-modal pattern of rainfall that normally exceeds 1000 mm per annum within a growing season of 120-150 days. Mean monthly temperature ranges from 18-26ºC. The site has red to brown clay to loamy soils that are predominantly highly weathered and leached ferralsols with very strong acidity (pH 4.5), low reserves of primary minerals, and high levels of aluminum and manganese.

5.2.2 Mating design and field trial design

Botanical seeds of cassava were generated in 2009/10 season through hand pollination using a 5x5 half diallel mating design, where each parent was crossed with each of the other four parents. No selfing of clones was allowed to avoid inbreeding (Calle et al., 2005; Jaramillo et al., 2005). The crosses were made in one direction only without reciprocals. It was intended that the diallel would be based on 10 parents, which were selected jointly by farmers and scientists following a farmer-participatory germplasm evaluation. However, only five of the parents flowered within the first 12 months and could therefore be used as parents in the crossing block. The 10 families of seedlings from the 5 x 5 half diallel mating were raised in a field nursery at Mutanda research station over a period of 12 months. A minimum of 30 full-sibs was selected from each of the families (solely on the basis of those that produced at least six cuttings, each 15 cm in length) and planted in the seedling stage trial in 2010/11 season from which no data was collected. Cuttings from each of the 30 full-sibs of the 10 families were planted 15th December 2011 at Mutanda in a 30 x 2, row-column design with three replications to constitute the clonal evaluation trial. Each replication was planted to the 10 families, each of which consisted of 30 full-sibs that were planted on two ridges. Each full-sib clone was represented by two cuttings in each replication planted at a spacing of 1 x 1 m, equivalent to 10 000 plants ha^{-1}. Cuttings of parent clones (male and female) pertaining to each family were planted between families (Appendix 5.1). Unfortunately one of the replications was tampered with by unknown people who harvested cassava leaves and cut the tips of the plants, rendering the replication useless. Therefore, only two replications were considered for data collection. The F_1 progeny and their parents were harvested in September 2012 at 9 MAP months after planting. The trial

was harvested this early to assess the early bulking potential of the progeny. Earliness was one of the desirable attributes strongly identified by farmers in the PRA study.

5.2.3 Inoculation technique

The clones were artificially infested with CGM from a screenhouse-raised colony by attaching two infested leaves, which had at least twenty adult mites each, onto each of the two plants per clone in every replication (Habekub et al., 2000). The petiole of each detached infested leaf was lightly tied with a string to the petiole of the attached first and second fully expanded leaf from the top of each of the two plants per clone. The infested and uninfested leaves were placed with their abaxial surfaces in contact with each other. The main lobes were lightly held together with a plastic coated paper clip leaving the other leaf lobes freely open (Figure 5.1). The infester leaves and paper clips were removed after three days. Inoculation was repeated soon after the cold season in August. No fertilizers or herbicides were applied, but the trial was kept weed-free by frequent hand weeding.

Figure 5.1 Inoculation by attachment of CGM-infested leaves onto a test plant

5.2.4 Data collection

The cassava green mite population density (CGM PD) was estimated as suggested by Hahn et al. (1989), by counting adult mites on the third fully expanded leaf from the top on each plant. Leaf damage caused by CGM (CGM LD) was also assessed by estimating the proportion of leaf area (cm^2) covered by chlorotic spots on the same leaf. The CGM LD was scored in the warm dry season at 9 MAP and the scoring was based on a scale of 1-5, where: 1 = no obvious symptoms; 2 = moderate damage, no reduction in leaf size, scattered chlorotic spots on young leaves, 1-2 spots cm^{-2}; 3 = severe chlorotic symptoms, light reduction in leaf size, stunted shoot, 5-10 spots cm^{-2}; 4 = severe chlorotic symptoms and leaf size of young leaves severely reduced;

and 5 = tips of affected plants defoliated, resulting in a candle stick appearance of shoot tips. Plants with scores of 1 and 2 were considered to be resistant, whereas plants with scores of 3 to 5 were considered to be susceptible to CGM.

Each clone was scored for the following traits on a 1 to 3 scale: (i) the pubescence (Pbs) of the apical leaves; where: 1 = glabrous, 2 = moderately pubescent, and 3 = highly pubescent; (ii) size of shoot apices (TS), where: 1 = small, 2 = medium, and 3 = large; (iii) compactness of shoot apices (TC), where: 1 = loose, 2 = moderately compact, and 3 = compact; (iv) leaf longevity assessed by scoring for leaf retention (LR) and stay green (SG), where for LR: 1 = poor (<50% of the leaves retained), 2 = moderately good (50-74% of the leaves are retained), and 3 = very good (≥75% of the leaves retained); and for SG: 1 = poor (<50% of the leaves are live and green), 2 = moderately good (50-74% of the leaves are live and green), and 3 = very good (≥75% of the leaves are live and green).

The severity of CMD symptoms was scored based on a 1 to 5 scale as described by Banito et al. (2007), where: 1 = no symptoms of CMD; 2 = mild chlorotic pattern and slight distortion of only the base leaves; 3 = mosaic pattern on all leaves, leaf distortion; 4 = mosaic pattern on all leaves, leaf distortion and general reduction in leaf size; and 5 = leaves twisted/misshapen, and stunting of the whole plant.

Two plants per clone in each of the replications were uprooted for determination of (FSRY) and storage root dry mass percentage (SRDM%). Fresh mass of all the developed storage roots was recorded to estimate FSRY. The SRDM% was determined from a 150 g sub-sample of thinly sliced fresh chips, obtained from the bulk of storage roots of two plants per clone in each replication, which was then dried to a constant mass in a forced draught electric oven at 72°C. Using the formula indicated below, dry mass was then calculated and expressed as a percentage (Ceballos et al., 2012).

$$\text{SRDM \%} = \left(\frac{\text{Oven dry mass of sample}}{\text{150g fresh mass sample}}\right) \text{x } 100$$

The size of leaves was determined by measuring the length and width of the middle lobe according to Fukuda et al. (2010). Lobe length (LL) was measured from the point of intersection of leaf lobes to the apex of the middle lobe (Figure 5. 2). Leaf width (LW) was measured at the widest part of the middle lobe (Figure 5.3). The measurements of leaf size were taken on the fourth and fifth fully expanded leaves from the top on each of the two plants per clone in each replication. Plant growth habit was assessed by measuring plant height (PH) and stem diameter (StD), height to the first branching level (FBH), and number of branches (NBr). The PH was

measured on each of the two plants per clone using a graduated 3 m measuring stick, while StD at about 15 cm above soil level was recorded using digital vernier calipers. The FBH was measured from soil level to the topmost growing point of the main shoot. For branching type, the NBr were counted per plant, while a zero was recorded for non-branching clones

Figure 5.2 Measuring the length of the middle leaf lobe

Figure 5.3 Measuring the width of the middle leaf lobe

Harvest index (HI) was determined as the proportion of FSRY to whole-plant biomass yield. This was done by taking the mass of the stems, branches and leaves of harvested plants together in each plot. Storage roots were then weighed separately and HI was then calculated as:

$$HI = \left[\frac{\text{Mass of storage roots}}{\text{Mass of storage roots} + \text{above ground biomass}}\right]$$

5.2.5 Data analysis

Data from the clonal evaluation trial were analysed using residual maximum likelihood (REML) in Genstat 14 (Payne et al., 2011) at both family and individual progeny within family level. Families were considered to be fixed while replications were considered as random effects in the REML model. The general combining ability (GCA) effects and specific combining ability (SCA) effects were generated using the statistical software package DIAL 98 developed by Ukai Yasuo (Ahmad and Aurangzeb, 2003) specifically for the analysis of a full and half diallel tables. The relative importance of additive to non-additive gene action in the expression of the traits was determined from the ratio of the GCA SS to SCA SS (Shattuck et al., 1993). Pearson's phenotypic correlations between traits were also performed using Genstat 14 for the family means.

Estimating heterosis

Best-parent heterosis $H_{(BP)}$ was calculated for all the traits:

$$H_{(BP)}\ (\%) = \left[\frac{(\bar{X}_i F1 - \bar{X}BP)}{\bar{X}BP}\right] \times 100$$

where $\bar{X}_i F1$ = trait mean for the i^{th} F_1 progeny, $\bar{X}BP$ = trait mean for the best parent in the entire trial.

To identify high yielding F_1 progeny with good heterotic performances for FSRY and CGM resistance, genotypes that combined large positive $H_{(BP)}$ for FSRY with large negative $H_{(BP)}$ for CGM PD and CGM LD were identified (Tables 5.4). The identification was a four step process as follows:

i) Firstly, all F_1 progeny that had positive $H_{(BP)}$ for FSRY, regardless of its magnitude, were identified from the entire population of 300 F_1 progeny, and set aside to constitute the first subset.
ii) Secondly, F_1 progeny that had negative $H_{(BP)}$ for CGM LD were also identified from first subset and set aside to constitute the second subset.
iii) Thirdly, F_1 progeny with negative $H_{(BP)}$ for CGM PD were identified from the second subset and set aside to constitute the third subset.
iv) Finally, F_1 progeny with highest FSRY were selected from the third subset.

Estimating narrow-sense heritability

Narrow-sense heritability was estimated through the regression of the family mean of F_1 progeny on the mean of each pair of respective parents. The regression coefficient was taken to represent heritability in the narrow-sense for a given trait.

Participatory formulation of selection criteria

A total of 30 farmers were involved in the formulation of selection criteria for cassava. Using preference scoring farmers ranked cassava varietal attributes in their order of importance (Figure 5.3).

Figure 5.3 Farmers ranking desirable varietal attributes for formulation of a selection index for cassava clones at Mutanda research station, Zambia

A selection index (SI) was then formulated by assigning weights (ranks) to respective variables, (Becker, 1967; Ceballos et al., 2004) as follows:

$$SI: (X_1. \times W_1) + (X_2. \times W_2) + (X_3. \times W_3) + \ldots + (X_n. \times W_n)$$

Where: W_1, W_2, W_3,… W_n are the respective weights for each variable. To avoid the problems associated with differences in units among variables, the variables were standardized as follows:

$$X_i' = \left(\frac{X_i - \mu}{SD}\right)$$

where X_i' is the standardized value, X_i is the original value, μ is the mean of the population, and SD is the standard deviation for the variable analysed. Finally a selection index was formulated as follows:

$$PSI = (FSRY*8) + (SRDM*7) + \left[\frac{(CMD^{*}-5)+(CGM^{*}-5)}{2}\right] + (LR*3) + (SG*3),$$

Where: PSI = participatory selection index, FSRY = mean for fresh storage root yield; SRDM% = mean for storage root dry mass percentage; CMD = score for cassava mosaic disease severity; CGM = score for cassava green mite leaf damage; LR = score for leaf retention; SG = score for stay green. The index was used for selection of F_1 genotypes.

5.3 Results

Insufficient cuttings were obtained from the seedling stage plants in this study, despite having applied irrigation, to carry out multi-locational testing at the clonal stage. Therefore the study

was only conducted at one site. In some plots, plants died due to termite damage, leaving less than 30 full sibs per family in a replication. To get deal with this problem, harmonic mean instead of arithmetic mean for the families was used (Becker, 1967; Cach et al., 2005).

5.3.1 Combining ability mean squares

The GCA and SCA mean squares (MS) were significant (P<0.01) for CGM PD, CGM LD, TC, Pbs and LR (Table 5.1). The GCA and SCA MS were not significant for CMD severity, SGA, LLL, LLW, NBr, NSR, SRDM%, and FSRY (Table 5.1 and 5.2)

Ratios of GCA SS to SCA SS greater than unity were obtained for CGM PD, CGM LD, CMD severity, Pbs, LR, and NBr, while other traits had ratios less than unity (Table 5.1). The lowest ratio of 0.31 was obtained for NBr, followed by SRDM% and FSRY both of which had a ratio of 0.44.

Table 5.1 General combining ability and specific combining ability mean squares for cassava green mite density and associated leaf damage, cassava mosaic diseases severity, and leaf morphological traits of five cassava parents and their ten F_1 families evaluated in a 5 x 5 half diallel

Source of variation	Df	CGM PD			CGM LD		
		SS	MS	F	SS	MS	F
Rep	1	3.00	3.00	21.91	0.02	0.22	12.31
GCA	4	229.71	57.43	420.13**	1.04	0.26	142.30**
SCA	5	108.99	21.80	159.47**	0.72	0.14	79.49**
Error	9	1.23	0.14	21.93	0.72	0.00	47.79
Total	19	342.93	48.94	8.46	1.80	0.30	7.95
	Df	CMD Severity			TS		
		SS	MS	F	SS	MS	F
Rep	1	0.05	0.05	5.57	0.02	0.02	9.59
GCA	4	2.75	0.69	75.06	0.31	0.08	34.93**
SCA	5	2.01	0.40	43.87	0.59	0.12	53.26
Error	9	0.08	0.01	12.52	0.02	0.00	4.15
Total	19	4.89	0.41	3.52	0.94	1.01	26.34
	Df	TC			Pbs		
		SS	MS	F	SS	MS	F
Rep	1	0.012	0.012	48.15	0.06	0.06	7.01
GCA	4	0.278	0.070	278.65**	0.72	0.18	20.77**
SCA	5	0.395	0.079	317.01**	0.78	0.16	18.14**
Error	9	0.002	0.000	23.98	0.08	0.01	5.33
Total	19	0.688	0.760	10.57	1.64	0.07	2.34
	Df	LR			SG		
		SS	MS	F	SS	MS	F
Rep	1	0.0001	0.0001	0.89	0.073	0.073	0.67
GCA	4	0.6471	0.1618	1775.63**	0.272	0.068	0.62
SCA	5	0.6351	0.1270	1394.04**	0.447	0.089	0.82
Error	9	0.0008	0.0001	86.44	0.981	0.109	4.16
Total	19	1.2831	0.2763	32.12	1.773	0.075	0.79

CGM PD= cassava green mite population density; CGM LD = leaf damage due to CGM scored on a 1-5 scale where 1 = no symptoms, and 5 = very severe symptoms; CMD severity = the severity of cassava mosaic disease symptoms scored on a 1-5 scale, where 1 = no apparent symptoms, and 5 = very severe symptoms, TS = tip size scored on a 1-3 scale, where 1 = small, and 3 = large; TC = tip compactness scored on 1-3 scale, where 1 = loose, and 3 = compact; Pbs = leaf pubescence scored on a 1-3 scale, where 1 = glabrous, and 3 = highly pubescent; LR = leaf retention scored on a 1-3 scale, where 1 = lowest, and 3 = highest; SG = stay green; GCA = general combining ability; SCA = specific combining ability; SS = sum of squares; MS = mean square; F = F-probability for test of significance; *P<0.05; **P<0.01; ***P<0.001.

Table 5.2 General combining ability and specific combining ability mean squares for leaf lobe length and width, number of branches, number of storage roots, and storage root dry mass and fresh root yield of five cassava parents and their ten F_1 families evaluated in a 5 x 5 half-diallel

Source of variation	Df	LLL			LLW		
		SS	MS	F	SS	MS	F
Rep	1	0.090	0.090	0.34	33.592	33.592	1712.15
GCA	4	0.918	0.229	0.86	0.052	0.052	0.66
SCA	5	4.150	0.830	3.11	0.125	0.125	1.27
Error	9	2.401	0.267	20.91	0.177	0.177	1.58
Total	19	7.558	3.154	6.20	33.945	33.945	1.00
		NBr			NSR		
	Df	SS	MS	F	SS	MS	F
Rep	1	1.389	1.389	0.33	0.634	0.634	0.57
GCA	4	11.842	2.961	0.71	2.169	0.542	0.48
SCA	5	6.868	1.374	0.33	6.935	1.387	1.24
Error	9	37.360	4.151	0.02	10.071	1.119	8.51
Total	19	57.459	5.871	2.02	19.808	2.272	2.17
		SRDM (%)			FSRY		
	Df	SS	MS	F	SS	MS	F
Rep	1	0.42	0.42	0.06	5.481	5.481	0.86
GCA	4	40.79	10.20	1.49	42.638	10.660	1.67
SCA	5	92.91	18.58	2.72	54.461	10.892	1.71
Error	9	61.45	6.83		57.487	6.387	5.23
Total	19	195.57			160.067	4.159	0.90

LLL = leaf lobe length (cm) measured from the intersection of the middle lobe; LLW = leaf lobe width (cm) measured from the widest part of the middle lobe; NBr = number of branches; NSR = total number of storage roots per plant; SRDM% = storage root dry mass expressed as a percentage; FSRY = fresh storage root yield (t ha^{-1}); Df = degrees of freedom; SS = sums of squares; MS = mean square; F = level of significance of F-test; GCA = general combining ability; SCA = specific combining ability

5.3.2 General combining ability effects

Cassava green mite population density and leaf damage: Negative GCA effects for CGM LD were recorded for parents 4(2)1425, and I92/000. Although Mweru's GCA effect for CGM PD was positive, its GCA effect for CGM LD was desirably negative and small. Parents L9.304/147 and I92/0061 recorded high, but undesirably positive, GCA effects for CGM PD. Parents L9.304/147 and I92/0061 also had positive GCA effects for CGM LD.

Cassava mosaic disease severity: Positive GCA effects for CMD severity were obtained for parents L9.304/147 and I92/0061, while the other three parents namely Mweru, 4(2)1425, and I92/000 had negative GCA effects (Table 5.3).

Table 5.3 Means and estimates of general combining ability effects for cassava green mite density and leaf damage, and cassava mosaic disease severity of five cassava parents evaluated in a 5 x 5 half-diallel

Character	Genotype	Mean	GCA	GCA SE
CGM PD	Mweru	11.28	0.19	0.16
	4(2)1425	7.78	-4.86	0.16
	L9.304/147	15.50	2.90	0.16
	I92/0061	11.92	2.40	0.16
	I92/000	10.67	-0.63	0.16
	$LSD_{(0.05)}$	**0.88**		
CGM LD	Mweru	1.94	-0.04	0.02
	4(2)1425	1.81	-0.24	0.02
	L9.304/147	2.30	0.11	0.02
	I92/0061	1.98	0.30	0.02
	I92/000	1.90	-0.10	0.02
	$LSD_{(0.05)}$	**0.10**		
CMD severity	Mweru	1.82	-0.28	0.16
	4(2)1425	1.80	-0.04	0.16
	L9.304/147	2.10	0.17	0.16
	I92/0061	2.39	0.49	0.16
	I92/000	1.77	-0.35	0.16
	$LSD_{(0.05)}$	**0.09**		

CGM PD = population counts of cassava green mites per leaf; CGM LD = cassava green mite leaf damage scored on a 1–5 scale, where 1= no damage, and 5 = very severe damage; CMD severity = score for the degree of cassava mosaic disease infection scored on a 1-5 scale, where 1 = no symptoms, and 5 = very severe; GCA = general combining ability effects; SE = standard error; $LSD_{(0.05)}$ = least significant difference, $P<0.05$.

Tip size: Parents I92/0061 and I92/000 had positive GCA effects for TS, while parents Mweru, 4(2)1425, and L9.304/147 had negative GCA effects for TS (Table 5.4). The smallest TS was recorded by L9.304/147 with a mean of 1.51 ($P<0.01$), while I92/0061 had significantly ($P<0.01$) the largest TS with a mean score of 1.92.

Tip compactness: As for TS, parents I92/0061 and I92/000 had positive GCA effects for TC, while Mweru, 4(2)1425, and L9.304/147 had negative GCA effects for the trait. The parent Mweru had significantly ($P<0.05$) the smallest TC of 1.65.

Leaf pubescence: Positive but small GCA effects for Pbs were recorded for parents Mweru, 4(2)1425, and I92/000. On the other hand, parents L9.304/147 and I92/000 had negative GCA effects for the trait (Table 5.4). The most pubescent parent was 4(2)1425 (2.33) followed by Mweru (2.01).

Leaf retention: Mweru, 4(2)1425, and I92/0061 had positive GCA effects for LR while negative GCA effects were recorded for L9.304/147 and I92/000 (Table 5.4).

Table 5.4 Means and estimates of general combining ability effects for leaf retention and plant shoot tip characteristics of five cassava parents evaluated in a 5 x 5 half-diallel

Character	Genotype	Mean	GCA	GCA SE
TS	Mweru	1.74	-0.003	0.018
	4(2)1425	1.62	-0.060	0.018
	L9.304/147	1.51	-0.137	0.018
	I92/0061	1.92	0.173	0.018
	I92/000	1.76	0.023	0.018
	$LSD_{(0.05)}$	0.04		
TC	Mweru	1.65	-0.056	0.006
	4(2)1425	1.69	-0.006	0.006
	L9.304/147	1.75	-0.123	0.006
	I92/0061	1.72	0.167	0.006
	I92/000	1.70	0.017	0.006
	$LSD_{(0.05)}$	0.03		
Pbs	Mweru	2.01	0.190	0.032
	4(2)1425	2.33	0.130	0.032
	L9.304/147	1.74	-0.230	0.032
	I92/0061	1.88	0.010	0.032
	I92/000	1.78	0.100	0.032
	$LSD_{(0.05)}$	0.07		
LR	Mweru	1.94	0.177	0.003
	4(2)1425	2.15	0.134	0.003
	L9.304/147	1.74	-0.203	0.003
	I92/0061	1.87	0.027	0.003
	I92/000	1.71	0.126	0.003
	$LSD_{(0.05)}$	0.02		

TS = tip size scored on a 1-3 scale, where 1 = small, and 3 = large; TC = tip compactness scored on a 1-3 scale, where 1 = loose, and 3 = compact; Pbs = leaf pubescence scored on a 1-3 scale, where 1 = glabrous, and 3 = highly pubescent; LR = leaf retention scored on a 1-3 scale, where 1 = lowest, and 3 = highest; GCA = general combining ability; SE = standard error; $LSD_{(0.05)}$ = least significant difference, $P<0.05$.

5.3.3 Specific combining ability effects

Cassava green mite population density: Among the 10 families, Mweru x L9.304/147, 4(2)1425 x L9.304/147, and 4(2)1425 x I92/000 had the lowest mean CGM PD of 6.60, 4.58, and 8.58, respectively (Table 5.5). Families which had negative SCA effects for the trait were Mweru x I92/0061, Mweru x I92/000, 4(2)01425 x l9.304/147, L9.304/147 x I92/000, and I92/0061 x I92/000. All the families which had negative SCA effects also recorded significantly lower number of mites relative to the family L9.304/147 x I92/0061 which recorded the highest number (20.1) of mites per leaf (Table 5.5).

Cassava green mite leaf damage: Five families namely 4(2)1425 x L9.304/147, Mweru x L9.304/147, 4(2)1425 x I92/0061, Mweru x I92/0061, and L9.304/147 x I92/000 scored significantly ($P<0.05$) lower levels of CGM LD than L9.304/147 x I92/0061 which had the highest CGM LD with a mean of 2.73 (Table 5.5). Six families had negative SCA effects for the trait, namely Mweru x I92/0061, Mweru x I92/000, 4(2)1425 x L9.304/147, L9.304/147 x I92/000, and I92/0061 x I92/000.

Cassava mosaic disease severity: Four of the families, namely Mweru x I92/000, Mweru x 4(2)1425, 4(2)1425 x L9.304/147, and L9.304/147 x I92/000 had negative SCA effects for CMD severity. All the families that had negative SCA effects, correspondingly expressed low

symptoms of the disease as indicated by the lower mean severity scores (Table 5.5). The families Mweru x I92/000, 4(2)1425 x L9.304/147, and L9.304/147 x I92/000 exhibited combined resistance to CMD and CGM with negative SCA effects for CGM PD, CGM LD, and CMD severity.

Table 5.5 Specific combining ability effects for cassava green mite density and leaf damage, cassava mosaic disease severity, of ten F_1 cassava families from a 5 x 5 half-diallel

Family	CGM PD		CGM LD		CMD severity	
	Mean	SCA effects	Mean	SCA effects	Mean	SCA Effects
Mweru x L9.304/147	6.60	0.16	1.75	0.07	1.80	0.09
Mweru x I92/0061	12.10	-2.15	1.82	-0.22	2.48	0.51
Mweru x I92/000	11.20	-2.56	2.05	-0.18	1.64	-0.39
Mweru x 4(2)1425	15.20	4.55	2.15	0.33	1.35	-0.54
4(2)1425 x I92/0061	10.20	1.00	1.80	-0.03	1.77	0.08
4(2)1425 x I92/000	8.58	-0.09	2.03	0.01	2.55	0.25
4(2)1425 x L9.304/147	4.58	-1.06	1.58	-0.04	1.87	-0.06
L9.304/147 x I92/0061	20.10	3.65	2.73	0.35	2.93	0.22
L9.304/147 x I92/000	10.90	-2.50	1.87	-0.11	1.48	-0.37
I92/0061 x I92/000	11.90	-0.99	1.98	-0.18	2.37	0.20
Mean	11.10		1.98		2.02	
SED	0.37		0.01		0.10	
SCA SE		0.30		0.02		0.04

CGM PD = population counts of cassava green mites per leaf; CGM LD = cassava green mite leaf damage scored on a 1–5 scale, where 1 = no damage, and 5 = very severe damage; CMD severity = score for the degree of cassava mosaic disease infection scored on a scale of 1-5, where 1 = no symptoms, and 5 = very severe; SCA = specific combining ability; SE = standard error; SED = standard error of difference.

Tip size: Four of the families, Mweru x I92/0061, Mweru x I92/000, L9.304/147 x I92/000, and 4(2)1425 x L9.304/147 had positive SCA effects for TS. Of these families, Mweru x I92/000 recorded the largest mean scores for the trait (Table 5.6). However, negative SCA effects were recorded for 4(2)1425 x I92/0061, which also had the smallest mean TS score.

Tip compactness: All the families except Mweru x 4(2)1425, L9.304/147 x I92/000, and I92/0061 x I92/000, had positive SCA effects for TC. The family 4(2)1425 x I92/0061 had the largest TS mean score with a positive SCA effect, while Mweru x 4(2)1425 had the smallest TS mean score with a negative SCA effect for the trait (Table 5.6).

Leaf pubescence: Both positive and negative SCA effects were recorded for Pbs by the families. Positive SCA effects were recorded for families Mweru x L9.304/147, Mweru x 4(2)1425, and 4(2)1425 x I92/000, L9.304/147 x I92/000, and I92/0061 x and I92/000. Mweru x L9.304/147 had the largest mean Pbs score, followed by 4(2)1425 x I92/000, and Mweru x 4(2)1425, while lowest Pbs was scored by two of the families namely 4(2)1425 x L9.304/147 (Table 5.6).

Leaf retention: Four families, namely Mweru x L9.304/147, Mweru x 4(2)1425, 4(2)1425 x I92/000, and L9.304/147 x I92/000 had positive SCA effects for LR. The first three of these families also had correspondingly large mean scores for LR (Table 5.6).

Table 5.6 Mean and estimates of specific combining ability for tip size and compactness, leaf pubescence and leaf retention of ten F_1 cassava families evaluated in a 5 x 5 half-diallel

Family	TS		TC		Pbs		LR	
	Mean	SCA Effects	Mean	SCA effects	Mean	SCA effects	Mean	SCA effects
Mweru x L9.304/147	1.62	-0.07	1.67	0.04	2.33	0.11	2.15	0.04
Mweru x I92/0061	1.67	0.06	1.56	0.04	1.74	-0.08	1.74	-0.04
Mweru x I92/000	2.12	0.20	1.89	0.09	1.87	-0.18	1.86	-0.14
Mweru x 4(2)1425	1.57	-0.20	1.48	-0.17	2.10	0.15	2.00	0.15
4(2)1425 x I92/0061	1.34	-0.21	1.32	0.23	1.74	-0.01	1.73	-0.01
4(2)1425 x I92/000	1.97	0.11	1.97	0.11	2.29	0.30	2.27	0.30
4(2)1425 x L9.304/147	1.88	0.17	1.78	0.08	1.49	-0.40	1.47	-0.34
L9.304/147 x I92/0061	1.69	-0.10	1.68	0.05	1.49	-0.14	1.47	-0.16
L9.304/147 x I92/000	1.88	0.25	1.82	-0.24	1.74	0.23	1.67	0.20
I92/0061 x I92/000	1.72	-0.22	1.72	-0.15	1.78	0.02	1.70	-0.01
SED	0.05		0.02		0.08		0.01	
SCA SE		1.75		1.69		1.85		0.01

TS = tip size scored on a 1-3 scale, where 1 = small, and 3 = large;TC = tip compactness scored on a 1-3 scale, where 1 = loose, and 3 = compact; Pbs = leaf pubescence scored on a 1-3 scale, where 1 = glabrous, and 3 = highly pubescent; LR = leaf retention scored on a 1-3 scale, where 1 = low, and 3 = high; Mean = trait mean for respective families; SCA = specific combining ability; SE = standard error; SED = standard error of difference.

5.3.4 Phenotypic correlation between cassava green mite resistance traits and shoot morphological and storage root yield traits

A significant, negative correlation was recorded between CGM PD and LR (r =-0.790, P<0.01) and a significant, negative correlation between CGM LD and LR (r = -0.806, P<0.01) (Table 5.7). There was a significant (P<0.05), negative correlation (r = -0.717) between CMD severity and LR. However, a significant (P<0.05) but positive correlation (r = 0.714) was recorded between NBr and CGM LD. Similarly, NBr was positively but non-significantly correlated with CGM PD and CMD severity (r = 0.558 and r = 0.502, respectively). A negative but non-significant correlation (r = -0.502) was recorded between CGM LD and FSRY. CGM PD was significantly and negatively correlated with FSRY (r = -0.657, StD (r =-0.625), TS (r =-0.625), and Pbs (r =-0.735).

The CGM LD was significantly, negatively correlated with a number of other traits such as LW (r = -0.677, P<0.05), LL (r = -0.742, P<0.05), StD (-0.853, P<0.01), PH (r = -0.650, P<0.05), TC (r = -0.846, P<0.01), SGA (r = -0.764, P<0.05), and TS (r = -0.843, P<0.01) in addition to LR(r = -0.806, P<0.01). The CGM LD also had a negative, though non-significant, correlation with FSRY (r = -0.502, P>0.05) and Pbs (r = -0.437, P>0.05). A significant (P<0.05) negative correlation (r = -0.625) was recorded between CMD severity and FSRY (Table 5.7).

Table 5.7 Phenotypic correlation coefficients for cassava green mite population density and associated leaf damage, cassava mosaic disease severity, leaf morphological, and other agronomic traits

Trait	CGM PD	CGM LD	CMD severity
TS	-0.625*	-0.843***	-0.523
TC	-0.596	-0.846**	-0.729*
Pbs	-0.735*	-0.437	-0.736*
LL	-0.551	-0.742*	-0.526
LW	-0.545	-0.677*	-0.678*
LR	-0.790**	-0.806**	-0.717*
SG	-0.311	-0.764*	-0.681*
NBr	0.558	0.714*	0.502
FBH	-0.779**	-0.454	-0.542
PH	-0.410	-0.650*	-0.250
StD	-0.751*	-0.853**	-0.752*
NSR	0.338	0.480	0.198
FSRY	-0.657*	-0.502	-0.623*

CGM PD = population density of cassava green mite; CGM LD = leaf damage due to cassava green mite scored on a 1-5 scale, where 1 = no symptoms, and 5 = very severe symptoms; CMD severity = the severity of cassava mosaic disease symptoms scored on a 1-5 scale, where 1 = no apparent symptoms, and 5 = very severe symptoms; TS = tip size scored on a 1-3 scale, where 1 = small, and 3 = large; TC = tip compactness scored on a 1-3 scale, where 1 = loose, and 3 = compact; Pbs = leaf pubescence scored on a 1-3 scale, where 1 = glabrous, and 3 = highly pubescent; LL = leaf lobe length (cm) measured from the intersection of the middle lobe; LW = leaf lobe width (cm) measured from the widest part of the middle lobe; LR = leaf retention scored on a 1-3 scale, where 1 = lowest, and 3 = highest; SG = ability of leaves to stay green scored on a 1-3 scale, where 1 = lowest, and 3 = highest; NBr = number of branches; FBH = height to first branching level (cm); PH = total plant height (m); StD = stem diameter; NSR = total number of storage roots per plant; FSRY = fresh storage root yield (t ha^{-1})

5.3.5 Estimates of heterosis

All the families exhibited negative $H_{(BP)}$ for CGM PD and CGM LD, but none of the families had positive $H_{(BP)}$ for FSRY, StD, NBr, and PH (Appendix 5.2). However, 24 high yielding F_1 progeny which combined desirable heterotic performance for FSRY and CGM resistance were identified. Seven of such progeny combined negative $H_{(BP)}$ for CGM PD, CGM LD, and CMD severity, with positive $H_{(BP)}$ for FSRY and SRDM% (Table 5.8). These were progeny No. 4 from Mweru x 4(2)1425, progeny No. 9 from Mweru x L.304/147, progeny No. 12 and progeny No. 14 both from Mweru x I92/000, progeny No. 17 from 4(2)1425 x L9.304/147, progeny No. 18 from 4(2)01425 x I92/0061, and progeny No. 24 from L9.304/147 x I92/000. Apart from progeny No.17 and progeny No. 18 which had positive $H_{(BP)}$ for LR and LL, respectively, all the F_1 progeny had negative $H_{(BP)}$ for shoot morphological traits and NBr (Table 5.8). Only five out of 24 high yield F_1 progeny had positive $H_{(BP)}$ for Pbs, but all of them had positive $H_{(BP)}$ for CMD.

Table 5.8 Twenty four top performing F_1 progeny combining positive heterosis for storage root yield with negative heterosis for leaf damage due to cassava green mite based on the best parent in the trial

		Best parent heterosis																
Progeny No.	**Pedigree**	**CGM PD**	**CGM LD**	**CMD Severity**	**TS**	**TC**	**Pbs**	**LL**	**LW**	**LR**	**SG**	**NBr**	**FBH**	**PH**	**StD**	**NSR**	**FSRY**	**SRDM%**
1	Mweru x 4(2)1425	-37.6	-69.0	23.5	-20.0	-16.7	7.1	21.1	-13.3	-13.0	8.7	-30.0	-35.0	-11.6	10.1	-21.4	16.3	6.3
2	Mweru x 4(2)1425	-12.6	-31.7	-40.5	-60.0	-54.5	-64.3	-5.3	-6.7	8.7	1.4	5.0	-66.3	-27.9	-21.3	-64.3	7.9	-10.9
3	Mweru x 4(2)1425	-56.3	-93.6	25.7	-60.0	-54.5	-28.6	-15.8	-26.7	-5.8	23.2	-75.0	-10.0	-5.6	-20.9	7.1	9.3	14.1
4	Mweru x 4(2)1425	-50.1	-75.4	-0.8	-60.0	-54.5	-64.3	-10.5	-13.3	-20.3	-42.0	-70.0	-45.6	-25.2	-9.0	-21.4	3.7	10.9
5	Mweru x 4(2)1425	-50.1	-86.3	32.3	-20.0	-9.1	7.1	-10.5	-26.7	8.7	8.7	-70.0	-18.8	-21.9	-17.0	-14.3	7.0	-9.4
6	Mweru x L9.304/147	-62.5	-100.0	58.7	-20.0	-9.1	-28.6	-15.8	-23.3	-5.8	1.4	-50.0	-56.3	-40.3	-22.8	14.3	17.2	26.0
7	Mweru x L9.304/147	-37.6	-49.9	19.0	20.0	36.4	7.1	-5.3	-3.3	1.4	8.7	40.0	-17.5	-5.1	-26.0	-57.1	11.2	1.6
8	Mweru x L9.304/147	-37.6	-70.9	71.9	-20.0	-9.1	-28.6	-10.5	-3.3	-13.0	-5.8	-55.0	-56.9	-29.5	-11.6	28.6	16.3	26.6
9	Mweru x L9.304/147	-18.9	-40.8	-40.5	-60.0	-54.5	-28.6	-15.8	-26.7	-27.5	8.7	-30.0	-45.0	-2.9	-33.2	-64.3	14.4	18.8
10	Mweru x I92/0061	-50.1	-86.3	45.5	-20.0	-9.1	-64.3	10.5	-16.7	1.4	8.7	-30.0	-19.4	-4.6	-11.4	0.0	23.3	20.3
11	Mweru x I92/0061	-43.8	-72.7	32.3	20.0	36.4	-64.3	31.6	6.7	-27.5	1.4	-35.0	-21.9	-10.0	-17.6	-42.9	13.5	-17.2
12	Mweru x I92/000	-31.3	-29.9	-14.0	-20.0	-9.1	-28.6	-10.5	-11.7	-13.0	8.7	-40.0	-36.3	8.5	-4.6	-64.3	7.0	12.5
13	Mweru x I92/000	-12.6	-54.5	25.7	-60.0	-54.5	-28.6	-5.3	-23.3	1.4	16.0	-30.0	-58.8	-4.0	10.1	7.1	7.9	-10.9
14	Mweru x I92/000	-43.8	-71.8	-33.8	-60.0	-54.5	-64.3	-5.3	0.0	-5.8	1.4	-35.0	-28.1	-12.1	-8.5	-57.1	7.4	9.4
15	4(2)1425 x L9.304/147	-37.6	-63.6	12.4	-20.0	-9.1	7.1	21.1	-1.7	23.2	8.7	-70.0	-44.4	-15.9	-12.3	-35.7	20.0	-21.9
16	4(2)1425 x L9.304/147	-62.5	-100.0	-14.0	-60.0	-54.5	-64.3	-10.5	-6.7	8.7	8.7	-55.0	-28.1	5.7	-17.7	-35.7	15.3	-3.1
17	4(2)1425 x L9.304/147	-62.5	-100.0	-25.0	-60.0	-47.0	-28.6	-5.3	-13.3	23.2	8.7	-50.0	-50.6	-1.3	-8.0	-50.0	15.7	7.8
18	4(2)1425 x I92/0061	-0.1	-39.9	-27.3	-20.0	-9.1	-28.6	15.8	0.0	-5.8	23.2	-60.0	-40.6	-7.8	-19.0	-78.6	48.0	18.7
19	4(2)1425 x I92/000	-56.3	-96.4	19.0	20.0	36.4	-64.3	5.3	3.3	23.2	23.2	-35.0	-42.5	-25.2	1.7	-57.1	10.7	20.1
20	4(2)1425 x I92/000	-56.3	-81.8	52.1	-20.0	-9.1	-64.3	15.8	0.0	1.4	8.7	70.0	-43.8	-37.6	8.4	7.1	10.7	-0.8
21	4(2)1425 x I92/000	-18.9	-45.4	14.6	-60.0	-47.0	-64.3	0.0	8.3	1.4	16.0	-65.0	7.5	11.7	-19.6	-7.1	19.1	9.4
22	L9.304/147 x I92/000	-62.5	-100.0	34.5	-60.0	-1.5	-64.3	-10.5	-50.0	-13.0	-13.0	15.0	-11.3	-8.9	-15.7	0.0	9.8	2.1
23	L9.304/147 x I92/000	-37.6	-72.7	14.6	-20.0	-1.5	7.1	0.0	-33.3	-20.3	8.7	-55.0	-30.0	-10.0	-28.5	-35.7	15.3	10.4
24	L9.304/147 x I92/000	-62.5	-95.4	-11.8	-60.0	-1.5	-64.3	0.0	-25.0	-20.3	-20.3	-60.0	-36.3	-5.6	-18.6	-50.0	9.3	21.3

CGM PD = population counts of cassava green mites per leaf; CGM LD = leaf damage due to cassava green mite scored on 1-5 scale where 1 = no symptoms, and 5 = very severe symptoms; CMD severity = the severity of cassava mosaic disease symptoms scored on 1-5 scale, where 1 = no apparent symptoms, and 5 = very severe symptom; TS = tip size scored on 1-3 scale, where 1 = small, and 3 = large; TC = tip compactness scored on 1-3 scale, where 1 = loose, and 3 = compact; Pbs = leaf pubescence scored on 1-3 scale, where 1 = glabrous, and 3 = highly pubescent;LL = leaf lobe length (cm) measured from the intersection of the middle lobe; LW = leaf lobe width (cm) measured from the widest part of the middle lobe; LR = leaf retention scored on 1-3 scale, where 1 = lowest, and 3 = highest; SG = ability of leaves to stay green scored on 1-3 scale, where 1= lowest, and 3 = highest; NBr = number of branches; FBH = height to first branching level (cm); PH = total plant height (cm); StD = stem diameter; NSR = total number of storage roots per plant; FSRY = fresh storage root yield (t ha^{-1}); SRDM% = storage root dry mass expressed as a percentage.

5.3.6 Heritability estimates

Large heritability estimates were obtained for CGM PD (h^2 = 71%), CGM LD (h^2 = 86%), LR (h^2 = 80%) and TC (h^2 = 88%). Of all the traits, TS had the largest narrow sense heritability of 91%, while low heritability estimates were obtained for FSRY and SRDM% (Figure 5.4).

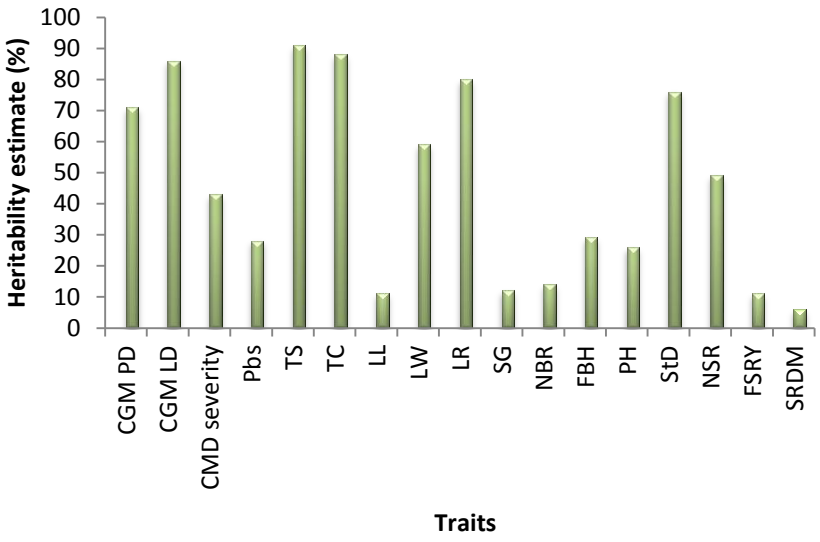

Figure 5.4 Narrow sense heritability estimates for cassava green mite and cassava mosaic disease resistance and other plant morphological traits

5.3.7 Selection of F_1 progeny based on farmer preferred traits

A total of 30 F_1 progeny were selected using the PSI (Table 5.9) at the predetermined 10% selection intensity. Of these progeny (Table 5.9), progeny No. 3 and progeny No. 6 both of which resulted from 4(2)1425 x L9.304/147 had no CGM LD. Similarly, no CMD LD was recorded by progeny No. 10 from Mweru x L9.304/147. This high resistance was also combined with high FSRY and SRDM% in the three genotypes. Progeny No. 5 from Mweru x I92/0061 had the highest yield of 26.5 t ha^{-1} with SRDM of 38.5%. Progeny No. 22 from L9.304/147 x I92/000, recorded the highest SRDM% (49.7%) but it had just slightly above average FSRY (17.6 t ha^{-1}). Similarly, progeny No 18 from L9.304 x I92/000, had second highest SRDM% (47.3%), but recorded the least FSRY (16.8 t ha^{-1}) among the selected genotypes. All the selected genotypes were early-bulking. They all recorded greater than 16 t ha^{-1} FSRY at 9 MAP, with progeny No. 2 from 4(2)1425 x L9.304/147 producing the highest FSRY of 31.8 t ha^{-1}, which is equivalent to the average yields currently obtained from improved genotypes at 24 MAP in Zambia.

Table 5.9 Overall mean performances of the 30 best F_1 progeny selected by the farmer participatory-formulated selection index, with respect to cassava green mite population density and associated leaf damage, cassava mosaic disease severity, shoot morphological traits, fresh storage root yield and storage root dry mass percentage

Progeny No	Progenitor	CGM PD	CGM LD	CMD severity	Pbs	TS	TC	LR	SG	FSRY	SRDM%
1	4(2)1425 x L9.304/147	26.5	3.2	1.9	2.2	1.0	1.2	2.5	2.7	17.3	34.5
2	4(2)1425 x I92/0061	11.0	2.7	1.8	2.0	2.0	2.0	2.2	2.8	31.8	38.0
3	4(2)1425 x L9.304/147	0.0	1.0	2.2	2.2	1.0	1.0	2.5	2.5	24.8	31.0
4	I92/0061 x L9.304/147	8.3	2.3	2.7	1.4	3.0	3.0	2.8	2.5	21.4	40.3
5	Mweru x I92/0061	2.5	1.3	3.7	2.0	2.0	2.0	2.3	2.5	26.5	38.5
6	4(2)1425 x L9.304/147	0.0	1.0	1.9	1.8	1.0	1.2	2.8	2.5	24.9	34.5
7	4(2)1425 x I92/000	3.3	1.2	3.8	1.8	2.0	2.0	2.3	2.5	23.8	31.8
8	4(2)1425 x I92/000	10.0	2.2	2.9	1.8	1.0	1.2	2.3	2.7	25.6	35.0
9	4(2)1425 x L9.304/147	2.5	1.3	4.3	1.5	2.0	2.0	2.3	2.3	21.0	40.0
10	Mweru x L9.304/147	0.0	1.0	4.0	1.6	2.0	2.0	2.2	2.3	25.2	40.3
11	Mweru x I92/000	5.2	1.5	1.7	1.3	1.0	1.0	2.2	2.3	23.1	35.0
12	L9.304/147 x I92/000	12.5	1.8	2.8	1.7	2.0	2.0	2.2	1.7	18.9	42.3
13	Mweru x L9.304/147	15.2	2.5	3.2	2.2	1.0	1.0	2.2	2.3	19.4	36.0
14	Mweru x L9.304/147	5.3	1.7	4.3	1.7	2.0	2.0	2.0	2.2	25.0	40.5
15	Mweru x4(2)1425	1.2	1.2	3.2	2.0	1.0	1.0	2.2	2.8	23.5	36.5
16	Mweru x L9.304/147	10.8	2.2	1.5	2.0	1.0	1.0	1.7	2.5	24.6	38.0
17	I92/0061 x L9.304/147	9.7	2.0	1.2	2.3	1.0	1.2	2.5	2.0	19.2	41.0
18	L9.304/147 x I92/000	13.7	2.3	3.5	1.8	2.0	1.0	2.2	2.2	16.8	47.3
19	Mweru x4(2)1425	5.7	1.7	3.1	1.4	2.0	1.8	2.0	2.5	25.0	34.0
20	4(2)1425 x L9.304/147	9.5	2.0	4.2	1.5	2.0	2.0	2.7	2.8	19.4	34.5
21	L9.304/147 x I92/000	8.2	1.7	2.7	1.7	2.0	3.0	2.5	2.2	19.6	37.3
22	L9.304/147 x I92/000	6.7	1.5	2.7	1.6	1.0	1.0	2.2	2.2	17.6	49.7
23	4(2)1425 x L9.304/147	5.0	1.7	2.9	1.9	2.0	2.2	1.8	2.5	24.8	35.3
24	4(2)1425 x L9.304/147	6.5	1.5	3.6	1.7	1.0	1.2	2.3	2.5	19.4	32.0
25	I92/0061 x L9.304/147	16.7	2.7	3.3	2.0	3.0	3.0	2.5	2.7	19.4	38.2
26	4(2)1425 x I92/0061	13.3	2.3	2.0	1.6	2.0	2.0	2.5	2.3	19.9	38.3
27	4(2)1425 x L9.304/147	6.7	1.7	2.8	2.0	2.0	2.0	2.8	2.5	25.8	25.0
28	L9.304/147 x I92/000	2.5	1.3	4.7	1.8	3.0	3.0	2.0	2.2	20.6	38.0
29	Mweru x I92/000	14.3	2.2	2.2	1.8	2.0	2.0	2.3	2.7	21.3	30.0
30	4(2)1425 x I92/000	0.7	1.2	3.0	1.9	3.0	3.0	2.8	2.8	23.8	38.4
Checks											
Mweru		11.3	1.9	1.8	2.0	1.7	1.6	1.7	2.0	15.5	28.0
4(2)1425		7.8	1.8	1.8	2.3	1.6	1.7	2.2	2.0	21.7	19.0
L9.304/147		15.5	2.3	2.1	1.7	1.5	1.8	1.7	2.3	15.2	23.0
I92/0061		11.9	2.0	2.4	1.9	1.9	1.7	1.9	1.4	15.6	28.0
I92/000		10.6	1.9	1.8	1.8	1.8	1.7	1.7	1.8	18.8	26.0
Maximum		37.5	3.7	6.2	121.0	3.0	3.0	2.8	2.8	31.8	49.7
Minimum		0.0	1.0	1.0	10.5	1.0	1.0	1.0	1.2	9.0	22.0
Average		8.5	1.9	2.8	52.4	1.7	1.7	1.9	2.1	16.6	34.2
LSD(0.05)		1.3	0.1	0.1	0.1	0.1	0.1	0.4	0.5	3.9	3.3
CV(%)		18.8	9.9	21.8	3.6	7.9	10.2	36.4	38.6	73.3	15.6

CGM PD = population counts of cassava green mites per leaf; CGM LD = leaf damage due to cassava green mite scored on 1-5 scale where 1 = no symptoms, and 5 = very severe symptoms; CMD severity = the severity of cassava mosaic disease symptoms scored on 1-5 scale, where 1 = no apparent symptoms, and 5 = very severe symptoms, TS = tip size scored on 1-3 scale, where 1 = small, and 3 = large; TC = tip compactness scored on 1-3 scale, where 1 = loose, and 3 = compact; Pbs = leaf pubescence scored on 1-3 scale, where 1 = glabrous, and 3 = highly pubescent; LR = leaf retention scored on 1-3 scale, where 1 = lowest, and 3 = highest; SG = ability of leaves to stay green scored on 1-3 scale, where 1= lowest, and 3 = highest; FSRY = fresh storage root yield (t ha^{-1}); SRDM% = storage root dry mass expressed as a percentage; $LSD_{(0.05)}$ = least significant difference, $P<0.05$; CV% = Coefficient of variation percentage.

5.4 Discussion and conclusions

The current study provides important information about the role of various plant morphological traits as indirect defense mechanisms against CGM and the potential for improving them through plant breeding is evident. The study indicated that both GCA and SCA effects were significant for CGM PD and CGM LD, and for the various plant morphological traits that were measured, suggesting that both additive and non-additive genetic effects play a role in the expression of these traits. The predominance of GCA SS over SCA SS for CGM LD, CGM PD, TS, TC, Pbs, and LR indicated that additive gene action is the major determinant of the expression of these traits. These findings are consistent with those of Calle et al. (2005), Jaramillo et al. (2005), and Perez et al. (2005) who reported on the greater importance of GCA effects relative to SCA effects for CGM and whiteflies (*Aleurotrachelus socialis* Bondar) resistance. The predominance of GCA effects i.e. additive gene action improves the inheritance of these traits in the sexual generation of a breeding programme (Ceballos et al., 2004; Perez et al., 2005; Mhike et al., 2011).

In breeding to improve the resistance of cassava to CGM, breeders select genotypes that are least attractive to mites (lowest CMD PD) and exhibit low level of damage (lowest CGM LD). Therefore, for traits that are measured with low scores in this manner, negative SCA effects in the families are desirable. The best families for resistance against CGM were identified as 4(2)1425 x L9.304/147 and Mweru x L9.304/147. These families had negative SCA effects for CGM PD and CGM LD, and had one parent L9.304/147 in common which had positive but large GCA for CGM PD, while the other parents, 4(2)1425 and Mweru, in the respective families had negative GCA effects for the two traits. This indicates that it is possible to obtain families with high negative SCA effects for CGM PD from crossing any combination of parents with large positive and negative GCA effects for the trait. The current results indicate that it is possible to select parents for CGM resistance breeding based on their *per se* performances (Banziger and Paterson, 1992).

Identification of F_1 progeny which have good level of resistance to insect pests and mites requires the imposition of high selection pressures under field conditions. The 'leaf attachment' method for artificial infestation used in this study proved to be not only cost-effective but also technically efficient. The method boosted natural population pest levels and maintained adequate selection pressure that revealed differences among genotypes. Unlike the use of clip cages (Crafts-Brandner and Chu, 1999), the 'leaf attachment' method does not seem to affect the microenvironment of the leaf and consequently its physiology. Crafts-Brandner and Chu (1999) observed a significant rapid increase in chlorophyll content and temperature, and decreased incident radiation on leaves in clip cages within 24 hrs.

Progeny Nos 3, 6, and 10, exhibited high resistance to CGM which was also combined with high FSRY and SRDM% suggesting that improving resistance to CGM would result in increased yield and dry mass of cassava storage roots. However, the study also shows that breeding efforts to improve SRDM% has a limit which varies with genotypes. All the selected genotypes were early-bulking, indicating the positive contribution of the study to improvement of cassava genotypes for farmer desired traits.

Previous studies have shown that Pbs is a desirable trait that helps to reduce CGM populations in cassava (Hahn et al., 1980, 1989; Raji et al., 2008). Corroborating these reports, the current study recorded negative correlations of CGM PD and CMD with Pbs. This has been attributed to the leaf hairs limiting the movement of CGM and whitefly on leaves, which in turn results in reduced reproductive capacity of these pests and the associated leaf damage. On the other hand, Pbs, especially of immature leaves and shoot apices, has been reported to provide suitable habitat for *T. aripo*, a phytoseiid predatory mite. In two experiments, Onzo et al. (2012) recorded 480 predatory mites (*T. aripo*) on pubescent apices of cassava plants as opposed to 280 mites on glabrous apices, confirming that *T. aripo* is attracted mainly to apices of the pubescent cultivars in presence of the prey. These authors have also reported that pubescent cultivars produce a certain odour that attracts *T. aripo* to the shoot apices of cassava. This predatory mite has proved to be the most successful natural enemy against CGM, whiteflies and thrips in Africa (Yaninek and Hanna, 2003) and South America (Amusa and Ojo, 2005; Onzo et al., 2005), where it is also reported to contribute to low severity of insect-vectored diseases such cassava anthracnose disease and CMD.

In this study, the best families for CGM resistance, namely Mweru x L9.304/147 and 4(2)1425 x L9.304/147 combined high Pbs with high LR. According to Hahn et al. (1989), Pbs is a heritable character and resistance to CGM can be improved by incorporating Pbs into high-yielding but CGM susceptible varieties. However, in the present study there were apparent inconsistencies in at least one family, 4(2)1425 x L9.304/147, which despite having the lowest mean for Pbs, recorded the highest level of resistance to CGM in terms of CGM PD and CGM LD. These inconsistencies, however, corroborate the observations made by workers at CIAT that some glabrous genotypes have been observed to be very resistant to CGM (Antony Bellotti[1], *personal communication*), confirming that Pbs is not always the only mechanism (direct or indirect) for resistance of cassava to CGM.

According to Zundel et al. (2009), cassava genotypes that have large and compact shoot apices plus prolonged LR and SG support *T. aripo* better than genotypes with small, loose tips. In the

[1]Antony Bellotti (PhD) is an emeritus scientist currently a consultant in entomology, agro-biodiversity and integrated pest management (Present address: International Centre for Tropical Agriculture (CIAT), A.A. 6713, Cali, Colombia, Email: a.bellotti@cgiar.org)

current study, CGM PD and CGM LD were negatively correlated with TS and TC. Though the genotypes in this study were evaluated in the absence of *T.aripo*, the significant negative correlations of LR and SG with CGM PD, CGM LD and CMD severity are indicative that genotypes with prolonged leaf longevity have greater potential to resist CGM and CMD. This implies that large and compact shoot apices, LR and SG should be selected for and improved through breeding for resistance to CGM and CMD.

The positive correlation of TS with LR, PH, StD, TC, and SG, implies that these traits can be selected concurrently and can effectively be improved through breeding, with the assumption that the traits do not compete for plant assimilates. A significant positive correlation also existed between LR and Pbs. Plant vigour as represented by PH and StD, plant canopy and foliar density has been reported to play a significant role in supporting the continuous survival of *T. aripo* (Zundel et al., 2009) and other phytoseiid predatory mites (Pratt et al., 2002) during both the rainy and dry seasons. Since these traits were found to be largely determined by additive gene action in this study, time and resources may be saved in a breeding programme because selection may be practiced as early as the sexual stage i.e. the parental and F_1 seedling generations. Lenis et al. (2006) advocate for early selection of cassava genotypes based on SG, which is achievable even at the seedling stage as an alternative to selecting for high harvest index.

The family Mweru x I92/0061, despite having significantly the highest mean for CGM PD with a positive SCA effect for the trait, sustained very low leaf damage with a negative SCA effect for CGM LD. This indicates that although the family allowed or supported a high CGM PD, it was able to resist the associated damage to the leaves. This could imply that the family was exhibiting tolerance for CGM as a mechanism of resistance. According to Bynum et al. (2004), tolerance enables a plant to repair the damage caused by the mites feeding on the leaves, without affecting mite population dynamics. On the other hand, two families Mweru x L9.304/147 and 4(2)1425 x L9.304/147 had significantly the lowest CGM PD with negative SCA effects for the trait which corresponded with significantly the lowest CGM LD, probably suggesting that either non-preference or antixenosis may be the mechanism of resistance exhibited by these two families. Consistent with this observation Byrne et al. (1982) have reported antixenosis as the main mechanism of resistance of cassava to CGM. Thomas and Waage (1996) outline three possible effects of antixenosis. Firstly, antixenosis can parallel antibiosis by affecting oviposition of adults through non-preference for oviposition sites, which is equivalent to reducing fecundity. Antixenosis can affect the number of adults ovipositing by increasing emigration of pests from the crop. Secondly, it can increase larval/nymphal movements, thus slowing down development time, or it can increase juvenile mortality by increasing pest fall-off. Thirdly, antixenosis can affect the number of colonizing adults from outside the crop. However, regardless of the

underlying mechanism, stability of resistance needs to be ascertained under field conditions through multi-locational testing in target production environments.

This study generated transgressive segregates which outperformed the best parents across all the families in terms of CGM PD, CGM LD and CMD. Thirty percent of the F_1 progeny had significant positive $H_{(BP)}$ in LR, SG, FSRY, and SRDM%. These genotypes were able to maintain more than 70% of their leaves throughout the cold season. The prolonged leaf life cycle of these genotypes signifies their potential for cold tolerance, and is an indirect way of increasing FSRY (Ojulong et al., 2009). Genotypes with extended leaf longevity may also be drought tolerant and resistant to CGM (Nukenine et al., 1999).

None of the families had positive $H_{(BP)}$ for FSRY, StD, NBr, and PH. Cassava breeders should exercise care when choosing cuttings from seedling plants to make sure that uniformity, in terms of length and diameter, is maintained as much as possible for both the progeny and parents so as to avoid bias and unnecessary error. As reported from earlier studies, length, thickness, and mass of cuttings per unit volume have a significant impact on subsequent establishment, growth and FSRY. Cuttings taken from the lower portion of the main stem, which normally have high mass per unit volume, have been reported to give better sprouting and survival rate in both dry and wet seasons (Oka et al., 1987), while lower yields of stakes and storage roots were recorded from plants that were established from thin cuttings taken from upper portion of the main stem (Keating et al., 1988). This partly explains why the Root and Tuber Improvement Programme in Zambia maintains and evaluates cassava seedlings for a minimum of 24 months before advancing them to the clonal evaluation stage.

Low multiplication rates for cassava as compared to cereal crops, is a major challenge which retards progress in breeding cassava in southern Africa. Zambia experiences a mono-modal type of rainfall that lasts for four months and is followed by a three-month cold season during which frost is experienced in some parts of North-Western Province (SCRB, 2001). Due to the low temperatures in the cold season, growth of cassava is very much checked and severe shoot die-backs are normally encountered. Worse still, a sharp rise in CGM PD is encountered on the new, young leaves that emerge after the cold season, causing damage which worsens as the weather gets warmer and drier. This generally contributed to insufficient production quality cuttings in the study.

Though early branching and increased NBr could help in overcoming shortage of planting materials, these attributes have been shown to facilitate rapid spread of *M. tanajoa,* which results in increased CGM PD and CGM LD in cassava fields (Egesi et al., 2007). Branches may serve as bridges between and within plants that facilitate the migration of mites in search of suitable leaves and, in the process, increases the chances for mating and reproduction. This

provides an explanation for the positive correlation of NBr and negative correlation for FBH with CGM PD and CGM LD, respectively. Traditional cassava genotypes in Zambia take at least 24 months to mature, while existing improved genotypes take 14–16 months. Therefore in the first six months of cultivation, various crops are intercropped with cassava. For this practice, early branching genotypes are normally not preferred by farmers because they interfere with weeding and harvesting of the intercrops (Calle et al., 2005). Moreover, in confirmation of this study's findings, other studies have reported that FBH is positively correlated with FSRY (example Calle et al., 2005).

Findings from this study are consistent with those by Ntawuruhunga and Dixon (2010) who reported generally low and moderate heritability estimates for FSRY, storage root diameter, NSR and PH. However, inconsistencies among reported heritability estimates are not uncommon, simply because heritability estimates are highly dependent on the environment and source of germplasm used (Falconer and Mackay, 1996). Different heritability estimates have been reported for most traits at different stages of cassava evaluation, namely seedling or single-plant, single-row, advanced replicated trials (Kawano et al., 1987). High heritability indicates that traits have high genetic variance (Zacharias and Labuschagne, 2010). Generally low heritability estimates are expected for polygenically controlled traits such as FSRY, SRDM%, and PH (Aina et al., 2007). According to Ntawuruhunga et al. (2001), it would take more time to improve traits with moderate heritability because of their low genetic variance. Traits with high heritability such as CGM PD and CGM LD, LR, TS, and TC can be easily improved through phenotypic mass selection (Cach et al., 2005).

Though it was difficult to find one progeny which was best for all the traits, as is usually the case (Calle et al., 2005), the wide variability in $H_{(BP)}$ among F_1 progeny for various traits studied, signifies the contribution of breeding to improving the frequency of favourable genetic combinations in new cassava genotypes which should ultimately provide farmers in Zambia and perhaps elsewhere with a broader choice of genotypes. Bellotti et al. (2012) rightfully state: "An important objective of an HPR strategy is to develop cultivars that are not susceptible to CGM and that hopefully combine low-to-moderate levels of resistance." The new genotypes generated in the current study include at least eight most promising early-bulking genotypes that combine good levels of resistance to CGM and CMD with higher FSRY and SRDM% than any of the currently released cultivars.

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Appendix 5.1: Layout of the first replication of the cassava clonal evaluation trial used for evaluation of 300 F1 cassava progeny and parents at Mutanda research station, Zambia

----------REPLICATION I ----------

1	30	P1	1	30	P3	1	30	P1	1	30	P4	1	30	P1	1	30	P2	1	30	P4	1	30	P2	1	30	P3	1	30	P5	1	30	P4
1	30	P1	1	30	P3	1	30	P1	1	30	P4	1	30	P1	1	30	P2	1	30	P4	1	30	P2	1	30	P3	1	30	P5	1	30	P4
2	29	P1	2	29	P3	2	29	P1	2	29	P4	2	29	P1	2	29	P2	2	29	P4	2	29	P2	2	29	P3	2	29	P5	2	29	P4
2	29	P1	2	29	P3	2	29	P1	2	29	P4	2	29	P1	2	29	P2	2	29	P4	2	29	P2	2	29	P3	2	29	P5	2	29	P4
3	28	P1	3	28	P3	3	28	P1	3	28	P4	3	28	P1	3	28	P2	3	28	P4	3	28	P2	3	28	P3	3	28	P5	3	28	P4
3	28	P1	3	28	P3	3	28	P1	3	28	P4	3	28	P1	3	28	P2	3	28	P4	3	28	P2	3	28	P3	3	28	P5	3	28	P4
4	27	P1	4	27	P3	4	27	P1	4	27	P4	4	27	P1	4	27	P2	4	27	P4	4	27	P2	4	27	P3	4	27	P5	4	27	P4
4	27	P1	4	27	P3	4	27	P1	4	27	P4	4	27	P1	4	27	P2	4	27	P4	4	27	P2	4	27	P3	4	27	P5	4	27	P4
5	26	P1	5	26	P3	5	26	P1	5	26	P4	5	26	P1	5	26	P2	5	26	P4	5	26	P2	5	26	P3	5	26	P5	5	26	P4
5	26	P1	5	26	P3	5	26	P1	5	26	P4	5	26	P1	5	26	P2	5	26	P4	5	26	P2	5	26	P3	5	26	P5	5	26	P4
6	25	P1	6	25	P3	6	25	P1	6	25	P4	6	25	P1	6	25	P2	6	25	P4	6	25	P2	6	25	P3	6	25	P5	6	25	P4
6	25	P1	6	25	P3	6	25	P1	6	25	P4	6	25	P1	6	25	P2	6	25	P4	6	25	P2	6	25	P3	6	25	P5	6	25	P4
7	24	P1	7	24	P3	7	24	P1	7	24	P4	7	24	P1	7	24	P2	7	24	P4	7	24	P2	7	24	P3	7	24	P5	7	24	P4
7	24	P1	7	24	P3	7	24	P1	7	24	P4	7	24	P1	7	24	P2	7	24	P4	7	24	P2	7	24	P3	7	24	P5	7	24	P4
8	23	P1	8	23	P3	8	23	P1	8	23	P4	8	23	P1	8	23	P2	8	23	P4	8	23	P2	8	23	P3	8	23	P5	8	23	P4
8	23	P2	8	23	P1	8	23	P3	8	23	P1	8	23	P5	8	23	P3	8	23	P2	8	23	P5	8	23	P4	8	23	P3	8	23	P5
9	22	P2	9	22	P1	9	22	P3	9	22	P1	9	22	P5	9	22	P3	9	22	P2	9	22	P5	9	22	P4	9	22	P3	9	22	P5
9	22	P2	9	22	P1	9	22	P3	9	22	P1	9	22	P5	9	22	P3	9	22	P2	9	22	P5	9	22	P4	9	22	P3	9	22	P5
10	21	P2	10	21	P1	10	21	P3	10	21	P1	10	21	P5	10	21	P3	10	21	P2	10	21	P5	10	21	P4	10	21	P3	10	21	P5
10	21	P2	10	21	P1	10	21	P3	10	21	P1	10	21	P5	10	21	P3	10	21	P2	10	21	P5	10	21	P4	10	21	P3	10	21	P5
11	20	P2	11	20	P1	11	20	P3	11	20	P1	11	20	P5	11	20	P3	11	20	P2	11	20	P5	11	20	P4	11	20	P3	11	20	P5
11	20	P2	11	20	P1	11	20	P3	11	20	P1	11	20	P5	11	20	P3	11	20	P2	11	20	P5	11	20	P4	11	20	P3	11	20	P5
12	19	P2	12	19	P1	12	19	P3	12	19	P1	12	19	P5	12	19	P3	12	19	P2	12	19	P5	12	19	P4	12	19	P3	12	19	P5
12	19	P2	12	19	P1	12	19	P3	12	19	P1	12	19	P5	12	19	P3	12	19	P2	12	19	P5	12	19	P4	12	19	P3	12	19	P5
13	18	P2	13	18	P1	13	18	P3	13	18	P1	13	18	P5	13	18	P3	13	18	P2	13	18	P5	13	18	P4	13	18	P3	13	18	P5
13	18	P2	13	18	P1	13	18	P3	13	18	P1	13	18	P5	13	18	P3	13	18	P2	13	18	P5	13	18	P4	13	18	P3	13	18	P5
14	17	P2	14	17	P1	14	17	P3	14	17	P1	14	17	P5	14	17	P3	14	17	P2	14	17	P5	14	17	P4	14	17	P3	14	17	P5
14	17	P2	14	17	P1	14	17	P3	14	17	P1	14	17	P5	14	17	P3	14	17	P2	14	17	P5	14	17	P4	14	17	P3	14	17	P5
15	16	P2	15	16	P1	15	16	P3	15	16	P1	15	16	P5	15	16	P3	15	16	P2	15	16	P5	15	16	P4	15	16	P3	15	16	P5
15	16	P2	15	16	P1	15	16	P3	15	16	P1	15	16	P5	15	16	P3	15	16	P2	15	16	P5	15	16	P4	15	16	P3	15	16	P5

30 Progeny + 2 Parents = Family plot

F_1 clone = 2 plants

Appendix 5.2: Best parent heterosis of families of cassava genotypes for cassava green mite density and leaf damage, cassava mosaic disease severity, shoot morphological traits, storage root yield and storage root dry mass percentage

Family	Best parent heterosis															
	CGM PD	CGM LD	CMD severity	TS	TC	Pbs	LL	LW	LR	SG	NBr	FBH	PH	StD	NSR	FSRY	SRDM%
Mweru x L9.304/147	-67.9	-35.0	16.5	-40.0	-25.5	-28.6	-4.8	-11.1	0.2	-8.8	-45.4	-35.7	-10.8	-9.5	-19.0	-21.2	1.8
Mweru x I92/0061	-54.1	-32.6	12.7	-33.3	-28.8	-38.1	-5.3	-17.7	-13.0	-5.6	-27.2	-39.5	-15.5	-19.4	-24.5	-19.2	4.2
Mweru x I92/000	-57.1	-31.3	29.6	-20.0	-14.6	-33.3	8.4	-7.8	-11.8	-4.8	-50.7	-25.9	-2.4	-15.8	-15.5	-22.4	1.6
Mweru x 4(2)1425	-41.6	-24.9	2.2	-38.7	-32.1	-28.6	-2.5	-15.8	-15.7	-8.2	-18.5	-38.6	-14.0	-3.9	-32.9	-16.3	2.4
4(2)1425 x I92/0061	-55.7	-35.7	12.4	-46.7	-37.1	-38.1	7.9	-2.1	-10.9	-0.7	-29.7	-28.9	-9.2	-16.6	-17.4	-20.2	-0.9
4(2)1425 x I92/000	-58.6	-30.1	7.2	-22.7	-9.6	-19.0	-1.8	-8.7	-15.9	-17.4	-38.5	-40.3	-12.8	-10.2	-40.2	-27.0	8.2
4(2)1425 x L9.304/147	-74.9	-41.3	2.1	-26.7	-18.2	-41.7	7.7	-13.9	-15.2	-15.9	-39.3	-27.1	-11.2	-7.1	-41.7	-27.6	11.1
L9.304/147 x I92/0061	-19.9	-6.2	-0.1	-33.3	-21.0	-39.3	-6.5	-23.4	-22.5	-14.3	-28.3	-38.4	-12.8	-14.5	-40.7	-29.6	15.5
L9.304/147 x I92/000	-55.6	-35.9	18.8	-25.3	-15.4	-32.1	-0.7	-17.7	-20.3	-13.3	-22.5	-36.8	-18.2	-21.6	-25.0	-23.3	17.2
I92/0061 x I92/000	-51.1	-27.8	12.5	-32.0	-21.0	-39.3	-0.7	-20.8	-18.6	-16.9	-40.8	-36.2	-10.5	-5.4	-23.3	-29.8	8.0

CGM PD = population counts of cassava green mites per leaf; CGM LD = score for the level of leaf injury caused by cassava green mite scored on a 1–5 scale; CMD severity = score for the severity of symptoms of cassava mosaic disease; TS = size of shoot apices scored on a 1-3 scale; TC = compactness of shoot apices scored on a 1-3 scale; Pbs = pubescence which is the degree of hairiness of leaves scored on a 1–3 scale; LL = leaf lobe length (cm) measured on the middle lobe from the intersection of lobes; LW = leaf lobe width (cm) measured from the widest part of the middle lobe; LR = proportion of leaves retained on a plant scored on a 1-3 scale; SG = stay green scored on a 1-3 scale; NBr = number of branches; FBH = height the first branching level (cm; PH = plant height (m); StD = stem diameter (cm); NSR = number of storage roots per plant; FSRY= fresh storage root yield in t ha^{-1}; SRDM%= storage root dry mass percentage.

CHAPTER 6

General overview

Cassava is the second most important food crop with potential for industrial use in Zambia after maize. However, its productivity is low due to widespread use of landraces, most of which are susceptible to cassava green mite (CGM) and cassava mosaic disease (CMD). The control of major pests of cassava in Zambia has mainly been based on biological control through the use of exotic parasitoids and phytoseiid predatory mites. However, lack of suitable cassava clones to support continuous inhabitance of natural enemies limits the success of biological control in Zambia. Understanding direct and indirect defense mechanisms that enhance host plant resistance (HPR) and biological control is critical for successful development of an integrated pest management approach. Lack of information on gene action and farmers' perception of CGM and preferred varietal attributes also limits success of resistance breeding and adoption of cultivars. It was envisaged that integration of HPR and classical biological control approaches would lead to a more sustainable pest management of CGM in view of anticipated climate change. This research was therefore undertaken with a view to contributing to the broadening of genetic diversity of cassava as well as to generate information that would be useful for enhancement of HPR and biological control of CGM in Zambia. The study was divided into three main parts. The first part was a participatory rural appraisal (PRA) study which was conducted in two major cassava growing areas of North-Western Province in Zambia, in order to obtain information on farmers' perceptions of the distribution and importance of major cassava pests and traditional coping strategies thereof. The second part involved screening of germplasm for new sources of resistance. The last part involved a genetic study to determine the nature of gene action controlling the inheritance of resistance to CGM and other relevant plant morphological traits in cassava.

The PRA study which made use of individual and focus group interviews was conducted with farmers in Solwezi and Mwinilunga districts. The study was aimed at gathering traditional knowledge on desirable and non-desirable varietal attributes, and cultural practices and plant attributes that are associated with reduced CGM population density (CGM PD) and leaf damage (CGM LD) in cassava fields, with a view to identify traits that can be promoted through conventional breeding. The findings were as listed below:

- Fresh storage root yield (FSRY), storage root dry mass percentage (SRDM %), earliness and resistance of cultivars to pests and diseases are the most important

attributes that determine adoption and retention of new cassava cultivars by farmers in Mwinilunga and Solwezi districts.

- Farmers are familiar with the symptoms of damage caused by CGM but most of them do not know the actual pest responsible for such damage. Farmers are able to estimate the distribution and extent of pest damage in their own fields, with minimal guidance on pest and symptom identification. Use of photographs and live infested plant samples can give farmers good guidance in this regard.
- Major pests of cassava in North-Western Province include moles, termites, CGM, scale insects, and cassava mealybug (CM). Termites, CGM and moles are the most widely distributed and most damaging.
- Generally farmers prefer cassava genotypes that combine FSRY with high SRDM%, earliness and extended underground storability or resistance to storage root rot (SRR). However, the choice of genotypes by farmers is location specific and end-use dependent. Farmers growing cassava for sale of unprocessed storage roots and leaves, are more concerned with quality traits such as sweetness, increased leaf retention (LR) and stay green (SG) for continuous supply of pest-free leaves for vegetable, while farmers who grow cassava mainly for own consumption in the form of flour are more concerned about earliness combined with extended underground storability of storage roots.
- According to the farmers, 'big heads' (large shoot apices), and hairy leaves are highly associated with reduced CGM LD. Leaf pubescence (Pbs) is associated with tender leaves, which is an indication of high palatability for cassava leaf vegetable preferred by women.
- The intensity of anthocyanin in the leaves, petioles and stems of cassava plants is also associated with increased resistance to CGM. The "purple or pink cassava" (cassava plants which combine purple or pink mature and immature leave and purple or pink petioles with purple or pink stems) is not attacked by CGM. However such cultivars are rare and their leaves are not preferred for consumption as a leaf vegetable.
- Canopy size and LR were also considered by the farmers to be highly associated with reduced damage due to termites and scales in cassava fields. Bitter cassava varieties are less preferred by termites and moles as compared to sweet ones, when grown in a mixture.
- Removal of cassava shoot tips and selective pruning of infested shoots are the most effective traditional cultural practices in reducing the population of both CGM and CM. According to the farmers, these practices help to escape insect and frost damage in cassava fields if applied just after the rainy season but before the onset of the cold season.

Multi-location trials were conducted using 19 cultivars which include landraces, locally improved, and introduced genotypes from international institute of tropical agriculture to identify the best performing genotypes in each environment; identify locations that best represent target environment for low to no CGM LD and high FSRY performances, as well as to study inter-season and intra-annual stability of genotypes for CGM resistance-related traits. The additive main effects and multiplicative interaction (AMMI) stability value (ASV) (Purchase et al., 2000) was used to study the stability of genotypes, environments, and traits. The genotype selection index which integrates stability and trait mean performance was used to categorize genotypes and environments into groups of adaptability (Farshadfar 2008). The findings were:

- Most of the traits studied are less influenced by the environmental effects, implying that the genetic differences among genotypes caused most of the variations in the resistance to CGM, FSRY, SRDM%, LR, Pbs, SG, as well as in the size and compactness of shoot apices of cassava.
- The Spearman's correlation of rank order calculated between pairs of stability indices indicate that the ASV is highly correlated with four other stability indices including stability variance, ecovalance stability index, and the environmental variance.
- The CGM LD and Pbs are among the most stable traits across the environments.
- Widely adapted genotypes for specific traits have been identified, with genotypes L9.304/147, 92/000, TME2, 4(2)1425, and L9.304/175 combining wide adaptability with best overall mean performance across traits.
- Genotypes Kapeza, M86/0016, I60/42, Manyopola, and TME2 were found to be adapted to moderately high pest pressure environments.
- The study showed that at least three genotypes, namely Kapeza, L9.304/147 and 4(2)1425 were able to consistently yield above 13 t ha^{-1} at 9 months after planting both in the 2010/11 and 2011/12 seasons, suggesting their potential as early bulking genotypes.
- Though storage root rots can be encountered at all stages of plant growth, the study indicated that the incidence of root rots varies with genotype, implying that there is genetic variability in the cassava germplasm available in Zambia.
- Stable high yielding genotypes were identified such as Kaleleki, Mweru and L9.304/175 which also combine stability with very high SRDM% and resistance to SRR, suggesting that it is possible to combine earliness with prolonged underground storability in cassava as desired by farmers. However, in future research the evaluation of the genotypes must extend over 36 months which is the longest period that farmers keep the crop in the field.

Overall the study indicated that there is sufficient genetic variability in the Zambian germplasm to enable breeders to improve cassava for resistance against CGM, and to select for genotypes that provide suitable habitat for the natural enemies of CGM enabling biological control of the pest. Stable sources of genes for farmer-preferred traits were identified, which should speed up the progress in breeding improved cassava cultivars.

Diallel analysis was performed for 300 F_1 cassava genotypes that were obtained from 10 families. The study was aimed at investigating the combining abilities of the parents and progeny, and to establish the nature of the gene action controlling inheritance of CGM resistance traits and associated plant morphological traits in cassava. The F_1 genotypes and their respective parents were evaluated in the field for a period of nine months. The findings were:

- Both general combining ability (GCA) and specific combining ability (SCA) effects were significant for the reaction of cassava genotypes to CGM, and for the various plant morphological traits that were measured, which suggested that both additive and non-additive gene effects are important in the expression of these traits.
- However, the predominance of GCA sums of squares over SCA sums of squares for all the traits indicated that additive gene action is the major determinant in the expression of these traits.
- The best parent for CGM resistance was 4(2)1425 which had a mean score of 2.0 for CGM LD, and its combination with Mweru gave the best mean of 1.75 for CGM LD.
- The best parent for CMD resistance was 92/000 with a mean score of 1.4, and in combination with 92/0061 had the best mean of 1.6 for CMD severity.
- The best parent for FSRY was 4(2)1425 which had a mean yield of 20.3 t ha^{-1}, and in combination with genotype 92/000 gave the best mean of 21.7 t ha^{-1}.
- Large narrow sense heritability(h^2) estimates were obtained for CGM PD (71%), CGM LD (86%), LR (80%), TC (88%) and TS (91%), while low heritability estimates were obtained for FSRY and SRDM%. These results indicate that CGM resistance and LR are highly heritable traits, and it should be relatively easy to improve them through breeding, suggesting that there is scope to integrate HPR with biological control for sustainable pest management that is both farmer- and environmentally-friendly.

Overall implications of the study for cassava breeding

The current study presents a challenge to breeders to develop fast-growing and high yielding cassava genotypes that can easily suppress weeds, bulk early, and resist SRR. The increasing importance of cassava leaves as a cheap source of protein emphasises the need for breeders to improve LR and SG in cassava in association with FSRY and SRDM% (Lenis et al., 2006). Farmers should be trained and sensitized about the benefits of natural enemies of CGM and the requirements for their existence in cassava fields. Active involvement of

both educated and uneducated farmers at all stages of an integrated pest management programme to control CGM is likely to contribute to its effectiveness and sustainability.

Farmers desire cultivars that are consistently high yielders, and therefore, breeders should evaluate genotypes in a range of environments and select for both high yield and stability of performance to mitigate the effects of genotype by environment interaction and to make the selection of genotypes more precise and refined. For this reason the AMMI-based genotype selection index which proved to be very suitable for selection of both high yielding and stable genotypes for all the seven traits of cassava is recommended. In this study, genotypes that were highly stable and high yielding are widely adapted and can, therefore, be recommended for production in any of the six environments, while genotypes that exhibited specific adaptability to certain environments should be recommended for production in those particular environments.

Among all the genotypes, L9.304/147, L9.304/175, 4(2)1425, I60/42 exhibited the highest levels of intra-season and inter-season stability combined with high CGM resistance. These genotypes should be used as sources of resistance and high FSRY in future breeding programmes.

One of the major impediments to breeding for resistance against CGM has been the lack of an efficient technique for maintaining constant and effective levels of infestation pressure in the field. The seasonal changes in temperature and rainfall cause fluctuations in natural populations of mites resulting in patchy and uneven distribution of mites in cassava field trials. In this study a simple technique for generating optimal CGM PD that should reveal differences in the resistance of genotypes in the field throughout the experimental period was described. The method, however, requires the continuous maintenance of a live colony of mites in a screenhouse for artificial infection purposes.

It is clear from the diallel analysis that both additive and non-additive gene actions were involved in the expression of the traits evaluated. The implication of the predominance of GCA effects over SCA effects for CGM resistance and associated traits is that for such traits, a hybridization scheme followed by phenotypic mass selection with appropriate selection pressures applied should be effective in identifying desirable recombinants. Similarly the high heritability estimates obtained for CGM resistance, LR, and TS, imply that such traits can be easily improved through phenotypic mass selection, while different selection strategies such as phenotypic recurrent selection should be recommended for low heritability traits (Cach et al., 2005). The significant negative correlations of Pbs, LR and SG to CGM PD, CGM LD, and CMD severity recorded in this study are also indicative that cultivars with enhanced LR, and Pbs have the potential to resist CGM and CMD, and that these traits can be jointly improved. Ultimately, with proper selection of parents, considerable resources are

likely to be saved since, as has been demonstrated in this study, a single breeding programme can lead to the genetic improvement of CGM and CMD resistance, Pbs, LR, and SG.

The current study has identified stable, low pest pressure sites which can be used for the multiplication of planting materials and moderately high to high pest pressure zones that can be used for screening of germplasm for CGM resistance. The current study has also contributed to broadening the genetic base of cassava germplasm in Zambia through the generation of genetic diversity. The products of the current study include at least eight most promising genotypes that combine earliness and good levels of resistance to CGM and CMD with higher FSRY and SRDM% than any of the existing released cassava cultivars in Zambia.

The most promising genotypes that combine CGM resistance, high FSRY, with various farmer-preferred traits need to be further tested in the presence of *T.aripo* in different locations, so as to confirm their suitability for integrated pest management, as well as the general stability of their performance.

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